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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN ADULT LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human adult liver is described. Also described are single exon nucleic acid probes expressed in
the adult liver and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_ADULT_LIVER.txt,
25 created 24 January 2001, having 26,335,065 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

adult liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert *et al.*, *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick *et al.*, *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis
25 and prognosis of diseases of the liver particularly those diseases with polygenic etiologies.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human adult liver, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,109 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,995 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 13,110 - 25,995, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,109.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human adult liver which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,109 or a complementary sequence or a
30 fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human adult liver.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a
35 nucleotide sequence as set out in any of SEQ ID NOS.:

13,110 - 25,995 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human adult liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,996 - 38,578 or a complementary sequence or a fragment thereof wherein said probe
10 hybridizes at high stringency to a nucleic acid expressed in the human adult liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first
35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is
20 provided a method of measuring gene expression in a sample derived from human adult liver, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said
25 first collection of nucleic acids derived from mRNA of human adult liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
35 labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the adult liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 25,995 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,110 - 25,995, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 13,109.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,996 - 38,578.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,996 - 38,578, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described, *inter alia*, in Brenner
et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);
in such case, the term "microarray" and phrase "nucleic
acid microarray" refer to the plurality of beads in
5 aggregate.

As used herein with respect to a nucleic acid
microarray, the term "probe" refers to the nucleic acid
that is, or is intended to be, bound to the substrate; in
such context, the term "target" thus refers to nucleic acid
10 intended to be bound thereto by Watson-Crick
complementarity. As used herein with respect to solution
phase hybridization, the term "probe" refers to the nucleic
acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising
15 SEQ ID NO.", and variants thereof, intends a nucleic acid
probe, at least a portion of which probe has either (i) the
sequence directly as given in the referenced SEQ ID NO., or
(ii) a sequence complementary to the sequence as given in
the referenced SEQ ID NO., the choice as between sequence
20 directly as given and complement thereof dictated by the
requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and
the equivalent acronym "ORF" refer to that portion of an
exon that can be translated in its entirety into a sequence
25 of contiguous amino acids i.e. a nucleic acid sequence
that, in at least one reading frame, does not possess stop
codons; the term does not require that the ORF encode the
entirety of a natural protein.

As used herein, the term "amplicon" refers to a
30 PCR product amplified from human genomic DNA, containing
the predicted exon.

As used herein the term "exon" refers to the
consensus prediction of the various exon and gene
predicting algorithms i.e. a nucleic acid sequence
35 bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
5 eukaryotic organisms will also prove useful as genomic
sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
10 are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
15 regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into
process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
25 given genomic region. In such case, the input often will
be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
30 experimental confirmation is identified. Experimental
confirmation can involve physical and/or bioinformatic
assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
35 this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in
5 process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can
10 be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a
15 combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation
20 can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the
25 like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an
30 experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly
35 to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements
35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are
35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

 Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.

- 20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

- As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic
5 recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for
10 identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the
15 novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative
20 coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more
25 software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

30 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region,
35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although
5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be
10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as
15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated
20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene
25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way,
30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be
35 identified is coding of protein sequence, and a first used

approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

 Predicted functional sequence, optionally representing a consensus among a plurality of methods and
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

 In the preferred embodiment of the methods of the present invention, wherein the function sought to be
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-
30 specific ORFs can be chosen for subsequent use in gene expression assay.

 Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative
35 exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of
35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by
5 process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture
10 the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying
15 length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the
20 methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can
25 alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or
30 intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about
35 300, 400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified
5 product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
10 complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

15 Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined,
20 including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon,
25 and positively-charged derivatized nylon membranes.

Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No.
30 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however,
35 provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure

expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

10 With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater

15 specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain

20 artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific

25 primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such

30 "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon

35 microarray of the present invention can be made without

such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus,
5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved
10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of
15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used
20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention
25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the
30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides
35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered
15 (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the
35 melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to
10 standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query – including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence –
5 can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process
10 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the
15 record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored
20 locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at
25 which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present
30 invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being
35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence
5 is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the
10 sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored
15 electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically — for example, by time-delayed appearance of
20 a small overlaid window upon movement of a cursor or other pointer over rectangle 89 — or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user
25 specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or
30 alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene
35 name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.

15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be
20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

 As earlier described, increased predictive reliability can be achieved by requiring consensus among
25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

 Although FIG. 3 shows three series of
30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as
5 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including
10 interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right
15 borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of
20 annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing
25 an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using
30 genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during
35 amplification and designed to permit reamplification of the

probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode
5 protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in
10 one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

15 Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray
20 hybridization analysis, the expression of 13,109 of these ORFs in adult liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in adult liver is currently
25 available for use in measuring the level of its ORF's expression in adult liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
30 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health
35 problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, *Prog. Liver Dis.* 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy findings were very similar, but there were wide differences between families.

Kalra et al., *Hum. Hered.* 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., *New Eng. J. Med.* 307:271-277 (1982) described 4 white American sibs who died between ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

Cloninger, *Science* 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL), low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation).

Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., Nature Genet. 18:369-373 (1998)) and chromosome 11 (Aouizerat et al., Am. J. Hum. Genet. 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary schlerosing cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher in PSC than normal individuals. Prochazka et al., New Eng. J. Med. 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75% of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary
25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen
35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrome 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, and hepatocellular cancer.

5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents, 10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following 15 *Schistosoma mansoni* infection.

 The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins, 20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have 25 genetic bases or contributions.

 Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a 30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35 The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of
35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the adult liver has been demonstrated are useful for both measurement in the adult liver and for survey of expression in other tissues.

15 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
30 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
35 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
5 for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405,
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
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"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements
5 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

10 The invention particularly provides genome-derived single-exon probes known to be expressed in adult liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
15 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
20 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
25 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
30 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
35 amplification technique. One such technique additional to

PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
15 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a
5 hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

10 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
15 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

20 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,110 – 25,995, respectively, for probe SEQ ID NOS. 1 – 13,109. The minimum amount of ORF required to be
25 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,110 – 25,995 individually by routine experimentation using standard high stringency
30 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
35 poly(dA), 0.2 µg/µl human cot1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
5 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second,
10 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen
15 for the common attribute of expression in the human adult liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell
20 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF
25 by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to
30 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-
35 derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human adult liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
5 consisting of SEQ ID NOS.: 1 - 13,109.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,109 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,110 - 25,995, that encodes
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 13,109 can be used, or that portion thereof in SEQ ID NOS. 13,110 - 25,995 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 13,110 - 25,995. Such amino acid sequences are set out in SEQ ID NOS: 25,996 - 38,578. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

30

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

35 Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

Bioinformatics Results

5 All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

10 After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
15 Markoff model, and DICTION, a program proprietary to
Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

20 The three gene finding programs yielded a range
of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
30 That is, 0.25% of the genomic sequence was identified by
all three of the programs as containing putative coding
region.

ORFs predicted by any two of the three programs
("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish *et al.*, *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2Gene Expression Measurements From Genome-Derived Single
5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series
10 of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message
15 pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial
20 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to
25 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II
30 enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5.
35 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μ l hybridization solution
5 containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2 μ g/ μ l human c_{ot}1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC,
10 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics
15 Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference
20 permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact,
25 both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when
30 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is
35 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-

05 to $1e-99$; black: E values $> 1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and
35 shows in blue the normalized Cy3 signal intensity for all

sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene
35 expression panel 24 human cDNAs) (OriGene Technologies,

Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Expressed Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai *et al.*, *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes *et al.*, *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,109 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 13,109 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,109. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the
30 exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,110 - 25,995, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human adult liver and thus presents the subset of probes that was recognized to be
5 useful for measuring expression of their cognate genes in human adult liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,110 - 25,995 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to
10 identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

15 The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as
20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the
25 SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of
30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is
35 found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ — which is probative evidence that the query sequence has previously been shown to be expressed — the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,109) and probe exon (SEQ ID NOs.: 13,110 - 25,995, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Adult liver

Table 4 (545 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human adult liver.

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
472	13543	26465	4.79				
914	13966	26913	10.74				
1071	14115		2.15				
1328	14392	27310	10.84				
1519	14550	27511	1.03				
1519	14550	27512	1.03				
1637	14637	27630	1.56				
1662	14692	27652	3.77				
1755	14782	27752	1.72				
1781	14807	27776	7.27				
1908	14930	27907	1.05				
1994	15012	28002	2.13				
2176	15190	28196	2.41				
2298	15306	28312	2.27				
2608	15606	28599	1.49				
2608	15606	28600	1.49				
3229	16277	29178	2.44				
3510	16548	29448	1.58				
3575	16612	29516	8.4				
3620	16656		0.8				
3725	16757	29645	1.21				
4025	17052		0.99				
4253	17307	30176	1.88				
4361	17375	30238	11.97				
4448	17457		1.55				
4500	17510	30376	0.65				
4950	17949	30807	1.16				
4986	17985		0.72				
5174	18166	31011	6.61				
5188	18180	31025	1.15				
5438	18520	31245	2.5				
5438	18520	31246	2.5				
5607	18683		3.94				
5791	18853		8.49				

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5876	18883		3.58				
5837	18004	32123	1.15				
5943	19070	32129	3.4				
6255	25845	32471	1.64				
6284	19335	32501	1.77				
6883	19719		1.31				
6829	19862	33074	1.26				
6829	19862	33075	1.26				
7485	20425	33705	1.39				
7485	20425	33706	1.39				
7811	20740	34043	1.28				
7811	20740	34044	1.28				
8330	21235		0.47				
8839	21570	34909	1.51				
9055	21884	35339	1.14				
9419	22347	35711	0.84				
9419	22347	35712	0.84				
10063	22879	36370	5.03				
10286	23178	36588	0.58				
10394	23283	36703	1.42				
10526	23412	36825	1.15				
10801	23687	37116	0.74				
10801	23687	37117	0.74				
10911	23796	37224	0.57				
10911	23796	37225	0.57				
11126	24056		3.49				
11487	24380		1.49				
11532	24442	37902	1.43				
11798	24720	38213	2.14				
11934	24778		2.59				
6287	19338	32605	15.42	9.8E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8585	21516	34860	1.8	9.8E+00	U92716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
10263	23153	36562	0.51	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
10263	23153	36563	0.51	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2

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Table 4
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7342	20338	33604	0.88	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7342	20338	33605	0.88	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10904	23789	37217	1.06	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor ILH polypeptide 2 (Gif2h2) genes, complete cds
10904	23789	37218	1.06	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor ILH polypeptide 2 (Gif2h2) genes, complete cds
2715	15709	28704	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2715	15709	28705	1	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2966	16018	28915	4	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
6580	19621	32806	0.51	9.4E+00	P75130	SWISSPROT	HYPOTHETICAL PROTEIN MG447 HOMOLOG
8677	21608	34950	1.22	9.3E+00	AF130990.1	NT	Homo sapiens actodysplasia-A receptor protein (EDAR) gene, exons 2, 3, and 4
9555	22482	36842	3.44	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
7874	20801	34104	0.44	9.2E+00	Q61767	SWISSPROT	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(5)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-6-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5479	18560	31403	2.54	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5479	18560	31404	2.54	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9684	22689		1.21	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6269	19320	32484	5.18	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3934592 3'
6841	19680	32870	2.11	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp1bx3 premature mRNA, partial cds
6841	19680	32871	2.11	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp1bx3 premature mRNA, partial cds
463	13535	28455	1.63	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9987	21345	34680	4.11	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11611	24519		1.73	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8730	21690		1.07	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7733	20665		1.9	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8933	21863	36219	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8933	21863	36220	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
6011	19074	32200	3.41	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
9313	22241	35602	3.81	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9313	22241	35603	3.81	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3018	16070	28971	3.82	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3018	16070	28972	3.82	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7380	20374	33643	0.52	7.2E+00	BE179090.1	EST_HUMAN	RC0-HT0613-200300-031-a07 HTD613 Homo sapiens cDNA
7509	20448	33731	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7509	20448	33732	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
10125	23016		10.66	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11823	24743	38234	2.63	7.1E+00	P05860	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
10488	23376	36791	2.64	7.0E+00	P48810	SWISSPROT	ARGININE KINASE (AK)
11696	24598	35076	1.82	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS18
8860	21790	35141	2.11	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10838	23724	37147	1.37	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10856	23742	37165	0.54	6.9E+00	P34226	SWISSPROT	SKT5 PROTEIN
8487	21418	34754	1.6	6.8E+00	W03412.1	EST_HUMAN	z007c11.11 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:281850 5'
8487	21418	34755	1.6	6.8E+00	W03412.1	EST_HUMAN	z007c11.11 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:281850 5'
9677	22603		1.5	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10705	23591	37018	3.32	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5466	18547		0.78	6.6E+00	Q99028	SWISSPROT	GATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6824	19857	33069	0.71	6.6E+00	BF672121.1	EST_HUMAN	602162573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
9585	25991		0.57	6.6E+00	P51825	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10576	23462	36884	2.64	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10576	23462	36885	2.64	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11598	24477		1.92	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9723	22848	36030	8.06	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10794	23680	37110	0.55	6.5E+00	BE866001.1	EST_HUMAN	601676435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5'
10262	23162	36561	1.31	6.2E+00	AY010901.1	NT	Schizaphyllum commune unknown mRNA
7387	20380	33649	1.35	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10993	23877	37306	0.65	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10993	23877	37307	0.65	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
							Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
6799	19832	33043	6.98	5.9E+00	AF155142.1	NT	
12060	24901		1.4	5.9E+00	BE568630.1	EST_HUMAN	601645276F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3930451 5'
3585	16822		0.92	5.8E+00	7661657	NT	Homo sapiens DESC1 protein (DESC1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7523	20462	33749	0.79	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7523	20462	33750	0.79	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
8002	20920		1.3	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11908	24008	37450	2.46	5.6E+00	Q56278	SWISSPROT	LYCOPENE BETA CYCLASE
8500	19544	32720	0.81	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCa
11218	24144		1.51	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11908	24008	37447	5.09	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
12163	24992		1.63	5.6E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
7259	20168	33407	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7259	20168	33408	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7715	20647		0.82	5.4E+00	Q99435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8373	21277	34809	0.48	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
							VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELIN LV-1N; LIPOVITELIN LV-1C;
8451	21383		1.58	5.4E+00	Q81062	SWISSPROT	LIPOVITELIN LV-2
8357	22285	35647	1	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8357	22285	35648	1	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10539	23425	36842	1.43	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
10539	23425	36843	1.43	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4897	17896	30781	1.38	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6763	19797		0.55	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN GEH-20
8657	21588		3.77	5.3E+00	P34098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
9535	22462		0.6	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
12054	24895	38309	3.68	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
5650	18724		1.18	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0691-270400-188-409 HT0691 Homo sapiens cDNA
10860	23746		0.89	5.2E+00	AF248070.1	NT	Drosophila orientacea R18 retrotransposable element reverse transcriptase gene, partial cds
11640	24546		2.11	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 81.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
9515	22442	35808	0.81	5.1E+00	Q16005	SWISSPROT	RHODOPSIN
10340	23229	36646	1.56	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
8539	19582	32766	0.92	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
9597	22523	35887	0.52	5.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10691	23577		0.81	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10912	23797	37226	3.92	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
11735	24637	38118	8.47	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10727	23613		0.78	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4147	17168		13.45	4.9E+00	AF185255.1	NT	Eniloe australis histone H3 (H3) gene, partial cds
9105	22033		5.61	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310100-002-004 BT0547 Homo sapiens cDNA
309	13402	26319	3.7	4.7E+00	BF240552.1	EST_HUMAN	601875554F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
310	13402	26319	3.33	4.7E+00	BF240552.1	EST_HUMAN	601875554F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089716 5'
3318	16365	29265	1	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8257	21162	34495	0.58	4.6E+00	U67559.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9738	22662	36048	1.04	4.6E+00	BE646437.1	EST_HUMAN	7688g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0845 PROTEIN, contains element PTR5 repetitive element
9738	22662	36047	1.04	4.6E+00	BE646437.1	EST_HUMAN	7688g10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0845 PROTEIN, contains element PTR5 repetitive element
10877	23763		0.73	4.6E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8239	21144		0.54	4.5E+00	AF126177.1	NT	Issatchenkia orientalis inositolphosphorylceramide synthase (PGT) gene, complete cds
12034	24876	38381	2.37	4.6E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
12175	25011	38515	1.86	4.5E+00	BF668841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
13107	25777		4.27	4.5E+00	BE089317.1	EST_HUMAN	QV3-BT0381-170100-060-012 BT0381 Homo sapiens cDNA
3087	16138	29035	1.02	4.4E+00	BF630893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3087	16138	29036	1.02	4.4E+00	BF630893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
6443	19489		1.76	4.4E+00	X13414.1	NT	Murine I gene for MHC class II(a) associated invariant chain
6515	19559	32741	0.61	4.4E+00	AF156596.1	NT	Nicotiana tabacum inorganic phosphate transporter (PT1) mRNA, complete cds
6357	19408		0.7	4.3E+00	AF059879.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7842	20769	34072	2.49	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R-var1 gene, exon 1
8060	20973	34289	0.8	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
11296	24216	37688	5.49	4.3E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11371	24288		1.59	4.3E+00	11528311	NT	Homo sapiens DiGeorge syndrome critical region gene 2 (DGCR2), mRNA
5707	18780		3.07	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5788	18860	31988	1.09	4.2E+00	P51826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6668	19035		0.62	4.2E+00	Q27830	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
7079	20285	33542	1.63	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7079	20295	33543	1.63	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9513	22440	35805	6.13	4.2E+00	A1809013.1	EST_HUMAN	wf57g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360682 3'
10429	23318	36736	1.42	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-1b) (DOCT1)
6161	25842	32360	0.55	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
6161	25842	32361	0.55	4.1E+00	O09185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7471	20411	33689	0.74	4.1E+00	BE253688.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351634 5'
7579	20515	33803	0.44	4.1E+00	BF247939.1	EST_HUMAN	601869030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4089768 5'
8111	21023	34349	7.96	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
8255	21160		0.58	4.1E+00	AB041523.1	NT	Pathoprotein yessensis mRNA for calcineurin A, complete cds
8255	21163	34496	4.78	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8255	21163	34497	4.78	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8495	21426	34707	1.14	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
10089	22995	36378	0.53	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
10197	23088	36489	1.6	4.1E+00	BF692425.1	EST_HUMAN	60224798F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10663	23549		0.65	4.1E+00	AJ238273.1	NT	Rickettsia prowazekii strain Madrid E, complete genome, segment 4/4
							CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10798	23682		0.54	4.1E+00	P46414	SWISSPROT	(P27KIP1)
11322	24241		3.68	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
11409	24326		14.72	4.1E+00	BE985880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908051 5'
3604	16841		0.72	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5644	20176	33417	0.96	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5644	20176	33418	0.96	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7267	20176	33417	0.88	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7267	20176	33418	0.88	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7553	20480	33779	1.15	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9431	22359	35722	0.61	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10452	23341	36756	0.54	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS)
10631	23547	36981	0.67	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
11905	24006	37446	1.77	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
							GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS (NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11881	24824	38319	2.61	4.0E+00	P07564	SWISSPROT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11981	24824	38320	2.61	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3560	16597	29501	5.4	3.9E+00	X64518.1	NT	N. leishmania chilensis gene 50 for class I chitinase C
4427	17438		0.79	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 89 (MSVSP89) gene, promoter region
5855	18926	32042	2.69	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5855	18926	32043	2.69	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6929	19955	33175	0.71	3.9E+00	AF288209.1	NT	Dicotyledonous discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6987	20014	33245	0.92	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRe1 gene, and sodium phosphate transporter (NPT3) gene, complete cds
7169	20169	33445	3.78	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7754	20884	33983	4.35	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8892	21822	35174	2.65	3.9E+00	X65865.1	NT	X. laevis mRNA for M4 muscarinic receptor
11829	23864	37399	4.12	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2676	15672		1.55	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6654	19893	32887	0.93	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
7078	20284	33541	0.52	3.8E+00	A1493849.1	EST_HUMAN	q25107.x1 NC1 CGAP_K411 Homo sapiens cDNA clone IMAGE:2030437 3'
9001	21930	35286	1.16	3.8E+00	D44725.1	EST_HUMAN	HUMSUJY135 Human brain cDNA Homo sapiens cDNA clone 148
10311	23200		0.69	3.8E+00	A390987.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
4106	17130	30004	11.53	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7529	20468		0.91	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9720	22845	38027	0.68	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11863	24753	38247	2.33	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11863	24753	38248	2.33	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
12339	25134		1.81	3.7E+00	AB013748.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
614	13679	28581	1.95	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
5436	18518	31243	0.56	3.6E+00	BF316316.1	EST_HUMAN	60101866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
9205	22133	35489	4.38	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
9205	22133	35490	4.38	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
10189	23079	36480	0.53	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds

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Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10188	23079	36481	0.53	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11288	24209			3.6E+00	M98795.1	NT	Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
3292	19339	29241	3.15	3.6E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
6232	19286		1.3	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6456	19501	32676	0.83	3.5E+00	R19745.1	EST_HUMAN	Yg40c08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34940 5'
8301	21205	34540	1.12	3.5E+00		EST_HUMAN	cd37f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618987 3' similar to gb.J04213
8343	21248	34583	0.52	3.5E+00	AA692102.1	EST_HUMAN	CELLULAR RETINALDEHYDE-BINDING PROTEIN (HUMAN);
9054	21983		0.51	3.5E+00	4505284	NT	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R) mRNA
9583	22510	35872	0.7	3.5E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9583	22510	35872	0.97	3.5E+00	AA190998.1	EST_HUMAN	zp86b04.s1 Stratiogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
10026	22926	35873	0.97	3.5E+00	AA180998.1	EST_HUMAN	zp86b04.s1 Stratiogene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
11000	23894	37316	1.2	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
1533	14563	27523	0.55	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
2614	15612	28607	3.15	3.4E+00	AF284577.1	NT	Brassica napus RPB5d mRNA, complete cds
7033	20069	33292	0.95	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7753	20663	33982	0.42	3.4E+00	U77617.1	NT	Chloranth-Aster yellows phytoplasma acetate kinase gene, complete cds
8157	21064	34394	2.63	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9235	22163		0.8	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9656	22592	35953		3.4E+00	U65408.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNU1) gene, complete cds
10757	23843	37076	0.79	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
11963	24806	38304	0.59	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSO1 gene, complete cds
6303	19354	32524	2.96	3.4E+00	L77570.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
6303	19354	32525	1.98	3.4E+00	Q09869	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
10942	23827	37253	0.84	3.3E+00	Q09869	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
10942	23827	37253	0.84	3.3E+00	Q09869	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
10942	23827	37253	1.06	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10942	23827	37254	1.39	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
523	13593	26505	1.39	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
523	13593	26505	1.59	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4110	13593	26505	0.94	3.2E+00	X98422.1	NT	D.rerio zp-50 POU gene
4841	17842	30711	1.49	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5760	18833	31934	1.43	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5760	18833	31935	1.43	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5766	18868	31976	2.58	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5766	18868	31977	2.58	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5561	19602	32787	1.89	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5561	19602	32788	1.89	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
8049	20962	34278	0.73	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8245	21150	34484	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf4, ycf3, rps18 genes
8245	21150	34485	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf4, ycf3, rps18 genes
9581	22508		6.46	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
10060	22976	36368	1.21	3.2E+00	M36383.1	NT	S.aeroviciae threonine deaminase (LV1) gene, complete cds
10640	23526	36961	2.39	3.2E+00	AB018081.2	NT	Onyias latipes OIGC8 gene for guanylyl cyclase C, complete cds
12303	25111		4.71	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
6080	19151	32287	1.91	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E202 IN CHROMOSOME 1
7785	20714	34016	0.88	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
8190	21097		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus peccate lyase (pelE) gene, complete cds
8666	21597	34937	0.58	3.1E+00	P40985	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
9164	22092	35449	5.22	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
9164	22092	35450	5.22	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
9801	22765		4.47	3.1E+00	Q14857	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9865	22780	36169	0.54	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10409	23297	36717	0.68	3.1E+00	7624759	NT	Chlorella vulgaris chloroplast, complete genome
10494	23382		0.62	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 58.3 KD PROTEIN F5209.5 IN CHROMOSOME III
10824	23710	37137	5.36	3.1E+00	P49385	SWISSPROT	DEOXYTHYMPINE SYNTHASE (DHS)
11895	23695		2.49	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11913	24760		4.16	3.1E+00	S56680.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
5522	18601	31450	1.42	3.0E+00	X53096.1	NT	S.aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6837	19869	33083	0.68	3.0E+00	X58037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6837	19869	33084	0.68	3.0E+00	X58037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7517	20458		10.11	3.0E+00	P18406	SWISSPROT	CYR81 PROTEIN PRECURSOR (3CH61)
7580	20497		0.75	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9464	22392		1.65	3.0E+00	X07838.1	NT	B. napus DNA for myosinase
10783	23669	37098	0.66	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11092	24023	37465	1.39	3.0E+00	Q16181	SWISSPROT	CDC10 PROTEIN HOMOLOG
11447	24363	37811	5.92	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11447	24363	37812	5.92	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
12016	24858	38358	1.56	3.0E+00	P34194	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
2024	15042	28036	2.11	2.9E+00	AE002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of the complete genome
6309	19359		0.86	2.9E+00	AB028033.1	NT	Bonapartia pediculus mitochondrial DNA for 16S ribosomal RNA
7237	20146	33388	10.73	2.9E+00	Z38879.1	NT	F. pringlei gdcPA gene for P-protein of the glycine cleavage system
7577	20513	33789	4.82	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7577	20513	33800	4.82	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7860	20787	34080	5.2	2.9E+00	P48589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8449	21381	34722	0.61	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE[CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; MINOR STRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8449	21381	34723	0.61	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE[CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; MINOR STRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8676	21607	34949	0.88	2.9E+00	BF344171.1	EST_HUMAN	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3
9779	22703		0.68	2.9E+00	AJ002153.2	NT	602017413F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4153059 5'
1476	14507	27468	3.83	2.8E+00	AF186398.1	NT	Sagittaria oedipus gene for seminal vesicle secreted protein semenogelin I
1657	14687		2.32	2.8E+00	AL161552.2	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
7601	20623	33023	5.61	2.8E+00	8393724	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
10140	23031		0.71	2.8E+00	BE605182.1	EST_HUMAN	Mus musculus endomucin (LOC63423), mRNA
11131	20623	33923	1.57	2.8E+00	8393724	NT	60134278F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
249	13347	26250	9.41	2.7E+00	6878306	NT	Mus musculus endomucin (LOC63423), mRNA
249	13347	26260	9.41	2.7E+00	6878306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5743	18816	31912	1.43	2.7E+00	L14005.1	NT	Homo sapiens epaA polymorphism Kingle IV gene, exons 1 and 2
8724	21654		0.7	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
9520	22447		2.43	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9966	21324	34657	0.64	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.xt NCI CGAP Bm35 Homo sapiens cDNA clone IMAGE:2891374 3' similar to gb:M17733
10978	23862		1.7	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4786	17791	30658	5.9	2.6E+00	AF068749.1	NT	GM0-BT0281-031199-087-H04 BT0281 Homo sapiens cDNA
5739	18812	31907	1.75	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5739	18812	31908	1.75	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
6038	19100		1.55	2.6E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7986	25984		0.79	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
8156	21063		8.98	2.6E+00	AF235502.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8637	21568	34905	1.33	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Shp) gene, exons 18 through 27, and complete cds
8637	21568	34906	1.33	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10182	23073	36473	2.87	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10841	23727		1.97	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
11488	24381	37828	1.48	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12889	26859		2.17	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1483	14514	27474	2.58	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1493	14514	27475	2.58	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
6024	19086	32210	1.99	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
6024	19086	32211	1.99	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6730	19086	32210	1.54	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6730	19086	32211	1.54	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
7032	20059	33291	0.68	2.5E+00	D30052.1	NT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
8227	21132	34482	1.08	2.5E+00	AW949158.1	EST_HUMAN	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds
8302	21206	34541	0.49	2.5E+00	4502902	NT	QV4-FT0005-110500-205-q07 FT0005 Homo sapiens cDNA
9848	22574	35945	1.64	2.5E+00	D50307.1	NT	Homo sapiens elafirin, heavy polypeptide-like 1 (CLTCL1) mRNA
10366	23255	36675	0.85	2.5E+00	BE297758.1	EST_HUMAN	Rice DNA for aldolase C-1, complete cds
11971	24814		2.02	2.5E+00	P40170	SWISSPROT	60115779FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631090 5'
12300	25109		2.91	2.5E+00	AF289665.1	NT	DNAJ PROTEIN
3057	16109	29015	1.1	2.4E+00	M24282.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
5015	16013	30872	5.08	2.4E+00	4503352	NT	Chicken alpha-3 collagen type VI mRNA, 3' and
							Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6243	19297	32455	4.27	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7773	20703	34002	0.63	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7773	20703	34003	0.63	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7789	20718	34021	0.43	2.4E+00	P20126	SWISSPROT	RNA REPLICASE POLYPROTEIN
7789	20718	34022	0.43	2.4E+00	P20126	SWISSPROT	RNA REPLICASE POLYPROTEIN
8718	21649	34984	2.25	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8718	21649	34985	2.25	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8780	21720		3.32	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99, section 47 of 132 of the complete genome
9210	22138		1.82	2.4E+00	AW876126.1	EST_HUMAN	RC2-PT0004-031299-011-406 PT0004 Homo sapiens cDNA
9387	22316	35677	8.12	2.4E+00	P24091	SWISSPROT	ENDOCHITININASE B PRECURSOR (CHN-B)
10541	23427	36846	2.58	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10541	23427	36847	2.58	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10608	23494	36924	2.52	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10737	23823		7.42	2.4E+00	P08099	SWISSPROT	XYLOLOSE KINASE (XYLOKININASE)
10811	23697	37123	1.96	2.4E+00	BE328702.1	EST_HUMAN	tr63f06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10811	23697	37124	1.96	2.4E+00	BE328702.1	EST_HUMAN	tr63f06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
11063	23947	37385	1.4	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11797	24719	38212	2.5	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1281	14314	27263	9.93	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4217	17233		1.68	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
6048	19110		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7858	20786	34088	2.43	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
8038	25995		3.15	2.3E+00	P07189	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
8253	21189	34491	1.5	2.3E+00	X60265.1	NT	M.mezel dhak and dhaj genes homologues coding for Dnak and Dnal
9654	22560	35952	0.59	2.3E+00	5835317	NT	Polytelus ornamentalis mitochondrion, complete genome
9712	22837	36018	1.73	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
11241	24167	37613	3.36	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11714	24616	38092	1.58	2.3E+00	P28059	SWISSPROT	ENDOCHITININASE 3 PRECURSOR
12190	25029	38526	2.66	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12190	25029	38527	2.66	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12499	26238	31862	6.44	2.3E+00	BE895237.1	EST_HUMAN	601433873F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4103	17128	30003	0.91	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4418	17429	30281	5.4	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4418	17429	30292	5.4	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5526	18605	31453	11.77	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) [>
5526	18605	31454	11.77	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) [>
6067	19128	32259	1.04	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6067	19128	32260	1.04	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
8297	18348	32516	7.48	2.2E+00	BE250383.1	EST_HUMAN	60094340T11 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
6612	19653	32837	3.09	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6882	19912	33128	2.79	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7293	18482	33930	3.6	2.2E+00	AA694574.1	EST_HUMAN	1195802.61 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7701	20633	33930	0.87	2.2E+00	AA137027.1	EST_HUMAN	zn97104.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
8051	20964	34280	20.17	2.2E+00	AA449012.1	EST_HUMAN	2x05g10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786634 5'
8142	21051	34383	0.55	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8414	21316	34648	0.41	2.2E+00	O67099	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
8681	21612	34953	0.71	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
8681	21612	34954	0.71	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
9880	22755		13.66	2.2E+00	BE741678.1	EST_HUMAN	G01594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
10097	26691		2.64	2.2E+00	Q04706	SWISSPROT	TRANSPONIN TY1 PROTEIN A
10556	23442	36862	1.93	2.2E+00	A1290373.1	EST_HUMAN	qm88b03.x1 Soares_placenta_8to9weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:1893985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10556	23442	36863	1.93	2.2E+00	A1290373.1	EST_HUMAN	qm88b03.x1 Soares_placenta_8to9weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:1893985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10598	23484	36913	2.2	2.2E+00	BF246782.1	EST_HUMAN	G0185559F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10935	23820	37247	2.49	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein HGR14 homolog mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11039	23923	37366	0.51	2.2E+00	P22809	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR) (CA2-47)
11874	23974	37411	3.47	2.2E+00	P07911	SWISSPROT	(ALPHA-2D ADRENERGIC RECEPTOR)
12041	24883	38389	5.96	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
691	15878	26562	6.8	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
3649	16685		0.85	2.1E+00	AW449366.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
6372	19421		0.92	2.1E+00	P79357	SWISSPROT	U1H-B13-ak-e-08-Q-U1st NCL CGAP Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
7119	20323	33587	3.55	2.1E+00	O70169	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
7375	20369	33638	0.67	2.1E+00	4503430 NT		ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7397	20096	33330	5.68	2.1E+00	N29575.1	EST_HUMAN	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
9064	21983		2.3	2.1E+00	AU123630.1	EST_HUMAN	W08a10.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
1224	14261	27203	1.1	2.0E+00	AF180527.1	NT	TRANSCRIPTION INITIATION FACTOR TF1ID (HUMAN);
1224	14261	27204	1.1	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM200671 5'
1363	14394	27349	1.08	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1597	14828		3.72	2.0E+00	P25582	SWISSPROT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
2163	15175	28180	2.67	2.0E+00	Z78279.1	NT	Oryctolagus cuniculus Na ⁺ K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2163	15175	28181	2.67	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
4191	17211	30077	1.63	2.0E+00	AW664496.1	EST_HUMAN	R. norvegicus mRNA for collagen alpha1 type I
4191	17211	30078	1.63	2.0E+00	AW664496.1	EST_HUMAN	R. norvegicus mRNA for collagen alpha1 type I
7981	20902		0.84	2.0E+00	P07566	SWISSPROT	h13005.x1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
8602	21533	34874	4.37	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8602	21533	34875	4.37	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8602	21533	34876	4.37	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
9478	22406	35766	3.1	2.0E+00	F31500.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE
12808	26823	31483	6.51	2.0E+00	5834843 NT		GLYCOPROTEINS E1 AND E2
5792	18864	31971	4.67	1.8E+00	8754389 NT		GLYCOPROTEINS E1 AND E2
5792	18864	31972	4.67	1.8E+00	8754389 NT		GLYCOPROTEINS E1 AND E2
6337	19387	32556	1.21	1.9E+00	BE690895.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6947	19976		0.87	1.8E+00	AW845699.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds

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7053	20079		1.95	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
9027	21956	35314	2.43	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9027	21956	35315	2.43	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9217	22145		2.97	1.9E+00	BF300206.1	EST_HUMAN	CM2-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
9451	22379		2.45	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
10156	23047	36446	0.7	1.9E+00	AA669125.1	EST_HUMAN	ab94a04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
11038	23922	37365	0.84	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3141	16191	29084	2.04	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3185	16215	29104	1.09	1.8E+00	U04359.1	NT	Synectococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3185	16215	29105	1.09	1.8E+00	U04359.1	NT	Synectococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6082	19143		1.69	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6342	19392	32561	1.89	1.8E+00	BF311989.1	EST_HUMAN	601897864F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6983	19701		3.59	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
7044	20070	33304	1.26	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4136038 5'
7412	20111	33345	0.93	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7635	20570		0.74	1.8E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8694	21625	34968	0.95	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8694	21625	34969	0.95	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8694	21625	34969	0.95	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
9038	21667	35328	0.55	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9038	21667	35327	0.55	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9038	21667	35328	0.55	1.8E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9413	22341	35706	2.66	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9717	22642	36023	0.81	1.8E+00	R31042.1	EST_HUMAN	yh72c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9804	22710	36092	1.06	1.8E+00	AW880004.1	EST_HUMAN	QV6-O10030-070300-148-a03 O10030 Homo sapiens cDNA
10363	23252	36872	0.77	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10775	23661		3.37	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
11031	23915		0.92	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)

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12615	25797		6.13	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12692	25349		4.6	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
1135	14177	27114	2.24	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2290	15298	28305	4.2	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2396	15401	28405	2.03	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4570	17578	30440	1.92	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5807	18876	31985	1.95	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171289-127-605 BT0282 Homo sapiens cDNA
5807	18876	31986	1.95	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171289-127-605 BT0282 Homo sapiens cDNA
6069	19130	32263	0.49	1.7E+00	R58748.1	EST_HUMAN	G4846 Fetal heart Homo sapiens cDNA clone G4846 5' end
6250	19303	32464	3.4	1.7E+00	Q911R8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
6832	19884	33078	0.53	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPc)
7587	20523	33811	1.19	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7587	20523	33812	1.19	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8318	21223		0.44	1.7E+00	P06180	SWISSPROT	HISTONE-BINDING PROTEIN N1/N2
8437	21389	34710	1.19	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8611	21542	34884	1.3	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tall1), mRNA
8640	21571	34910	0.64	1.7E+00	BF530830.1	EST_HUMAN	602071817F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214669 5'
9106	22034	35388	0.56	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
9187	22115		1.5	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
9262	22190	35547	0.65	1.7E+00	XG6063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9262	22190	35548	0.65	1.7E+00	XG6063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9373	22301	35662	0.52	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9692	25690	35993	1.76	1.7E+00	Q60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9692	25690	35994	1.76	1.7E+00	Q60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
10133	23024		1.28	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
10668	23554		0.63	1.7E+00	AW953681.1	EST_HUMAN	EST365751 MAGE rescues, MAGC Homo sapiens cDNA
12028	24868	38370	1.83	1.7E+00	W22424.1	EST_HUMAN	67577 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
2047	15084	28065	10.72	1.6E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2057	15074	28074	3.51	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2063	15076	28079	1.14	1.6E+00	Y11344.1	NT	Mus musculus ST6GALNAcII gene, exon 2

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2303	16311		1.26	1.6E+00	X98373.1	NT	B.napus gene encoding endo-polygalacturonase
3002	16054	28958	1.25	1.6E+00	W58426.1	EST_HUMAN	z125101.1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
3825	16855		1.09	1.6E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4115	17138		6.97	1.6E+00	BF570077.1	EST_HUMAN	602186085T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4462	17473	30329	0.97	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4462	17473	30330	0.97	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5207	18198	31041	10.6	1.6E+00	AF127897.1	NT	Salmi botivensis olfactory receptor (SBO27) gene, partial cds
5218	18208	31053	3.06	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5218	18208	31054	3.06	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
6039	19101	32228	2.33	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2'01 gene, 3' end
6135	19104	32331	0.86	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6198	19254	32399	0.48	1.6E+00	BE971873.1	EST_HUMAN	601651111R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834443 3'
6198	19254	32400	0.48	1.6E+00	BE971873.1	EST_HUMAN	601651111R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834443 3'
6743	19777	32890	0.85	1.6E+00	BF360703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
7007	20034	33267	1.16	1.6E+00	AW294881.1	EST_HUMAN	U1H-B12-ahr-b-04-OUI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7615	20650	33842	2.24	1.6E+00	BE697287.1	EST_HUMAN	RC0-CT0415-200700-032-e10 CT0415 Homo sapiens cDNA
8608	21639		1.82	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8860	21880	35240	3.13	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9457	22365	35747	1.05	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9457	22365	35748	1.05	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9902	25688	34684	1.44	1.6E+00	X52048.1	NT	M. musculus COL3A1 gene for collagen alpha1
9992	25688	34685	1.44	1.6E+00	X52048.1	NT	M. musculus COL3A1 gene for collagen alpha1
10115	23008		0.67	1.6E+00	AF043488.1	NT	Thermotoga maritima ethanololysis D-xylose-binding protein (xylF) gene, complete cds
10254	23144	36553	1.6	1.6E+00	T41280.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hmcDNA library Homo sapiens cDNA clone ph6b6_19/1TV
10645	23531	36963	0.64	1.6E+00	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a (1AL), and zinc finger protein (DNZ1) genes, complete cds
10682	23568	36997	1.08	1.6E+00	AW835844.1	EST_HUMAN	QV4-L10016-090200-100-007 L10016 Homo sapiens cDNA
10682	23568	36998	1.08	1.6E+00	AW835844.1	EST_HUMAN	QV4-L10016-090200-100-007 L10016 Homo sapiens cDNA
11209	24135	37594	2.3	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
11246	24170	37617	2.47	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
11265	24189	37637	1.52	1.6E+00	AA216387.1	EST_HUMAN	nc16802.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008287 similar to contains element MER4 repetitive element;

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11281	19194	32331	5.56	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
12129	24970	38474	3.45	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
13084	25590		1.66	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08.5'
34	13150	26039	4.94	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
250	13348	26261	1.62	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
644	13705		1.65	1.5E+00	6752981	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagardin) (Adam15), mRNA
2434	15438	28438	2.19	1.5E+00	AJ131402.1	NT	Pdoto virus A RNA complete genome, isolate U
2641	15541	28540	2.39	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3183	15438	28438	1.89	1.5E+00	AJ131402.1	NT	Pdoto virus A RNA complete genome, isolate U
3433	16474	28381	0.75	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5930	18997	32116	1.1	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NC1_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.;
5930	18997	32117	1.1	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NC1_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.;
6577	19818		0.99	1.5E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6671	19708	32903	2.34	1.5E+00	R17879.1	EST_HUMAN	yg10602.r1 Soares infant brain N1B Homo sapiens cDNA clone IMAGE:31693 5'
7190	20190	33434	0.64	1.5E+00	BE90771.1	EST_HUMAN	601502041F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903659 5'
7488	20428		1.4	1.5E+00	BE785366.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881656 5'
7522	20461	33747	20.78	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7522	20461	33748	20.78	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7731	20663	33961	0.67	1.5E+00	AA889259.1	EST_HUMAN	ak26f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
8035	20950	34265	0.62	1.5E+00	AI003254.1	EST_HUMAN	en07b11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gb:S96936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8375	21279		0.66	1.5E+00	AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
8699	21630	34975	1.03	1.5E+00	BE887446.1	EST_HUMAN	601509556F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8782	21682	35025	0.64	1.5E+00	AB040887.1	NT	Homo sapiens IgM chain gene, mu-delta region
9204	22132	35488	1.11	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
10016	22916	36305	0.63	1.5E+00	R81928.1	EST_HUMAN	y03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
10161	23062	36453	1.33	1.5E+00	AW375687.1	EST_HUMAN	QV3-CT0192-261096-008-409 CT0102 Homo sapiens cDNA
10374	23263	36685	7.79	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-905 TN0078 Homo sapiens cDNA
10555	23441		1.41	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NC1_CGAP_Bn04 Homo sapiens cDNA clone IMAGE:4183865 5'
10692	23578	37007	4.46	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10692	23578	37008	4.46	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	24152	37603	1.63	1.5E+00	U78186.1	NT	Coprinus cinereus sec17-like protein (sec17) and hyphal tip 1 (hvt1) genes, complete cds
11836	24687	38176	4.39	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547P243 3'
11973	24816		4.68	1.5E+00	X07380.1	NT	Maize mitochondrial RNA-Ser gene and RNA-Phe pseudogene
12055	24896	38400	1.43	1.5E+00	AI400798.1	EST_HUMAN	ig94409.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12055	24896	38401	1.43	1.5E+00	AI400798.1	EST_HUMAN	ig94409.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12427	25189		2	1.5E+00	6753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
12776	25405		4.6	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
31	13147	26035	1.69	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
31	13147	26036	1.69	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2296	15304		1.03	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2356	15363		10.16	1.4E+00	U87922.1	NT	Ovis aries prion protein gene, complete cds
2718	15711	28709	1.85	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genome DNA
2823	15812	28808	2.74	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2823	15812	28809	2.74	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4354	17368	30231	1.54	1.4E+00	AW900455.1	EST_HUMAN	WSB1 protein (WSB1) genes, complete cds
4354	17368	30232	1.54	1.4E+00	AW900455.1	EST_HUMAN	GM0-NN1005-140300-286-106 NN1005 Homo sapiens cDNA
4699	17704		2.33	1.4E+00	BF681547.1	EST_HUMAN	GM0-NN1005-140300-286-106 NN1005 Homo sapiens cDNA
5557	18895	31515	1.04	1.4E+00	AW094976.1	EST_HUMAN	GM0-NN1005-140300-286-106 NN1005 Homo sapiens cDNA
5718	18791		4.98	1.4E+00	AB032983.1	NT	60216687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
6531	19575	32757	2.62	1.4E+00	Q13472	SWISSPROT	W445907.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
6548	25978		3.91	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6679	19716	32913	2.89	1.4E+00	Q92777	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6679	19716	32914	2.89	1.4E+00	Q92777	SWISSPROT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6726	18762	32869	0.51	1.4E+00	11096333	NT	SYNAPSIN II
6916	18946	33165	0.51	1.4E+00	BE007870.1	EST_HUMAN	SYNAPSIN II
6916	18946	33166	0.51	1.4E+00	BE007870.1	EST_HUMAN	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
7135	20243	33494	0.81	1.4E+00	AW893057.1	EST_HUMAN	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
7665	20599	33698	2.38	1.4E+00	AJ133269.1	NT	QV0-BN0148-050500-215-b11 BN0148 Homo sapiens cDNA
7683	20617	33917	1.19	1.4E+00	AW487760.1	EST_HUMAN	QV0-BN0148-050500-215-b12 NN0006 Homo sapiens cDNA
7749	20680	33979	0.65	1.4E+00	P55288	SWISSPROT	CM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA
							Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
							he23f05.x1 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7749	20680	33980	0.65	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7778	20707	34010	0.96	1.4E+00	Q80905	SWISSPROT	MINOR CAPSID PROTEIN L2
8910	21840		0.81	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8952	22280		5.77	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9639	22665	35934	1.63	1.4E+00	R20459.1	EST_HUMAN	Y633f12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9739	22663	36048	3.08	1.4E+00	BE084697.1	EST_HUMAN	RC1-BT0313-301289-012-05 BT0313 Homo sapiens cDNA
9773	22697	36083	0.7	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10704	23590	37017	1.05	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10745	23631	37063	0.91	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10745	23631	37064	0.91	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
11005	23889	37323	0.81	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11005	23889	37324	0.81	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11506	24416	37870	1.47	1.4E+00	AA195528.1	EST_HUMAN	zr36e09.r1 Soares_NhiHMFu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element MER22 repetitive element;
11674	24578	38054	6.73	1.4E+00	AB006682.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11842	24693	38182	5.4	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11842	24693	38183	5.4	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11859	24749	38241	2.89	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
11859	24749	38242	2.89	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
12426	25815		2.1	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12787	25969		1.92	1.4E+00	11546836	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen se70-2 (SE70-2), mRNA
592	13659		1.99	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydropyrimidin-thiopyran dehydrogenase
927	13979	26925	2.66	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1156	14197		13.38	1.3E+00	Y19213.1	NT	Homo sapiens putative psfH-taA pseudogene for hair keratin, exons 2 to 7
1323	14357	27304	11.53	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1323	14357	27305	11.53	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1384	14416		1.18	1.3E+00	U61730.2	NT	Coix laetyma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1633	14663		2.36	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 65 of the complete genome
2258	15268		1.02	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2429	15433	28433	0.92	1.3E+00	P26391	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2582	15581		3.91	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2581	16032	28333	0.94	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spm1), mRNA
3659	16694	28590	0.68	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5336	18320	31168	1.36	1.3E+00	AF080222.1	NT	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region
5336	18320	31168	1.36	1.3E+00	AF080222.1	NT	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region
5704	18777	31708	0.95	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5908	18977	32094	0.42	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6178	19235	32381	0.55	1.3E+00	BF668825.1	EST_HUMAN	602145284F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4306095 5'
6251	19304	32465	8.52	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291189-004-08 CT0289 Homo sapiens cDNA
6251	19304	32466	8.52	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291189-004-08 CT0289 Homo sapiens cDNA
6684	19720	32620	1.58	1.3E+00	M33496.1	NT	D melanogaster no-on-transient A gene product, complete cds
7055	20081		0.8	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
7097	20303		0.5	1.3E+00	P48940	SWISSPROT	SPORE GERMINATION PROTEIN KB
7153	20261	33515	1	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7268	25684	33419	0.42	1.3E+00	AW821580.1	EST_HUMAN	IL2-ST0311-020200-040-G12 ST0311 Homo sapiens cDNA
7285	20238	33488	0.89	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447865 5'
7459	20399	33672	0.96	1.3E+00	BE243671.1	EST_HUMAN	TCBAPT0959 Pediatric pre-B cell acute lymphoblastic leukemia BAYlor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP0959
7862	20789	34092	0.67	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8873	21803	35157	1.63	1.3E+00	AL009912.1	NT	Sus scrofa plp gene
9015	21844	35300	2.16	1.3E+00	BE963378.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
9124	22052	35412	0.95	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950632 3'
9268	22196		2.25	1.3E+00	8910247	NT	Homo sapiens GL004 protein (GL004), mRNA
9348	22276	35638	0.99	1.3E+00	A1927629.1	EST_HUMAN	w088a07.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2462100 3'
9689	22615	35988	0.65	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Scores breast 3Nbh8st Homo sapiens cDNA clone IMAGE:183076 3'
9689	22615	35989	0.65	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Scores breast 3Nbh8st Homo sapiens cDNA clone IMAGE:183076 3'
10046	22962		6.24	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
10054	22970	36358	2.7	1.3E+00	X72019.1	NT	S. alba pht-1 mRNA for photolase
10054	22970	36359	2.7	1.3E+00	X72019.1	NT	S. alba pht-1 mRNA for photolase
10150	23041	36440	1.16	1.3E+00	AF069250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10195	23086	36487	1.87	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID
10271	23181	36571	1.53	1.3E+00	AJ927628.1	EST_HUMAN	ALPHA-MANNOSIDASE (LAMAN)
10341	23230	36647	0.89	1.3E+00	AJ223962.1	NT	wc85a07.xl NCI_KR11 Homo sapiens cDNA clone IMAGE:2462100 3'
10341	23230	36648	0.89	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
10379	23268	36690	3.8	1.3E+00	BE963379.2	EST_HUMAN	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
10709	23595	37023	1.37	1.3E+00	AE004392.1	NT	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
10725	23611	37040	1.93	1.3E+00	M29953.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
11056	23840		1.04	1.3E+00	AL163302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
11135	24064		4.55	1.3E+00	Q14117	SWISSPROT	Homo sapiens chromosome 21 segment HS21C102
11344	24263	37703	2.47	1.3E+00	P25299	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11366	24284	37728	2.01	1.3E+00	Z18892.2	NT	MRNA 3'-END PROCESSING PROTEIN RNA15
11970	24813	38308	3.49	1.3E+00	D42042.1	NT	Mus musculus desmin gene
12049	24890	38394	5.06	1.3E+00	Z98692.1	NT	Human mRNA for KIAA0085 gene, partial cds
12224	26088		1.39	1.3E+00	AF174585.1	NT	Bacillus subtilis genomic DNA 23.8kb fragment
12556	26270		3.14	1.3E+00	AF187873.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
12722	26369	31800	3.77	1.3E+00	BF348043.1	EST_HUMAN	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12732	25724		1.49	1.3E+00	P33464	SWISSPROT	602023185F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158452 5'
12814	25436		1.8	1.3E+00	AF187035.1	NT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
13098	25614		1.54	1.3E+00	U39978.1	NT	Stumira lillum cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
673	13735	26647	7.6	1.2E+00	AA676246.1	EST_HUMAN	Necrophoreresultant-degrading bacterium Bm6 2,3-dihydroxyphenyl dioxygenase (bphCII) gene, complete cds
848	13903	26843	1.31	1.2E+00	P05228	SWISSPROT	z122a08.s1 Sceres_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
848	13903	26844	1.31	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
848	13903	26845	1.31	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
903	13955		1.84	1.2E+00	8924234	NT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
1188	14227	27168	3.19	1.2E+00	AF080245.2	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1233	14269	27212	1.25	1.2E+00	AJ252242.1	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1233	14269	27213	1.25	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2023	15041	28035	1.06	1.2E+00	AF140831.1	NT	pea seed-borne mosaic virus complete genome
2400	15405	28408	0.99	1.2E+00	AF156495.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3156	16206	28096	1.73	1.2E+00	AB020881.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
3207	16255	29152	8.26	1.2E+00	AL161563.2	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3207	16255	29153	8.26	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3330	16376		4.2	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3406	16448	29356	0.67	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3407	16449		1.23	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
3775	19808	29693	10.11	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (P07) gene, exons 1 to 9, partial cds
4072	17098	29981	2.44	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4401	16448	29356	0.67	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4583	17591		2.21	1.2E+00	M87060.1	NT	Rattus rattus cardiac AEs gene, exons 1-23
4676	17661	30549	1.86	1.2E+00	AF158495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4702	17707		7.25	1.2E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
4793	16449		0.8	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
5145	18140	30983	1.25	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
5145	18140	30984	1.25	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5145	18140	30985	1.25	1.2E+00	P06228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5623	18699	31597	1.33	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5748	18819	31916	2.08	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6007	19071		0.51	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
6089	19160	32286	0.92	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6392	19441	32508	2.21	1.2E+00	X74885.1	NT	D.hydrel ayl repeat cluster DNA, fragment D
6457	19502	32677	4.18	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6544	19587	32773	1.57	1.2E+00	X89084.1	NT	C.glutamicum pta gene and ackA gene
6544	19587	32774	1.57	1.2E+00	X89084.1	NT	C.glutamicum pta gene and ackA gene
6590	19631	32813	31.21	1.2E+00	AA759254.1	EST_HUMAN	an94g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
6704	19740	32941					y09b12.s1 Soares melanocyte 2NkHM Homo sapiens cDNA clone IMAGE:273599 3' similar to gbM87935HUMAAU472 Human carcinoma cell-derived Alu RNA transcript (rRNA); gb:J04970
6778	19812	33023	0.73	1.2E+00	N33295.1	EST_HUMAN	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6782	19815	33027	0.74	1.2E+00	P17671	SWISSPROT	ECODYSONE-INDUCIBLE PROTEIN E75-A
7243	20152	33391	2.02	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7257	20166	33405	1.02	1.2E+00	AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
			2.63	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7366	20379	33648	0.57	1.2E+00	AA167810.1	EST_HUMAN	zq9805.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632001 5' similar to gbD10522 Human mRNA for 80K-L protein, complete cds. (HUMAN);
7624	20559		0.75	1.2E+00	AJ271735.1	NT	Homo sapiens Xi pseudautosomal region; segment 1/2
7777	25676	34009	2.59	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cDNA Homo sapiens cDNA clone cDAAFH03 5'
8099	21011	34337	2.59	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8162	21069	34398	0.44	1.2E+00	J05218.1	NT	Chicken muscarinic acetylcholine receptor (m4 mAChR) gene, complete cds
8340	21245	34578	0.47	1.2E+00	BE787648.1	EST_HUMAN	601481761F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
8345	21250	34585	0.48	1.2E+00	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
9132	22060	35420	4.63	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
9221	22149	36502	0.86	1.2E+00	P38427	SWISSPROT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-GLUCOSEPHOSPHATE (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
9434	22302	36502	0.82	1.2E+00	7706271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
9576	22503	35867	2.33	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201089-001-e07 CT0222 Homo sapiens cDNA
9781	22706	36089	0.56	1.2E+00	H48599.1	EST_HUMAN	yq80a06.t1 Soares fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:202088 5'
9834	22839	36227	3.1	1.2E+00	Z32880.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
10132	23023	36419	1.9	1.2E+00	D11745.1	EST_HUMAN	HUM-HM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hmo01a01
10441	23330	36748	3.56	1.2E+00	X68832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10815	23701	36748	0.86	1.2E+00	AB009666.1	NT	Homo sapiens Molro gene, exon 1
11786	24708	38200	1.74	1.2E+00	AW817817.1	EST_HUMAN	PMO-ST0284-161189-001-401 ST0284 Homo sapiens cDNA
11822	24742	38200	1.24	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11890	23990	37429	5.19	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12523	25790	31577	36.12	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12543	25262	31577	2.45	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
496	13557	28479	1.31	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1787	14813	27782	1.2	1.1E+00	AW995353.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1917	14938	27915	1.21	1.1E+00	AW575889.1	EST_HUMAN	UI-HF-BR0p-ajk-f02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3377	16421	29323	11.07	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3377	16421	29324	11.07	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3545	16583	29488	0.89	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3640	16876	29574	1.05	1.1E+00	AI808350.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3782	16813	29699	1.79	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3782	16813	29700	1.79	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3801	16832	29718	1.96	1.1E+00	5729757	NT	Homo sapiens calpain 9 (nCL-9) (CAPN9) mRNA
3888	16917	29937	0.68	1.1E+00	X85374.1	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4021	17048	29937	0.57	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4079	17105	29984	0.72	1.1E+00	AB040053.1	NT	Oryza sativa subsp. japonica rCOP1 mRNA for COP1, complete cds
4311	17325		0.63	1.1E+00	5836331	NT	R. uncinatis complete mitochondrial genome
4794	17798		0.77	1.1E+00	U34992.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds
5113	18110	30955	5.02	1.1E+00	U18469.1	NT	African swine fever virus, complete genome
5114	18111	30956	2.46	1.1E+00	AJ271740.1	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5204	18195	31037	1.01	1.1E+00	X78425.1	NT	E. faecalis pbp5 gene
5407	18388		0.72	1.1E+00	AF140522.1	NT	Glossina morsitans morsitans salivary gland growth factor-2 (TSGF-2) mRNA, complete cds
5411	18392		0.98	1.1E+00	BE409837.1	EST_HUMAN	601298534F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3625605 5'
5448	18529	31255	0.45	1.1E+00	P13181	SWISSPROT	GALACTOSE TRANSPORTER (GALACTOSE PERMEASE)
5490	18570	31418	1.51	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5808	18880	31987	40.8	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
5828	18899	32013	14.89	1.1E+00	AI138592.1	EST_HUMAN	q685c03.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1736280 3'
6329	19379	32546	1.24	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC9A14), mRNA
6526	19570	32753	0.65	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6672	19709	32904	0.68	1.1E+00	R06037.1	EST_HUMAN	ye89603.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:124924 5'
7015	20042	33276	0.71	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7163	20270	33526	0.45	1.1E+00	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
7627	20562		0.68	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7676	20610	33909	0.68	1.1E+00	X55981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7881	20807	34112	0.61	1.1E+00	BF683714.1	EST_HUMAN	602139978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301322 5'
7811	20835	34137	2.14	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7911	20835	34138	2.14	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7934	20856	34164	8.75	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
8016	26692	34250	0.94	1.1E+00	11987960	NT	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog) like (Sir2l), mRNA
8709	21640	34987	3.73	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4248628 5'
8799	21729	35078	0.86	1.1E+00	AJ478339.1	EST_HUMAN	fm39h11.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
9286	22224	35583	1.08	1.1E+00	AB003088.1	NT	Acetabularia cellulosus mitochondrial COXI-like gene
9374	22302	35663	0.93	1.1E+00	S80750.1	NT	VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
9971	21329		0.58	1.1E+00	BE584876.1	EST_HUMAN	601216278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
10154	23046	36444	0.7	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10206	23097		0.83	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
10291	23181	36593	0.56	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10348	23237	36635	2.17	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
10446	23335	36753	5.97	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment (No. 27)
10503	23391	36802	20.33	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10979	23863	37290	1.18	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
11095	24026	37469	2.49	1.1E+00	11087384	NT	Homo sapiens KIAA0826 gene product (KIAA0826), mRNA
11150	24079		3.12	1.1E+00	AF088942.1	NT	Klebsormidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11526	24436	37694	1.68	1.1E+00	11439596	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 11 (KCNJ11), mRNA
11643	18425		4.92	1.1E+00	8922673	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11547	24456	37918	4.06	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11547	24456	37919	4.06	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11794	24716	38208	4.19	1.1E+00	AI809699.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
12002	24844	38340	1.5	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12002	24844	38341	1.5	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12496	29236		1.96	1.1E+00	P07860	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12591	25268	31842	2.59	1.1E+00	AF216898.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12714	25787		2.93	1.1E+00	AF234169.1	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
102	13215		2.91	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
117	13225	26137	2.72	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
441	13512		1.72	1.0E+00	AB021884.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
598	13665	26667	1.38	1.0E+00	ALJ251660.1	NT	Giardia ligria mRNA for homeodomain transcription factor (so gene)
700	13759	26676	8.98	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
702	13761		0.89	1.0E+00	AF125084.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1413	15900		1.41	1.0E+00	X80416.1	NT	V. carteri Aigal-CAM mRNA
2508	15509	28511	1.57	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2508	15509	28512	1.57	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2589	15587		0.95	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204, contains element MER22 MER22 repetitive element ;

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2919	15972	28869	4.6	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2919	16972	28870	4.6	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3009	16080		0.95	1.0E+00	O14226	SWISSPROT	HYPOPHOSPHATE 67.9 KD PROTEIN C6F1208G IN CHROMOSOME 1
3242	16260	29183	1.18	1.0E+00	AA628453.1	EST_HUMAN	af28908.s1 Soares, Jetal, Tetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3431	16472		0.65	1.0E+00	AF222761.1	NT	WP:CA2D8.3 CE04204 :contains element MER22 MER22 repetitive element :
3661	13215		0.98	1.0E+00	U23808.1	NT	Rattus norvegicus neuromedin U precursor (NmlU) gene, exons 5 and 8
3748	16780	29669	1.93	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
4157	17178	30050	1	1.0E+00	AF223391.1	NT	Agaricus bisporus mRNA for tyrosinase
5168	18158	31006	0.79	1.0E+00	AF092505.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5394	18376	31218	0.88	1.0E+00	BE142914.1	EST_HUMAN	Mus musculus dipeptidyl aminopeptidase-like protein 6 (Dpp6) gene, partial cds; and proximal Rump white inversion breakpoint
5464	18546	31386	2.68	1.0E+00	Z97022.1	NT	MRQ-HT0157-310300-010-gt11 HT0157 Homo sapiens cDNA
6063	19126	32263	4.77	1.0E+00	AF248084.1	NT	Hordeum vulgare gene encoding cysteine proteinase
6063	19126	32263	4.77	1.0E+00	AF248084.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6063	19126	32254	4.77	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6182	19230	32386	1.23	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA TCA contig fragment No. 6
6353	19402	32569	5.15	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6360	19409	32574	1.92	1.0E+00	AW452782.1	EST_HUMAN	UJ-H-B13-alk-d-09-0-UJ.s1 NCJ CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6765	19789	33011	2.14	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6820	19863	33066	0.74	1.0E+00	AF104689.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6821	19861		0.8	1.0E+00	P46506	SWISSPROT	SRB-17 PROTEIN
6860	19979	33202	0.48	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6950	19979	33203	0.48	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
7084	20290	33549	1	1.0E+00	Y11204.1	NT	V. carteri gene encoding valoxopsin
7174	18446	31315	0.56	1.0E+00	U63721.1	NT	Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds
7498	20438	33719	1.36	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7898	20824		9.02	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8171	21078	34408	1.51	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
8183	21095	34428	9.27	1.0E+00	AA775191.1	EST_HUMAN	ac78808.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:868791 3'
8407	21310		0.61	1.0E+00	BF078213.1	EST_HUMAN	602163702F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294727 5'
8539	21470	34810	1.18	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8539	21470	34811	1.18	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8720	18431		1.66	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
							PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8924	21854	35209	2.66	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8924	21854	35210	2.66	1.0E+00	Q02207	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
9047	21876		0.66	1.0E+00	P51784	SWISSPROT	SIMILAN IMMUNODEFICIENCY VIRUS GAG PROTEIN (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
9102	25689		2.23	1.0E+00	BE147331.1	EST_HUMAN	RC71-HT0229-181099-011-608 HT0229 Homo sapiens cDNA
9140	22068	35429	1.46	1.0E+00	U42720.2	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9283	22211	35569	1.71	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9811	22717	36099	1.83	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9903	22891	36275	0.58	1.0E+00	AF257519.1	NT	Dantio retro eukaryotic translation initiation factor eIF4E-1 mRNA, complete cds
9903	22891	36276	0.58	1.0E+00	AF257519.1	NT	Dantio retro eukaryotic translation initiation factor eIF4E-1 mRNA, complete cds
10014	22914	36303	1.43	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
10014	22914	36304	1.43	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
10137	23028	36425	1.87	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
10142	23033	36430	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
10142	23033	36431	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
10367	23256	36676	0.51	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10367	23256	36677	0.51	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10613	23499	36931	0.83	1.0E+00	5174862	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10613	23499	36932	0.83	1.0E+00	5174862	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10700	23686	37015	1.13	1.0E+00	A1077620.1	EST_HUMAN	oy15d07.s1 Soares_senescent_fibroblasts_NBHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10818	23702	37129	2.99	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW C04 5'
10955	23839	37268	21.78	1.0E+00	AA004882.1	EST_HUMAN	z194e02.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10955	23839	37267	21.78	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10988	23872	37300	1.11	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11528	24438	37896	1.59	1.0E+00	AA701494.1	EST_HUMAN	z163b11.s1 Soares_fetal_liver_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element;
12162	18545	31385	1.57	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
12368	25172		3.26	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12703	25358		2.04	1.0E+00	AW876184.1	EST_HUMAN	EST388283 MAGS resequences, MAGN Homo sapiens cDNA
2684	15878	28877	1.27	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3667	16701		0.95	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5830	18901	32016	11.74	9.9E-01	P49857	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6084	19145	32280	0.92	9.9E-01	Q08632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1280.5 IN CHROMOSOME II
6903	22709		1.76	9.9E-01	U65667.1	NT	Lycopersicon esculentum putative Mli1 copy 1 nematode-resistance gene
10084	22877		2.07	9.9E-01	Q28842	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
11157	24086	37533	2.46	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
546	13615	28623	1.13	9.8E-01	P22867	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2316	15324		1.1	9.8E-01	AJ003108.1	NT	Caillitrix jacchus UBE1 gene derived retroposon on the Y chromosome
7564	20501	33789	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7564	20501	33790	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
8094	21006	34330	1.23	9.8E-01	BF034016.1	EST_HUMAN	6014563337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8094	21006	34331	1.23	9.8E-01	BF034016.1	EST_HUMAN	6014563337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
9278	22206	35563	0.98	9.8E-01	P38852	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10918	23803		0.71	9.8E-01	AA825566.1	EST_HUMAN	cd55cd04.s1 NCI CGAP_QCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11432	24348	37793	2.02	9.8E-01	BE288705.1	EST_HUMAN	601110259F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11432	24348	37794	2.02	9.8E-01	BE288705.1	EST_HUMAN	601110259F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12598	25294		1.64	9.8E-01	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7520	20459	33745	2.22	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
9070	21999	35353	1.89	9.7E-01	AF149112.1	NT	Triticum aestivum sigma rust resistance protein Y10 (Y10) gene, complete cds
9078	22005	35359	1.49	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (moe) and restriction endonuclease (res)
9397	22325	35988	0.82	9.7E-01	BE798822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11612	24520		5.76	9.7E-01	BF311209.1	EST_HUMAN	U1-H-B14-act-e-07-Q-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
13705	25620		5.01	9.7E-01	AL114281.1	NT	Boltyis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4544	17553	30413	0.71	9.6E-01	AF197825.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4544	17553	30414	0.71	9.6E-01	AF197825.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4569	17577	30439	1.72	9.6E-01	AW798674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5660	19027	32147	3.54	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2394
5660	19027	32148	3.54	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2394
7051	20077	33310	0.55	9.6E-01	Z979341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FGA contig fragment No. 6
7747	20678	33976	0.5	9.6E-01	AF197881.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8963	21893		1.74	9.6E-01	X95275.1	NT	P.falcipterus complete gene map of plastid-like DNA (IR-A)
9410	22338	35702	0.85	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
11530	24440	37899	1.44	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11951	24785	38284	4.1	9.6E-01	AV752805.1	EST_HUMAN	AV752805 NPd Homo sapiens cDNA clone NPDBAG06 5'
11951	24785	38285	4.1	9.6E-01	AV752805.1	EST_HUMAN	AV752805 NPd Homo sapiens cDNA clone NPDBAG06 5'
12308	25115		2.73	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12887	25856	31473	1.88	9.6E-01	U91423.1	NT	Sahyana tiburo NADH dehydrogenase subunit 2 (NADPH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2498	15500	28501	1.34	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3947	16876	29759	2.53	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3658473 5'
3947	16876	29760	2.53	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3658473 5'
9553	22480	35839	0.83	9.5E-01	A190162.1	EST_HUMAN	qd57d07.x1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9560	22576	36947	1.2	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-602 CT0295 Homo sapiens cDNA
11690	24592	38070	1.89	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4103830 5'
11885	23985	37423	1.63	9.5E-01	AW293789.1	EST_HUMAN	U1-H-B12-ahp-f-03-Q-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
12196	25031	38532	2.32	9.5E-01	T67204.1	EST_HUMAN	ya53d04.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:66631 3'
3245	16238		4.67	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3264	16312		2.72	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9423	22351	35717	0.78	9.4E-01	M90724.1	NT	Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4
12547	25265		1.59	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3869929 5'
12886	25782		1.45	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastoid leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1762	14788		7.14	9.3E-01	AF242382.1	NT	Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5
2880	15675	28674	1.35	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0603-271199-011-B01 BT0603 Homo sapiens cDNA
4119	17142	30014	1.43	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4119	17142	30015	1.43	9.3E-01	M20218.1	NT	Bovine papillomavirus type 2, complete genome
5786	18959	31966	1.67	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5875	18943	32081	3.99	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7717	20649		0.84	9.3E-01	AF270648.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8844	21675	34912	2.15	9.3E-01	AA847040.1	EST_HUMAN	cc09b03.s1 NCI_CGAP_O12 Homo sapiens cDNA clone IMAGE:1385357
9372	22300		0.89	9.3E-01	AF061981.1	NT	Xenopus laevis CCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9493	22421	35784	0.89	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12991	25547	31753	1.62	9.3E-01	11440288	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA
12998	25551		2.01	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3285	16332	29238	5.18	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5919	18098		1.47	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (SLC30a4), mRNA
6218	19273	32427	4.94	9.2E-01	BF037686.1	EST_HUMAN	601481153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
6924	19953	33173	0.5	9.2E-01	M64703.1	NT	N. crassa val-1 mRNA
10184	23075	36476	0.87	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
10288	23159	36569	0.9	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10758	23644	37077	4.12	9.2E-01	11430983	NT	Homo sapiens lysosomal sialidase-like protein 1 (LALP1), mRNA
10899	23794	37210	1.63	9.2E-01	BF593251.1	EST_HUMAN	768606.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3576219 3' similar to SW:NU5M_TRYBB
11091	24022	37484	1.94	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
12144	24984	38484	1.72	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
1648	14879	27642	1.15	9.1E-01	T96875.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
2138	15151		0.96	9.1E-01	8923056	NT	ye5201.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element;
3249	16297	28200	0.98	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3249	16297	28201	0.98	9.1E-01	T26418.1	EST_HUMAN	AB20008R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB20008 5'
4547	17556		1.71	9.1E-01	D17428.1	NT	AB20008R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB20008 5'
6408	19459	32630	1.43	9.1E-01	L36033.1	NT	Corynebacterium glutamicum secA gene for SecA protein, complete cds
6783	19816	33028	3.41	9.1E-01	Q61704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
8010	20927	34244	17.06	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
8202	21108	34438	2.17	9.1E-01	U72895.1	NT	ob1908.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1336862 3'
							Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10672	23598	36990	0.71	9.1E-01	P38432	SWISSPROT	P80-COLLIN
12632	25849		28.85	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3251	16299	28204	1.05	9.0E-01	7661625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4486	17497	30357	1.31	9.0E-01	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
5139	18194	30977	0.83	9.0E-01	AF017729.1	NT	Oryzobolus curvicaudus Rad51 (RAD51) mRNA, complete cds
7790	20719	34023	0.71	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7822	20761		1.33	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds
9887	22802	36189	0.52	9.0E-01	AF086761.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
10349	23234	36652	0.52	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 61 of the complete genome
5805	18984	32081	2.54	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6497	19541		1.29	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA
6734	26653	32977	0.57	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6734	26653	32978	0.57	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
7567	20503		0.62	8.9E-01	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
7636	20571	33866	0.46	8.9E-01	AA194201.1	EST_HUMAN	z38c06.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7636	20571	33867	0.46	8.9E-01	AA194201.1	EST_HUMAN	z38c06.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:665674 5'
8789	21719		0.51	8.9E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8906	21925	35280	0.87	8.9E-01	AF259667.1	NT	Oliothona nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
12103	25028	38529	2.36	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12481	25225		3.78	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4658	17663	30531	2.44	8.9E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5347	18330	31179	0.96	8.8E-01	L41694.1	NT	Trypanosoma brucei microtubule-associated protein (MAP16) mRNA, 3' end of cds
5558	18636	31516	0.8	8.8E-01	AF310817.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
7957	20879	34190	0.47	8.8E-01	MB1182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10726	23612	37041	0.67	8.8E-01	7656878	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEB), mRNA
11520	24430	37888	2.8	8.8E-01	Z28337.1	NT	Maeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12323	28928		4.13	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719843
487	13588	26474	1.49	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2424	15428	28429	0.91	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2818	15971	28888	5.93	8.7E-01	AA585863.1	EST_HUMAN	nm05111.1 NCL CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6129	18126		3.62	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put>
5330	18314		0.75	8.7E-01	AJ288085.1	NT	Homo sapiens partial LGALS9 gene for galectin-9, exon 3
5359	18342	31186	0.73	8.7E-01	BF218306.1	EST_HUMAN	601883175F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095378 5'
8617	21548	34889	0.65	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9485	22413	35774	0.74	8.7E-01	A1239456.1	EST_HUMAN	q136e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9485	22413	35775	0.74	8.7E-01	A1239456.1	EST_HUMAN	q136e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
10258	23148	36556	1.77	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 624 of 529 of the complete genome
10793	23679	37108	0.59	8.7E-01	BF570169.1	EST_HUMAN	60218554T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
10793	23679	37109	0.59	8.7E-01	BF570169.1	EST_HUMAN	60218554T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309906 3'
11271	24163	37644	6.02	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12157	24956	38496	4.03	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12157	24956	38497	4.03	8.7E-01	BF107894.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12679	25755		2.12	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
497	13567		1.55	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
883	13936	26884	4.44	8.6E-01	W69089.1	EST_HUMAN	ztd4e03.r1 Soares_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2289	15297	28304	1.17	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthinohalosis), polypeptide 1 (CYP27A1b) mRNA
3686	18719	29611	0.9	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3865	18894	29778	1.54	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5413	18394		1.6	8.6E-01	AB014075.1	NT	Clostridium histolyticum genes for hypoxanthine-guanine phosphoribosyl-transferase (HGPRase), GTPase end 12 ORFs, complete and partial cds
6116	19175	32309	8.31	8.6E-01	XG0547.1	NT	Chicken lipoprotein lipase gene
6116	19175	32310	8.31	8.6E-01	XG0547.1	NT	Chicken lipoprotein lipase gene
6639	25651	32868	0.51	8.6E-01	S78772.1	NT	polyprotein [Coxsackie B4 virus CB4, host=mice, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
7006	20033	33265	1.98	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7006	20033	33266	1.98	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7957	20873		0.63	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 60 of 134 of the complete genome
8506	21437		1.45	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8620	21551	34892	0.78	8.6E-01	AF077837.1	NT	Bacillus halodurans genomic DNA, section 12/14
7027	20053	33285	1.25	8.5E-01	AF165214.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
7949	20871	34182	2.54	8.5E-01	BE642612.1	EST_HUMAN	Bacteriophage D3, complete genome
							601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8570	21501	34844	0.53	8.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8889	21918	35273	0.78	8.6E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8989	21918	35274	0.78	8.6E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
9071	22000	35354	1.41	8.6E-01	AJ249213.1	NT	Homo sapiens partial 5-HT ₄ receptor gene, exons 2 to 5
10837	23723	37145	2.64	8.6E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10837	23723	37146	2.64	8.6E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12617	25852		3.3	8.6E-01	11418543	NT	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVBP1), mRNA
12624	25308		7.93	8.6E-01	8607008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4299	17313	30180	1.03	8.4E-01	AF143509.1	NT	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds
5682	25631	31677	2.54	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5682	25631	31678	2.54	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
8322	21227	34561	0.52	8.4E-01	AF051142.1	NT	Manestra brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10464	23352		3.57	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
765	13822	28751	2.8	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cyoA) and CycB (cycB) genes, complete cds
3142	16162	29085	4.33	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3878	16907	29788	0.81	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4098	17123	30000	3.46	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5451	18532	31258	2.38	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10194	23065		3.67	8.3E-01	A1791952.1	EST_HUMAN	mm01112.y6 NC1_CGAP_Oc9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR11 THR repetitive element;
10611	23497	36928	1.42	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10714	23600	37027	4.01	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
11118	24048	37494	2.58	8.3E-01	AE000803.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
11133	24062		1.91	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11749	24690	38131	1.78	8.3E-01	AF020803.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
2086	15081	28080	1.68	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2102	15116		1.82	8.2E-01	AF145689.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2728	16721		1.47	8.2E-01	AW376900.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
3894	17021	29911	0.99	8.2E-01	AF063417.1	NT	Tanytulum orbiculare elongation factor 1-alpha mRNA, partial cds
5249	18236	31086	0.98	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6935	19964	33185	0.59	8.2E-01	X05283.1	NT	G. gallus mRNA for C-Serrat-1 protein
6935	19964	33186	0.59	8.2E-01	X05283.1	NT	G. gallus mRNA for C-Serrat-1 protein

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7081	20287	33546	0.82	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SC1125 protein
7226	20224	33472	3.3	8.2E-01	AW378433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7645	25673	33875	4.16	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
9012	21941	35297	0.62	8.2E-01	BE263145.1	EST_HUMAN	60114485F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412.5'
9492	22420	35782	0.57	8.2E-01	AW614205.1	EST_HUMAN	hg77g1.1.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2951684.3'
9492	22420	35783	0.57	8.2E-01	AW614205.1	EST_HUMAN	hg77g1.1.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2951684.3'
10528	23414	36828	0.6	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
10581	23447	36869	2.17	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
10719	23605	37034	0.56	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10719	23605	37035	0.56	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10873	23759	37185	4.09	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10873	23769	37185	4.09	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
12068	24909	38412	4	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
12151	24990	38490	6.37	8.2E-01	P10363	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12158	24997	38498	6.67	8.2E-01	H87398.1	EST_HUMAN	wt14d02.r1 Soares, placenta, 8 to 9 weeks, 2NBP8163W Homo sapiens cDNA clone IMAGE:252195.5'
12641	25317	31820	3.05	8.2E-01	AJ001261.1	NT	similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2809	15798		1.26	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3518	16556	29457	3.4	8.1E-01	AF055088.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3518	16556	29458	3.4	8.1E-01	AF055088.1	NT	Homo sapiens MHC class 1 region
5026	18026		0.67	8.1E-01	AF202634.1	NT	Homo sapiens MHC class 1 region
5906	18975	32093	0.51	8.1E-01	Q01727	SWISSPROT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6570	19811	32788	0.8	8.1E-01	U16790.1	NT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR) (MELANOCORTIN-1 RECEPTOR) (MC1-R)
6912	19942	33160	2.69	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6912	19942	33161	2.69	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7935	20857	34165	0.57	8.1E-01	O47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
							CYTOTOCHROME B
							Drosophila melanogaster putative inorganic phosphate cotransporter (Picoct) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gsrs) gene, partial cds
8490	21421	34759	1.21	8.1E-01	AF022713.2	NT	
							Drosophila melanogaster putative inorganic phosphate cotransporter (Picoct) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gsrs) gene, partial cds
8490	21421	34760	1.21	8.1E-01	AF022713.2	NT	

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9170	22098	35458	0.99	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
9170	22098	35459	0.99	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
9329	22257	35621	1.24	8.1E-01	AW242847.1	EST_HUMAN	nm01103.1 NCI_CGAP_Kid11 Homo sapiens cDNA IMAGE:2692469 3' similar to SW LYAR_MOUSE
10625	23511	35944	0.56	8.1E-01	P06425	SWISSPROT	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22.b1 PTRS repetitive element;
							PROBABLE E4 PROTEIN
							KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to
10896	23781	37208	0.55	8.1E-01	N84541.1	EST_HUMAN	EST(CLOWE C-OPE11)
11914	24761	38257	3.42	8.1E-01	BE93858.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11914	24761	38258	3.42	8.1E-01	BE93858.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12377	25157	31871	1.51	8.1E-01	AE001711.1	NT	Thermoga maritima section 23 of 136 of the complete genome
187	13266		2.84	8.0E-01	AJ271610.1	NT	Staphylococcus aureus partial pta gene for phosphate acetyltransferase allele 15
308	13401	26318	8.55	8.0E-01	AJ132772.1	NT	Bos taurus tub and rif genes
2049	15066		1.46	8.0E-01	BF530962.1	EST_HUMAN	G02072473F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4216091 5'
3126	16177	28072	1.18	8.0E-01	AF127897.1	NT	Salinri boliviensis olfactory receptor (SBO27) gene, partial cds
3358	16402	28303	0.9	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3767	16799		0.98	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4849	17855	30521	7.44	8.0E-01	X63739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5103	18100	30948	1.18	8.0E-01	7657352	NT	Mus musculus myosin Xb (Myc8b), mRNA
5345	18328	31177	0.91	8.0E-01	BE277215.1	EST_HUMAN	G0117857F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3051088 5'
8669	21600		1.06	8.0E-01	AW901489.1	EST_HUMAN	RC0-NN1012-270300-021-p06 NN1012 Homo sapiens cDNA
9089	22018	35374	1.38	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
11394	24310	37758	1.54	8.0E-01	Q82789	SWISSPROT	CREB-BINDING PROTEIN
476	13547	26467	1.01	7.9E-01	D11476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
738	13796		0.92	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1627	14657		16.76	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1462 protein, partial cds
1682	14712		0.97	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2280	15289	28297	6.28	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitogenin28, complete cds
2281	15290	28298	2.4	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3576	16613	29516	3.17	7.9E-01	AF228064.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4403	17415		0.67	7.9E-01	BE263612.1	EST_HUMAN	G01192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635785 5'
4722	17727	30590	0.82	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4722	17727	30591	0.82	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5320	18304		0.68	7.9E-01	AF139718.1	NT	Chrysomya bezziana peritrophin-48 precursor, gene, complete cds

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6602	19643	32825	0.69	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
6687	21618	34980	5.93	7.9E-01	X90996.1	NT	P. aethiops GR gene
10076	22991	36387	4.42	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vsg3M-B) mRNA, partial cds
10552	23438	36859	4.89	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10563	23479	36906	0.9	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
10989	23873	37301	0.97	7.9E-01	AB000831.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
11445	24361	38039	2.21	7.9E-01	768247.1	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11660	24566	38039	2.63	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
801	13853		1.78	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2294	15302	28308	3.77	7.8E-01	AW959567.1	EST_HUMAN	EST1371637 MAGE resequences, MAGF Homo sapiens cDNA
4613	17821	30484	0.87	7.8E-01	AE000869.1	NT	Methanobacterium thermoautotrophicum from bases 862690 to 876388 (section 75 of 148) of the complete genome
4814	17815	30682	1.15	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc51-1 mRNA, complete cds
5348	18331		0.72	7.8E-01	Z43786.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
6304	19355	32526	2.08	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6463	19508	32884	1	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6735	19769	32979	0.66	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8160	21087	34397	0.41	7.8E-01	Q09908	SWISSPROT	HYPOTHETICAL 60.7 KD PROTEIN C30D11.08C IN CHROMOSOME I
9060	21986	36342	1.28	7.8E-01	BF108927.1	EST_HUMAN	7154405.v1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE.3525176 3'
9775	22699	36085	1.44	7.8E-01	Y10169.1	NT	D. discoideum racGAP gene
9872	22787	36177	0.53	7.8E-01	4828673	NT	Homo sapiens nucleoprotein 214kD (CAIN) (NUP214), mRNA
10624	23510		1.15	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12611	25833		1.86	7.8E-01	L29280.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
149	13249	26166	5.28	7.7E-01	AF184346.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L-1) mRNA, complete cds
749	13806		1.94	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IA alpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NGS), butyrophilin-like
2761	15753	28749	1.85	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3065	16107	29013	11.84	7.7E-01	AB011094.1	NT	Homo sapiens mRNA for KIAA0522 protein, partial cds
3409	16451		0.79	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAc-T7), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3662	16696	29592	4.92	7.7E-01	AF118085.1	NT	Homo sapiens PRO1976 mRNA, complete cds
4503	17513	30379	2.52	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4503	17513	30380	2.52	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5752	18825	31923	1.38	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5752	18825	31924	1.38	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6181	19238	32385	0.86	7.7E-01	R08600.1	EST_HUMAN	W24b02.st Sceres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1277553'
10369	23248	36668	0.63	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12505	25240		6.05	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
6336	19386	32554	3.97	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6336	19386	32555	3.97	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6796	19829	33030	0.78	7.6E-01	P37638	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
7170	18442	31311	0.97	7.6E-01	A1253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7170	18442	31345	0.97	7.6E-01	A1253399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7404	20103	33338	0.93	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8642	21573	34911	1.44	7.6E-01	AF146783.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhlp (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8703	21634	34970	2.41	7.6E-01	6857752	NT	Mus musculus advillin (Adv4-pending), mRNA
8703	21634	34980	2.41	7.6E-01	6857752	NT	Mus musculus advillin (Adv4-pending), mRNA
8900	21830	35183	0.6	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8900	21830	35184	0.6	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9519	22446	35810	1.53	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b6, phenobarbital inducible, type a (Cyp2b9), mRNA
9819	22725	36108	3.76	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9819	22725	36109	3.76	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11796	24718	38210	2.5	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11796	24718	38211	2.5	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12133	24974		3.69	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12289	25100		5.4	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
536	13605		1.29	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
605	13671	28574	1.39	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3413	10455	29361	1.22	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'
4785	17760		1.71	7.5E-01	U48498.1	NT	Human skeletal muscle ryanodine receptor gene (RYR1), exon 92
5338	18415		1.15	7.5E-01	U48498.1	NT	Human skeletal muscle ryanodine receptor gene (RYR1), exon 92
7945	20867	34179	0.85	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12568	25274		4.74	7.5E-01	AF163161.2	NT	Homo sapiens dentin sialoprotein precursor (DSPP) gene, complete cds
13001	25593	31757	1.95	7.5E-01	D90907.1	NT	Synechocystis sp. PCC6803 complete genome, 027, 1056467-1188865
1157	14198	27134	1.1	7.4E-01	AI598146.1	EST_HUMAN	In14208.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
2366	15372	28375	1.03	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIA0534 protein, partial cds
3790	16821	29708	1.38	7.4E-01	AF112638.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
3973	17001	28888	0.69	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4416	17427	30289	4.86	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8428	21358	34697	1.09	7.4E-01	AL161651.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8426	21398	34698	1.09	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
9192	22120	35476	0.9	7.4E-01	BF346286.1	EST_HUMAN	602018456F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154340 5'
9272	22200		0.9	7.4E-01	U87860.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9642	22568	35939	7.39	7.4E-01	BE747503.1	EST_HUMAN	601573028F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9696	22624	36002	1.31	7.4E-01	AA187986.1	EST_HUMAN	Zp67n01.s1 Stratiagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10887	23772	37188	0.62	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12090	24931	38436	1.43	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
12090	24931	38437	1.43	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
12257	25077		5.27	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12363	25150		1.88	7.4E-01	AI472641.1	EST_HUMAN	ta13101.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4059	17065		0.72	7.3E-01	AP000062.1	NT	Aeropyrum pernix genomic DNA, section 5/7
4729	17734	30596	0.7	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4813	17814	30681	4.08	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5238	18225	31074	0.95	7.3E-01	O43103	SWISSPROT	FERRICHRONIE SIDEROPHORE PEPTIDE SYNTHETASE
6893	19823	33137	5.62	7.3E-01	L35772.1	NT	Mus musculus antigen (OD72) gene
6893	19923	33138	5.62	7.3E-01	L35772.1	NT	Mus musculus antigen (OD72) gene

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7453	26670	33664	0.9	7.3E-01	AJ011418.1	NT	Lyopersonicon esculentum mRNA for ubiquitin activating enzyme
7663	20780	34093	0.45	7.3E-01	Z14133.1	NT	D melanogaster Cdc mRNA for clathrin heavy chain
7977	20898	34211	8.65	7.3E-01	M26511.1	NT	V. alginolyticus sucrose (scfB) gene, complete cds
7977	20898	34212	8.65	7.3E-01	M26511.1	NT	V. alginolyticus sucrose (scfB) gene, complete cds
8332	21237	34570	0.51	7.3E-01	U34631.1	NT	Mus musculus alpha-4 integrin gene, exon 7
11862	24752	38245	3.93	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11862	24752	38246	3.93	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
856	13910		2.41	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1971	14989	27972	1.78	7.2E-01	X79140.1	NT	N. tabacum Nelf-4A13 mRNA
2485	15487	28488	1.5	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3115	16166	29060	1.5	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3514	16552	29452	2.37	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3678	16711	29602	1.43	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3940	16888	29851	0.97	7.2E-01	BF338350.1	EST_HUMAN	602035588F1 NCL CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183222 5'
4149	17170		0.78	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18
4882	17881	30748	2.94	7.2E-01	D60314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5264	18250	31100	1.27	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
5264	18250	31101	1.27	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
5396	18378	31220	1.94	7.2E-01	Z97335.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 0
7680	20618	33804	1.04	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8046	20959		0.44	7.2E-01	9625875	NT	Human herpesvirus 3, complete genome
8288	21192	34529	0.48	7.2E-01	AI610785.1	EST_HUMAN	tp388501.X1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2190025 3' similar to gbM23115 CALCIUM-TRANSPORTING ATPASE SARCOPASMIC RETICULUM TYPE, SLOW (HUMAN);
9022	21951	35307	1.44	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9516	22443		0.6	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10828	23714	37140	2.4	7.2E-01	BF070061.1	EST_HUMAN	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
11180	24108	37563	3.59	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome c mRNA, complete cds
11698	24600		1.49	7.2E-01	AW450487.1	EST_HUMAN	U1H-B13-aka-g-01-0UJ.s1 NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2735040 3'
12575	18427	31351	1.74	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polypeptide precursor (Dva) mRNA, complete cds

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12757	25391		4.27	7.2E-01	AF000063.1	NT	Aeropyrum pernix genomic DNA, section 8/7
716	13774	26594	11.44	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3110	16161	29057	20.14	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4304	17316	30186	5.04	7.1E-01	7305360	NT	Mus musculus obogelin (Olog), mRNA
4304	17318	30187	5.04	7.1E-01	7305360	NT	Mus musculus obogelin (Olog), mRNA
6173	19230	32376	1.65	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6173	19230	32377	1.65	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
7281	20234	33484	6.39	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvyltetrahydropterin synthase (pt) gene, complete cds
8769	21699	35044	0.58	7.1E-01	H54244.1	EST_HUMAN	Yq89d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202961 3'
9295	22223	35591	0.95	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
9295	22223	35582	0.95	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
10369	23298	36680	1.56	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10894	23779	37206	1.29	7.1E-01	M12681.1	NT	Human T-cell receptor gamma-chain J2 gene
12557	25768		2.16	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14292	27237	0.86	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14292	27238	0.86	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2473	15476	28478	1.54	7.0E-01	N62412.1	EST_HUMAN	Yz73607.s1 Soares multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2473	15476	28477	1.54	7.0E-01	N62412.1	EST_HUMAN	Yz73607.s1 Soares multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5169	18181		2.5	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6177	19234		0.86	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8949	21879		7.02	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
11560	24469	37934	1.62	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11560	24469	37935	1.62	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13055	26800	31581	2.38	7.0E-01	8630464	NT	Bacteriophage N15 virion, complete genome
995	14046	26989	66.92	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
995	14046	26990	66.92	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1336	14370	27320	2.26	6.9E-01	AA593530.1	EST_HUMAN	m28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085178 3'
3266	16314	29217	1.93	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5992	19057	32184	0.78	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds

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6221	19276	32430	0.63	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6630	19870	32855	1.62	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
8201	21105	34532	1.23	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8559	21490	34830	2.83	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8559	21490	34831	2.83	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9713	22638		0.72	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
10217	23108	36508	0.61	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10217	23108	36509	0.61	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11705	24607	38083	2.1	6.9E-01	D8013.1	NT	Homo sapiens DAN gene, complete cds
11705	24607	38084	2.1	6.9E-01	D8013.1	NT	Homo sapiens DAN gene, complete cds
12239	25763		1.75	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL-14)
983	14034	26977	1.36	6.9E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2723	16716		2.04	6.9E-01	D80817.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2877	14698	27631	1.19	6.9E-01	AA854476.1	EST_HUMAN	q75a05.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56441.1_maf1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4687	17692	30559	1.56	6.9E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
4966	17994	30822	0.7	6.9E-01	4758521	NT	Homo sapiens hevin (HEVIN) mRNA
10184	23055	38454	1.65	6.9E-01	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11529	24439	37897	2.17	6.9E-01	AJ276676.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11529	24439	37898	2.17	6.9E-01	AJ276675.1	NT	Stagonospora avenae bgf1 gene for beta-glucosidase, exons 1-4
11554	24463	37929	2.65	6.9E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11554	24463	37929	2.65	6.9E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11745	24646	38126	1.39	6.9E-01	AF164151.1	NT	Aropheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
12035	24877	38382	1.46	6.9E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
12035	24877	38383	1.46	6.9E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
318	13410	26328	24.93	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
359	13446	26358	25.65	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1828	14949		1.17	6.7E-01	M12132.1	NT	Quail fast skeletal muscle tropomyosin 1 gene, complete cds
2161	15173	28177	2.08	6.7E-01	AA451864.1	EST_HUMAN	z12g12.e1 Soares_t04_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2178	15918	28197	3.88	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relist) gene, complete cds, alternatively spliced
3039	16091	28993	4.8	6.7E-01	6878580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4563	17571	30434	0.67	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
5080	18077	30926	1.11	6.7E-01	AW079110.1	EST_HUMAN	xa95g12.x1 NC1_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3'
5699	18772	31700	0.87	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5699	18772	31701	0.87	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6189	19248	32392	0.89	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6579	19820	32804	1.86	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
6579	19820	32805	1.86	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
6907	19937	33155	0.48	6.7E-01	BE86241.2	EST_HUMAN	601660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6907	19937	33156	0.48	6.7E-01	BE86241.2	EST_HUMAN	601660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7699	20631		3.77	6.7E-01	AE004806.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7726	20658	33955	0.98	6.7E-01	AE004806.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10842	23528		0.89	6.7E-01	M34048.1	NT	Human placental protein 14 (PP14) gene, complete cds
11392	24308	37754	2.28	6.7E-01	BF354949.1	EST_HUMAN	OM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11891	28891	37430	3.38	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11
2524	15525	28528	1.41	6.6E-01	AF076240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2751	15742	28737	1.44	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3548	16586	28491	1.25	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3726	16768	28648	2.9	6.6E-01	Y07689.1	NT	G. albicans random DNA marker, 282bp
5167	18189	31007	0.83	6.6E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
5167	18189	31008	0.83	6.6E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
5589	19630	32812	4.18	6.6E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7482	20422	33701	0.98	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7482	20422	33702	0.98	6.6E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
8138	21047	34377	3.09	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLGID04 3'
9129	22057	35417	0.72	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
10189	23080		1.14	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment H921C078

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
647	13708	26616	1.33	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
647	13708	26616	1.33	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3494	16533	29433	5.85	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4121	17144	30017	1.01	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4380	17394	30289	4.79	6.5E-01	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5197	18189	31030	2.9	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5915	18984	32103	0.56	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
7026	20052	33284	1.31	6.5E-01	D88348.1	NT	Chicken mRNA for 116-kDa melanosomal matrix protein, complete cds
8025	20941	34256	0.78	6.5E-01	X04769.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
8119	21030	34357	0.9	6.5E-01	AJ799882.1	EST_HUMAN	uc46a02.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2321642 3'
10362	23241		0.85	6.5E-01	T78904.1	EST_HUMAN	yu21b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3'
10823	23709	37136	4.51	6.5E-01	AF119876.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
11079	24011	37452	2.87	6.5E-01	H87583.1	EST_HUMAN	yu17b06.r1 Soares placenta_809weeks_2NbpHP809W Homo sapiens cDNA clone IMAGE:252515 5'
11128	24058	37504	3.7	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCL CGAP_Pherf Homo sapiens cDNA clone IMAGE:1100748 3'
11230	24158		3.97	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
12029	24871	38374	2.3	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12808	25301		4.15	6.5E-01	BE465050.1	EST_HUMAN	h774a10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178130 3'
12828	25715		3.67	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
271	13366	26282	6.03	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
2826	15624	28617	1.03	6.4E-01	AF161184.1	NT	Pseudomonas fluorescens tytoplasmic halogenase (pma) gene, complete cds
3516	16554	28455	1.4	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3928	16956	29839	1.39	6.4E-01	AB049827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4358	17372		0.96	6.4E-01	Z74155.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL107w
4605	17613	30473	0.75	6.4E-01	Y12488.1	NT	M.musculus whn gene
4805	17613	30474	0.75	6.4E-01	Y12488.1	NT	M.musculus whn gene
5055	18052	30905	1.04	6.4E-01	AF239978.1	NT	Salmonella enteritidis SefR (sefR), hypothetical protein 7, and Dip (dip) genes, complete cds
9173	22101	35481	1.73	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10591	23477	36905	10.78	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10605	23491	36920	1.35	6.4E-01	BF870405.1	EST_HUMAN	602150289F1 NIH_MGC_B1 Homo sapiens cDNA clone IMAGE:4281126 5'
12718	26368		12.64	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
457	13529	26452	5.03	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
558	13627	26536	144.48	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2175	15187	28192	2.6	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2616	15614	28609	3.63	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2616	15614	28610	3.63	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3061	16113		0.86	6.3E-01	Y17275.1	NT	Lycopodium esculentum p69a gene, complete CDS
8299	16350	32518	0.87	6.3E-01	BE093606.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6885	18915	33131	1.02	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6885	18915	33132	1.02	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
9086	22015		3.21	6.3E-01	BE002044.1	EST_HUMAN	601876889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956351 5'
9443	22371	35735	0.98	6.3E-01	S82927.1	NT	glycoprotein illa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9761	22685	36072	0.67	6.3E-01	BF216084.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5'
9954	22659	36247	3.73	6.3E-01	9627521	NT	Varicella virus, complete genome
9954	22659	36248	3.73	6.3E-01	9627521	NT	Varicella virus, complete genome
10447	23336		0.75	6.3E-01	AE002328.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10909	23794	37223	1.46	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
11008	23882	37326	0.72	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
11500	24411	37865	2.1	6.3E-01	AA877715.1	EST_HUMAN	nr09008.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1181371 3' similar to TR:O02916 O02916 HLARK.;
11778	24678	38167	8.4	6.3E-01	A904160.1	EST_HUMAN	GM-BT043-090289-046 BT043 Homo sapiens cDNA
11857	24747	38239	1.75	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
12019	24861	38361	2.14	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12219	26063		1.56	6.3E-01	BF333356.1	EST_HUMAN	RCO-GI0037-250900-031-e09 GI0037 Homo sapiens cDNA
12341	25905	31365	13.98	6.3E-01	9910283	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12425	25188		1.61	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12623	26830		1.74	6.3E-01	X83528.1	NT	C. limicola psdD gene
5158	18151	30897	0.74	6.2E-01	AF157898.1	NT	Spermophilus sieversis isolate S47 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
6085	19146	32281	2.06	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7916	20840		2.84	6.2E-01	AF022263.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Cas-rs4) mRNA, partial cds
7973	25681	34207	1.15	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8876	21806	35169	5.59	6.2E-01	H72255.1	EST_HUMAN	Y601e08.s1 Soares fetal liver spleen 1NF5 Homo sapiens cDNA clone IMAGE:213542 3'
9415	22343	35708	0.63	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquininate dehydratase/shikimate:NAD(P) oxidoreductase gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9981	21339	34875	1.87	6.2E-01	BE562687.1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
10041	22041		3.87	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10560	23456	36891	7.51	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10717	23603	37031	0.6	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10717	23603	37032	0.6	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
11015	23898	37335	5.73	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
11015	23899	37336	5.73	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2417	15421		7.14	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
4651	17657	30523	12.86	6.1E-01	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
5726	18789	31892	1.21	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CelMyoD (hli-1) alternatively spliced genes, complete cds
7195	20195	33439	3.56	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7195	20195	33440	3.56	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7365	20359	33828	0.81	6.1E-01	AW105653.1	EST_HUMAN	cd50h03.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb.X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7464	20404	33680	0.53	6.1E-01	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8811	21741	35090	3.73	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
9353	22281	35641	1.39	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9353	22281	35642	1.39	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9949	22854	36241	23.9	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9949	22854	36242	23.9	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10357	23246	36865	1.08	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
10549	23435	36855	1.48	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
12156	24995	38494	2.24	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12156	24995	38495	2.24	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
517	13587	26500	6.03	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
563	13651		2.78	6.0E-01	5802989	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1389	14420	27375	1.67	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds

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Probe SEQ ID NO:	Exon: SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3885	16914	29792	0.93	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
5463	18544	31384	3.6	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5625	18701	31800	2.44	6.0E-01	AW139713.1	EST_HUMAN	UI-H-B11-aeb-a-10-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619.3'
6818	19851	33062	2.9	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6956	19984	33208	0.79	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7127	20331	33594	0.82	6.0E-01	L10234.1	NT	(CDW136) (CD136 ANTIGEN)
7127	20331	33595	0.82	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7742	20673	33871	6.6	6.0E-01	AJ277661.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
8701	21632	34977	4.43	6.0E-01	P02635	SWISSPROT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8701	21632	34978	4.43	6.0E-01	P02635	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10338	29227	36843	1.76	6.0E-01	AB008193.1	NT	SEGMENTATION PROTEIN FUSHI TARAZU
10768	23652		1.55	6.0E-01	Q01497	SWISSPROT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10871	23757		0.52	6.0E-01	BE637779.1	EST_HUMAN	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
11497	24408	37862	1.77	6.0E-01	AJ131892.1	NT	RC2-FN0094-190700-017-008 FN0094 Homo sapiens cDNA
11497	24408	37863	1.77	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperton protein, 419 kD isoform
11984	24827	38324	3.16	6.0E-01	A1420623.1	EST_HUMAN	Gallus gallus mRNA for Hyperton protein, 419 kD isoform
12688	26345	31826	1.52	6.0E-01	11421663	NT	60807.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2098621.3'
12960	25771	31576	2.29	6.0E-01	9055303	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12986	25709		5.41	6.0E-01	BE157617.1	EST_HUMAN	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
1028	14077	27017	0.95	5.9E-01	U32701.1	NT	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1427	14458	27411	1.18	5.9E-01	6880232	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3314	16361	29261	6.06	5.9E-01	AL163267.2	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3314	16361	29262	6.06	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4319	17333		3.5	5.9E-01	AF162756.1	NT	Homo sapiens chromosome 21 segment HS21C067
5236	18223	31072	2.12	5.9E-01	L27316.1	NT	Rattus norvegicus cerenxin 2 mRNA, partial cds
5326	18310	31160	2.5	5.9E-01	AF026566.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
6738	19772	32983	2.3	5.9E-01	AF085440.2	NT	Ovis aries SRY gene promoter region
7642	20577	33871	3.8	5.9E-01	AB023486.1	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7795	20724		0.56	5.9E-01	X68801.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
8578	21509	34855	0.61	5.9E-01	D80911.1	NT	G.gallus gene for skeletal alpha-actinin, exon EF2
							Synochocystis sp. PC06803 complete genome, 13/27, 1576593-1719843

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9197	22125	35481	0.54	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
10072	22987	36382	0.59	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KUW31/Ox major outer membrane protein (omp1) gene, complete cds
10424	23313		0.6	5.9E-01	P08463	SWISSPROT	E6 PROTEIN
10685	23571	37001	1.82	5.9E-01	P56284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
11119	24045	37491	2.77	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
11120	24050	37495	1.7	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11398	24314	37760	3.48	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-180100-002-H03 DT0041 Homo sapiens cDNA
11639	24545	38019	2.85	5.9E-01	AF084626.1	NT	Mus spretus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
11809	24757	38251	1.47	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
11909	24757	38252	1.47	5.9E-01	P47135	SWISSPROT	JSN1 PROTEIN
12376	25156	31870	1.8	5.9E-01	L42320.1	NT	Oryzopsis cuniculatus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12593	25289		3.38	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12784	25421		5.68	5.9E-01	P34826	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1923	14948	27922	1.05	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
4069	17095	29578	1.22	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4635	17641	30504	5.31	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4912	17911		1.23	5.8E-01	AF110848.1	NT	Megascelia scalaris sexilethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5659	18637		0.62	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5721	18794	31886	3.59	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6425	19472	32646	2.18	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-500E06 5'
6567	19608	32793	0.7	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
7124	20328		2	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8467	21398		2.69	5.8E-01	H41571.1	EST_HUMAN	yr81b03.e1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
8665	21596	34935	0.78	5.8E-01	A1280051.1	EST_HUMAN	gb-S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8665	21596	34936	0.78	5.8E-01	A1280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8768	21698	35042	2.74	5.8E-01	P14328	SWISSPROT	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779-3'
8768	21698	35043	2.74	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
9446	22376	35739	11.31	5.8E-01	AJ270774.1	NT	SPORE COAT PROTEIN SP96
9524	22451	35814	1.05	5.8E-01	Q27368	SWISSPROT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
10123	23014		0.64	5.8E-01	BF031606.1	EST_HUMAN	TRANSCRIPTION FACTOR E2F
11428	24344	37789	7.78	5.8E-01	AJ243213.1	NT	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11475	24388		3.57	5.8E-01	BF700092.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
							602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11582	24491		1.97	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
1612	14543	27604	1.03	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1612	14543	27605	1.03	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3090	16141		0.96	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3270	16318	29221	1.89	5.7E-01	Q9WJT2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3561	16598		3.73	5.7E-01	AB033503.1	NT	Populus euramericana pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6613	19554	32838	4.16	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3858590 5'
7008	20035	33268	0.78	5.7E-01	AA194201.1	EST_HUMAN	zr38c06.1 Soares_Nhr-IMPu_ST Homo sapiens cDNA clone IMAGE:665674 5'
7183	18455	31325	1.24	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8233	21138	34470	2	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8548	21479		0.57	5.7E-01	AJ251935.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc8 genes, alternative transcripts
8951	21881		0.84	5.7E-01	AI065061.1	EST_HUMAN	HA0805 Human fetal liver cDNA library Homo sapiens cDNA
10316	23205	36816	1.24	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10318	23205	36816	1.24	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
11048	23932	37372	1.07	5.7E-01	BF540962.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
3419	18461	29367	1.11	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3419	18461	29368	1.11	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3952	16980	28864	0.85	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
8159	21068	34396	0.41	5.6E-01	L44513.1	EST_HUMAN	HUMEST4B9 Human thymus NSTH II Homo sapiens cDNA
9361	22289	35654	4.78	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'
9361	22289	35655	4.78	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'
9914	22902	36289	1.51	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12244	25068		3.53	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3916457 5'
12686	16980	29864	3.48	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12715	25365		2.95	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13074	25598		3.35	5.6E-01	BF573929.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1239	14275	27218	1.54	5.5E-01	8393012	NT	Rattus norvegicus Prothymine A carboxylase, beta polypeptide (Pccb), mRNA
2752	15743	28738	4.81	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL
2752	15743	28739	4.81	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL
2861	16013	28911	1.09	5.5E-01	5902085	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3114	16165		1.76	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55V Homo sapiens cDNA clone IMAGE:178266 3'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3281	16329	29234	2.75	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3757	16789	29679	1.22	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
7628	20561	33854	0.56	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7628	20561	33854	0.56	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7666	20600	33855	0.68	5.5E-01	AF030001.1	NT	Carcinoma gene for gonadotropin II beta subunit, complete cds
9017	21946	33302	0.61	5.5E-01	A1791768.1	EST_HUMAN	cr82c01.y5 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
10287	23177	37176	0.77	5.5E-01	U89415.1	NT	Grimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10865	23751	37176	1.06	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Striatum (cat#936208) Homo sapiens cDNA clone HFB0335
11580	24489	37958	1.56	5.5E-01	BF129507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
150	13260	26167	7.75	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
150	13250	26168	7.75	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
606	13672	26575	1.71	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
606	13672	26576	1.71	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1298	14331	27277	2.28	5.4E-01	AW896087.1	EST_HUMAN	QY4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2118	15131	28288	1.71	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome
2271	15281	28288	2.29	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15.15' beta carotene dioxygenase (beta-diox gene)
5360	13672	26575	0.7	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
5360	13672	26576	0.7	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
5384	18366	32041	0.91	5.4E-01	X85973.1	NT	A.thaliana mRNA for phosphatidyl-specific phospholipase C
5864	18925	32041	0.79	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6432	19479	32656	1.52	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
6890	19728	32928	0.41	5.4E-01	11559824	NT	Homo sapiens hypothetical protein LOC683929 (LOC683929), mRNA
7376	20370	33639	0.63	5.4E-01	BE065592.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7721	20653	33948	0.69	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7721	20653	33949	0.69	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7723	20655	33952	1.67	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA)
10496	23394		2.35	5.4E-01	BF672536.1	EST_HUMAN	[INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA
11518	24428	37886	2.8	5.4E-01	P36858	SWISSPROT	DEHYDROGENASE]
12045	24886	38300	2.58	5.4E-01	Q60675	SWISSPROT	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
12045	24886	38391	2.58	5.4E-01	Q60675	SWISSPROT	NITRATE REDUCTASE [NADPH](NR)
12161	19479	32656	5.55	5.4E-01	AB025017.1	NT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
12301	25110		3.13	5.4E-01	A1855398.1	EST_HUMAN	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
539	13608	28518	2.16	5.3E-01	AF019413.1	NT	Rattus norvegicus gene for TIS11, complete cds
2154	15168	28169	0.94	5.3E-01	AF113919.1	NT	w137g04.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
2154	15168	28169	0.94	5.3E-01	AF113919.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-
2833	15822	28817	7.36	5.3E-01	4506328	NT	hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B
3299	16336	29239	4.03	5.3E-01	AF087658.1	NT	(B), and complement component C2 (C2) genes;>
4307	17321		2.5	5.3E-01	U36687.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
5843	18718	31621	1.43	5.3E-01	A1820921.1	EST_HUMAN	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
5843	18718	31622	1.43	5.3E-01	A1820921.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
5746	18818	31914	0.85	5.3E-01	AA183672.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
5746	18818	31915	0.85	5.3E-01	AA183672.1	EST_HUMAN	Homo sapiens secreted C-type lectin precursor (LSC1L) gene, complete cds
5842	18913	32029	1.93	5.3E-01	BE945620.1	EST_HUMAN	Mycoplasma genitalium section 9 of 51 of the complete genome
5842	18913	32030	1.93	5.3E-01	BE945620.1	EST_HUMAN	zu42h12.j5 Soares ovary tumor NthOT Homo sapiens cDNA clone IMAGE:740711 5'
9481	22389		1.81	5.3E-01	L01950.2	NT	zu42h12.j5 Soares ovary tumor NthOT Homo sapiens cDNA clone IMAGE:740711 5'
9510	22437	35801	0.84	5.3E-01	BF433958.1	EST_HUMAN	zu42g09.r1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:666112 5'
9510	22437	35802	0.84	5.3E-01	BF433958.1	EST_HUMAN	zu42g09.r1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:666112 5'
							7e73c12.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
							PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
							7e73c12.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
							PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
							Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for
							chloroplast product
							7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29
							repetitive element;
							7q71c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29
							repetitive element;

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10707	23593	37020	0.8	5.3E-01	A1954210.1	EST_HUMAN	wx94b02.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to
11073	23957	37393	0.52	5.3E-01	11428833	NT	SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11993	24836	38333	5.76	5.3E-01	BE566291.1	EST_HUMAN	Homo sapiens nucleoporin 214KD (CAIN) (NUP214), mRNA
12238	25769		4.27	5.3E-01	AA916053.1	EST_HUMAN	601338867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3882168 5'
841	13896	26833	13.58	5.2E-01	L20770.1	NT	og30e05.s1 NCI_CGAP_B-7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
1191	14230	27169	7.93	5.2E-01	Q8WV30	SWISSPROT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
1213	14257	27197	2.31	5.2E-01	AF224492.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1906	14927		2.81	5.2E-01	AL163285.2	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5(T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
2160	15172	28176	2.02	5.2E-01	AB018283.2	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
3164	16214	29103	1.48	5.2E-01	U65942.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
3465	16605		1.94	5.2E-01	AL116780.1	NT	Homo sapiens chromosome 21 segment HS21C085
3503	16543	29443	2.26	5.2E-01	AA984165.1	EST_HUMAN	Homo sapiens mRNA for KIAA0740 protein, partial cds
3699	16731		1.03	5.2E-01	AF020269.1	NT	Chlamydomonas abortus strain S263 POMP91A and POMP90A precursor, genes, complete cds
4717	17722	30584	0.69	5.2E-01	6762947	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5850	18921	32036	0.92	5.2E-01	AA284261.1	EST_HUMAN	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
10251	25693	36549	0.82	5.2E-01	X02218.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding
10251	25693	36550	0.82	5.2E-01	X02218.1	NT	Mus musculus acetylcholine receptor beta (Acbt), mRNA
10530	23416	36830	1.28	5.2E-01	AF143952.2	NT	zc44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
13051	25583		4.1	5.2E-01	P18516	SWISSPROT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
640	13701	26608	1.85	5.1E-01	M58509.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
671	13733	26644	3.66	5.1E-01	AJ233944.1	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
671	13733	26646	3.66	5.1E-01	AJ233944.1	NT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
1679	14709		1.08	5.1E-01	X87885.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
4163	17184	30057	5.45	5.1E-01	AB58495.1	EST_HUMAN	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
4283	17297	30163	3.94	5.1E-01	P96380	SWISSPROT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
6467	19512	32687	0.64	5.1E-01	BE541068.1	EST_HUMAN	R norvegicus mRNA for mammalian fusca protein
6528	19572		0.91	5.1E-01	AV712328.1	EST_HUMAN	w39b12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
7248	20155	33395	1.3	5.1E-01	R80873.1	EST_HUMAN	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
8856	21786	35135	0.52	5.1E-01	BE772052.1	EST_HUMAN	601063606F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3460000 5'
							AV712328 DCA Homo sapiens cDNA clone DCAAUF07 5'
							y194d09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
							CM4-FT0103-220600-210-012 FT0103 Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9135	22063	35422	0.81	5.1E-01	AW808881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9136	22063	35423	0.81	5.1E-01	AW808881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
10209	23100	36500	4.79	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
10211	23102	36503	3.8	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tap5091-cleaved sublibrary Homo sapiens cDNA not directional
10856	23542	36976	1.02	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12434	25702		2.66	5.1E-01	BF030207.1	EST_HUMAN	601555863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE3826767 5'
12664	25335		1.86	5.1E-01	BF439982.1	EST_HUMAN	rac51110.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE3406218 3' similar to contains element
2148	15161	28162	0.98	5.0E-01	4885552	NT	TAR1 repetitive element;
2148	15161	28163	0.98	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
							Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
							Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGA-HFEB), and putative chromosome replication protein (gida) genes, complete cds; and termination factor Rho (rho) gene>
2159	15171	28174	1.28	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGA-HFEB), and putative chromosome replication protein (gida) genes, complete cds; and termination factor Rho (rho) gene>
2159	15171	28175	1.28	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGA-HFEB), and putative chromosome replication protein (gida) genes, complete cds; and termination factor Rho (rho) gene>
3904	19933	29812	1.11	5.0E-01	L39483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3942	19970	29852	3.68	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
5776	18848	31952	0.44	5.0E-01	U30320.1	NT	Spartus aurata gonadotropin-releasing hormone (ebGrRH) precursor mRNA, complete cds
5776	18848	31953	0.44	5.0E-01	U30320.1	NT	Spartus aurata gonadotropin-releasing hormone (ebGrRH) precursor mRNA, complete cds
6936	19965		0.62	5.0E-01	BF576198.1	EST_HUMAN	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE4271939 5'
7029	20055	33288	0.55	5.0E-01	AF042848.1	NT	Homo sapiens EMMPRIN gene, promoter and exon 1
8115	21026	34351	0.73	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8115	21026	34352	0.73	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8371	21275		0.44	5.0E-01	Z71580.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL284c
9094	22023		1.97	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
9228	22156	35509	0.69	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE4043486 3'
9900	21348	34682	3.39	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE4136632 5'
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10151	23042	36441	1.63	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10151	23042	36442	1.63	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10876	23764		0.86	5.0E-01	BE69218.1	EST_HUMAN	601446024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
11066	23850	37386	0.59	5.0E-01	AW845172.1	EST_HUMAN	QV0-CT0010-100689-009 CT0010 Homo sapiens cDNA
12380	25160		4.42	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13028	25568		3.91	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13039	25576		3	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
816	13871	26808	1.95	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1686	14716	27677	1.09	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
4788	17792		0.99	4.9E-01	AW668760.1	EST_HUMAN	EST380866 IMAGE resequences, MAGJ Homo sapiens cDNA
5591	18667	31545	1.38	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6270	19321	32485	2.64	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6270	19321	32486	2.64	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7856	20783	34086	1.65	4.9E-01	AB040051.1	NT	Oryza sativa subsp. Japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
8164	21071	34400	0.7	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
8184	21071	34401	0.7	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9541	22468		2.01	4.9E-01	BF20791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9729	22654	36037	1.17	4.9E-01	AW339905.1	EST_HUMAN	h090c02.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2907268 3' similar to TR:095714
9836	25992		2.07	4.9E-01	10948863	NT	O85714 HERC2.1
10807	23693	37120	1.11	4.9E-01	AF063680.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
11002	23866	37319	0.53	4.9E-01	X60000.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
13020	25942		4.94	4.9E-01	AA613562.1	EST_HUMAN	H.sapiens DNA for BCL7A gene and BCL7A/IGH locus fusion
13029	25559	31738	1.58	4.9E-01	AL163301.2	NT	ng22e11.s1 NCJ_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
4440	17451		0.72	4.8E-01	4504850	NT	Homo sapiens chromosome 21 segment HS21C101 products
4787	17451		0.8	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5697	18770	31698	8.47	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6975	20002	33234	0.75	4.8E-01	U92882.1	NT	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
6985	20012		4.23	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.s1 NCJ_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1217513
7700	20632		2	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
8118	21029	34356	0.88	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
8229	21134	34465	3.51	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8229	21134	34465	3.51	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8484	21415	34752	1.2	4.8E-01	AB20744.1	EST_HUMAN	XJ7710.y5 Soares breast 2NbHBat Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element
9787	22761		1.05	4.8E-01	BE165148.1	EST_HUMAN	MER6 repetitive element.
10513	23400		0.58	4.8E-01	BF568633.1	EST_HUMAN	PM1-HT0350-201299-004-B04 HT0350 Homo sapiens cDNA
11170	24098		2.4	4.8E-01	X83502.1	NT	60218-287F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
12357	25146		1.66	4.8E-01	AL163227.2	NT	S.cerevisiae ORFs from chromosome X
12561	25735		4.16	4.8E-01	AF227565.1	NT	Homo sapiens chromosome 21 segment HS21C027
3123	16174		0.74	4.7E-01	AF192387.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
6793	19826	33039	8.84	4.7E-01	BF217173.1	EST_HUMAN	Felis catus feline leukemia virus subgroup C receptor (FLVGR1) mRNA, complete cds
7392	20091	33325	0.74	4.7E-01	AI204374.1	EST_HUMAN	601883880F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4096387 5'
8446	21378	34719	0.68	4.7E-01	T11414.1	EST_HUMAN	q72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
8446	21378	34720	0.68	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
11282	24203		5.26	4.7E-01	AF102673.1	NT	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
11525	24435	37893	2.11	4.7E-01	U47069.1	NT	Influenza A virus isolate HK51697 hemagglutinin (HA) gene, partial cds
11728	24690	38110	1.4	4.7E-01	BF529658.1	EST_HUMAN	Human collagen alpha2(XI)(COL11A2) gene, exons 6 through 16, and partial cds
11815	24736	38227	1.58	4.7E-01	AW89448.1	EST_HUMAN	602043889F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181303 5'
12463	25210		2.06	4.7E-01	BE887763.1	EST_HUMAN	RC8-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
3806	16837	29723	2.16	4.6E-01	BF693300.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
5604	18680	31557	0.93	4.6E-01	BF315593.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5604	18680	31558	0.93	4.6E-01	BF315593.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5659	18733	31639	3.46	4.6E-01	Q90643	SWISSPROT	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5659	18733	31640	3.46	4.6E-01	Q90643	SWISSPROT	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5737	18810	31904	2.35	4.6E-01	BE734781.1	EST_HUMAN	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5761	18824	31921	2.32	4.6E-01	AL247679.1	EST_HUMAN	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5761	18824	31922	2.32	4.6E-01	AL247679.1	EST_HUMAN	q59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5759	18832	31933	1.62	4.6E-01	P20050	SWISSPROT	TR-O15338 015338 BUTYROPHILIN.
5843	18914		0.66	4.6E-01	AF212124.1	NT	q59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to
5834	19001		0.85	4.6E-01	BE817247.1	EST_HUMAN	TR-O15338 015338 BUTYROPHILIN.
6117	19176	32311	0.46	4.6E-01	D26215.1	NT	MEIOSIS SPECIFIC PROTEIN HOP1
6506	19550	32730	0.95	4.6E-01	AE000894.1	NT	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
							PM0-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
							Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
							Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome

Table 4
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7020	20048	33281	0.49	4.6E-01	AF115340.1	NT	Bacillus subtilis Bbma (bbma) gene, complete cds
7073	20279	33533	1.88	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7073	20279	33534	1.86	4.6E-01	U62332.1	NT	Emricella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7600	25672	33824	0.63	4.6E-01	L07320.1	NT	Marine cytomagalovirus epsilon protein gene, complete cds
8182	21089	34428	0.74	4.6E-01	AA46377.1	EST_HUMAN	h04h05.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8228	21131		0.49	4.6E-01	Q90069	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NPA) (NP)
8300	21204		0.55	4.6E-01	AE004031.1	NT	Xyella fastidiosa, section 177 of 229 of the complete genome
8895	21825	35177	19.05	4.6E-01	BF697389.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
8906	22234	35594	0.51	4.6E-01	AA932237.1	EST_HUMAN	0076008.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9308	22234	35595	0.51	4.6E-01	AA932237.1	EST_HUMAN	0076008.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9841	22746	36128	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9841	22746	36129	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10482	23370	36782	1.64	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10482	23370	36783	1.84	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
11429	24345		2.79	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
11438	24354	37801	5.16	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11438	24354	37802	5.16	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11903	24003	37442	5.82	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11903	24003	37443	5.82	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12209	25043	38546	1.43	4.6E-01	M23080.1	NT	Hordeum vulgare alpha-hordeoflavin (Hbf-1) gene, complete cds
1733	14760		1.89	4.5E-01	BE311420.1	EST_HUMAN	601142103F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505993 5'
1927	14948	27924	1	4.5E-01	AE001931.1	NT	Danio rerio radioluciferase R1 section 68 of 229 of the complete chromosome 1
1927	14948	27925	1	4.5E-01	AE001931.1	NT	Danio rerio radioluciferase R1 section 68 of 229 of the complete chromosome 1
2813	15968	28865	5.96	4.5E-01	AA877086.1	EST_HUMAN	255502.61 Soares_fetal_liver_NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3362	16408	29307	8.69	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3435	16476	29382	1.71	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4112	17136		1.38	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4161	17182	30055	0.89	4.5E-01	A1708908.1	EST_HUMAN	COLLAGEN ALPHA 6(V) CHAIN
4272	18412		4.08	4.5E-01	AW873495.1	EST_HUMAN	as96c09.x1 Barstead acota HPLR88 Homo sapiens cDNA clone IMAGE:2353480 3'
5057	18054	30907	1.33	4.5E-01	BE963445.2	EST_HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5740	18813	31909	1.49	4.5E-01	AW508814.1	EST_HUMAN	501657228R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
6892	18922		1.6	4.5E-01	Q00956	SWISSPROT	QV2-P10012-140100-031-c09 P10012 Homo sapiens cDNA
7813	20742	34046	0.68	4.5E-01	M37036.1	NT	COAT PROTEIN
8053	20968	34281	2.54	4.5E-01	A1858849.1	EST_HUMAN	Rat nuclear proteins B23.1 and B23.2
8882	21812		1.43	4.5E-01	M32681.1	NT	w83e02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2428618 3' similar to TR:Q92923 Q92923
8974	21904	35260	2.98	4.5E-01	A1648593.1	EST_HUMAN	SWISNIF COMPLEX 170 KDA SUBUNIT. ; D.melanogaster Shaw2 protein mRNA, complete cds
							tz56g11.x1 NCI_CGAP_Oy35 Homo sapiens cDNA clone IMAGE:2292844 3'
9122	22050	35410	0.8	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE)
9340	22668		2.07	4.5E-01	11444786	NT	(PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
9551	22478	35837	0.83	4.5E-01	AE000218.1	NT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
10450	23339		1.02	4.5E-01	9630816	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
10973	23857	37284	24.51	4.5E-01	M86006.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10973	23857	37285	24.91	4.5E-01	M86006.1	EST_HUMAN	Bombyx mori nuclear polyhedrosis virus, complete genome
11298	24217	37667	2.63	4.5E-01	AW591271.1	EST_HUMAN	EST02531 Fetal brain, Striatum (cat836208) Homo sapiens cDNA clone HFBCY17
11699	24601		1.43	4.5E-01	AV719382.1	EST_HUMAN	EST02531 Fetal brain, Striatum (cat836208) Homo sapiens cDNA clone HFBCY17
12253	25932		4.79	4.5E-01	BE871481.1	EST_HUMAN	xc714h01.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
12935	25503		5.32	4.5E-01	11422099	NT	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
2050	15087		0.85	4.4E-01	8680303	NT	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'
							601448201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852861 5'
							Homo sapiens testis-specific kinase 2 (TESK2), mRNA
							Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2412	15416	28418	4.14	4.4E-01	P46765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3360	16404	29305	1.59	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3360	16404	29306	1.59	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3364	16408	29309	2.86	4.4E-01	BF056726.1	EST_HUMAN	7f91402.y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3993785 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4334	17348		1.95	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3809393 5'
5605	18681	31559	1.37	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5605	18681	31560	1.37	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5886	18955	32072	1.57	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5904	18973	32091	1.92	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLG Homo sapiens cDNA clone GLCC5C12 5'
6179	19236	32382	1.09	4.4E-01	A1198413.1	EST_HUMAN	q162h11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6179	19236	32383	1.09	4.4E-01	A1198413.1	EST_HUMAN	q162h11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6486	19532	32711	1.6	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:Q95154 Q95154
6585	19623		0.98	4.4E-01	AA776132.1	EST_HUMAN	AFLATOXIN B1-ALDEHYDE REDUCTASE. ;
7796	20725	34027	0.86	4.4E-01	AE000571.1	NT	aa55011.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038
8361	25687		0.64	4.4E-01	AE001188.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN);
8423	21355		13.12	4.4E-01	Z11878.1	NT	Helicobacter pylori 26895 section 49 of 134 of the complete genome
9322	22250	35614	1	4.4E-01	AA056427.1	EST_HUMAN	Treponema pallidum section 4 of 87 of the complete genome
9694	22619	35997	0.78	4.4E-01	AF112540.1	NT	S. tuberculosis mRNA for induced stolon tip protein (partial)
9725	22650	36032	0.68	4.4E-01	AW612578.1	EST_HUMAN	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9830	22735	36118	1.27	4.4E-01	O62836	SWISSPROT	h105c08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2854222 3' similar to
10468	23355	36771	2.12	4.4E-01	A1268680.1	EST_HUMAN	SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
10469	23357		2.33	4.4E-01	P28922	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10599	23485	36914	4.95	4.4E-01	P35590	SWISSPROT	q39099.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
10882	23748	37172	1.99	4.4E-01	S76404.1	NT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10882	23748	37173	1.89	4.4E-01	S76404.1	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
12491	25232	31859	4.51	4.4E-01	AL163282.2	NT	beta-HKA=H.K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12501	25873		15.77	4.4E-01	AF155218.1	NT	beta-HKA=H.K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
434	13505	26429	1.87	4.3E-01	AF155218.1	EST_HUMAN	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
434	13505	26430	1.87	4.3E-01	AF155218.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
1626	14636	27620	1.25	4.3E-01	AW86550.1	EST_HUMAN	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2915	15908		1.02	4.3E-01	AW935288.1	EST_HUMAN	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4249	17265	30132	1.59	4.3E-01	J00306.1	NT	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
4512	13505	26429	1.01	4.3E-01	AF155218.1	NT	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
							Human somatostatin 1 gene and flanks
							Callithrix jacchus MW/LW opsin gene, upstream flanking region

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4512	13505	26430	1.01	4.3E-01	AF16218.1	NT	Calithrix jacchus MW/LW opsin gene, upstream flanking region
5281	18247		1.11	4.3E-01	9635260	NT	Xestia c-nigrum granulovirus, complete genome
5549	18627	31503	0.9	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5549	18627	31504	0.9	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6105	19169	32299	1.15	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-408 HT0638 Homo sapiens cDNA
6125	19184	32319	2.07	4.3E-01	AF179825.1	NT	Salini sciureus olfactory receptor (SSC186) gene, partial cds
7005	20032	33264	4.36	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica ifnG gene
7094	20300	33561	0.66	4.3E-01	AF076629.1	NT	Equus caballus microsatellite LEX027
7191	20191		0.7	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7832	20761		1.55	4.3E-01	BF348001.1	EST_HUMAN	602023134FT NC1 CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4158286 5'
8333	21238		0.44	4.3E-01	M58643.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
8897	21826		3.19	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
9797	22761	38146	1.17	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
10247	29138	38543	1.91	4.3E-01	AW630048.1	EST_HUMAN	h74e10.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
10247	23138	38544	1.91	4.3E-01	AW630048.1	EST_HUMAN	h74e10.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
10723	23609	37039	0.68	4.3E-01	AW170559.1	EST_HUMAN	xn03605.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10891	23875	37304	0.59	4.3E-01	H65292.1	EST_HUMAN	TR:000189 000189 MU-ADAPTIN-RELATED PROTEIN 2. ;
11369	20300	33561	2.26	4.3E-01	AF075829.1	NT	y44505.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208209 3'
12163	24996	38500	1.53	4.3E-01	A1874332.1	EST_HUMAN	Equus caballus microsatellite LEX027
1385	15899	27371	1.38	4.2E-01	Q39102	SWISSPROT	t284004.x1 NC1 CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2283351 3'
3673	16706	29598	6.15	4.2E-01	AE003947.1	NT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3705	16737	29628	1.13	4.2E-01	A1280338.1	EST_HUMAN	Xyella fastidiosa, section 63 of 229 of the complete genome
3774	18411		0.7	4.2E-01	N81203.1	EST_HUMAN	q94401.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876945 3'
4067	17063	29977	1.16	4.2E-01	Q04886	SWISSPROT	7881E1 fetal brain cDNA Homo sapiens cDNA clone 7881E1-K similar to R07879, Z40498
4810	17811	30877	6.24	4.2E-01	AA534083.1	EST_HUMAN	SOX-8 PROTEIN
4894	17853	30759	4.12	4.2E-01	R13487.1	EST_HUMAN	q96h01.s1 NC1 CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:U63600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN DR-1 BETA CHAIN (HUMAN);
5914	18983	32102	1.58	4.2E-01	BF242055.1	EST_HUMAN	y77601.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:28278 5'
5990	19065	32182	1.71	4.2E-01	AW854182.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
6446	19492	32659	1.05	4.2E-01	AL163247.2	NT	RC3-CT0234-060400-029-g04 CT0234 Homo sapiens cDNA
7283	20236	33486	9.31	4.2E-01	AU158472.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
7283	20236	33487	9.31	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7355	25668	33618	2.39	4.2E-01	S82604.1	NT	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
							Brcal1-breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7452	20393	33633	6.45	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
8005	20922	34238	0.47	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8572	21503	34846	3.88	4.2E-01	AW057448.1	EST_HUMAN	EST369413 MAGE sequences; MAGE Homo sapiens cDNA
8572	21503	34847	3.88	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE sequences; MAGE Homo sapiens cDNA
8784	21714	35051	0.58	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
8851	22766	36150	0.53	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
8851	22766	36151	0.53	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
10476	23364		0.66	4.2E-01	AA705007.1	EST_HUMAN	z95601.s1 Soares fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10877	23563	36993	0.55	4.2E-01	AF181854.1	NT	Laesa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10874	23858	37286	1.07	4.2E-01	AW863666.1	EST_HUMAN	MR3-SN0010-280300-103-t07 SN0010 Homo sapiens cDNA
11479	24392	37842	1.93	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11833	24684	38173	2.4	4.2E-01	BE066485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3506085 3'
1121	14163	27100	1.72	4.1E-01	AI905481.1	EST_HUMAN	RC-BT081-210169-142 BT081 Homo sapiens cDNA
1130	14172	27109	1.01	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1130	14172	27110	1.01	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1632	14862	27625	1.02	4.1E-01	AI905849.1	EST_HUMAN	PM-BT103-270489-684 BT103 Homo sapiens cDNA
2760	15751	28747	1.51	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2882	16033	28934	2.77	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2882	16033	28935	2.77	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3347	16393	29294	1.07	4.1E-01	AA906344.1	EST_HUMAN	q94b08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3839	16868	29751	1.67	4.1E-01	AW981292.1	EST_HUMAN	EST373364 MAGE sequences; MAGE Homo sapiens cDNA
3839	16868	29752	1.67	4.1E-01	AW981292.1	EST_HUMAN	EST373364 MAGE sequences; MAGE Homo sapiens cDNA
4373	17387	30251	3.51	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD48 isoC, isoD, isoE, isoF, isoG and isoH genes
4409	17421		0.69	4.1E-01	AA909257.1	EST_HUMAN	cm33d02.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4572	17580	30442	1.03	4.1E-01	AI290232.1	EST_HUMAN	q185a10.x1 Soares NIH-MPp_S1 Homo sapiens cDNA clone IMAGE:1879098 3'
4778	17783	30653	1.49	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF-10 5'
4792	17796	30664	0.97	4.1E-01	AA460067.1	EST_HUMAN	z66607.1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786429 5'
4987	17956	30843	0.95	4.1E-01	BE621909.1	EST_HUMAN	601493807T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895232 3'
5319	18303	31153	0.65	4.1E-01	6895993	NT	Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA
5319	18303	31154	0.65	4.1E-01	6895993	NT	Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA
6220	19275	32429	4.22	4.1E-01	BF081393.1	EST_HUMAN	60215650F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7016	20043	33277	0.68	4.1E-01	U02288.1	NT	Mus musculus NIH 3T3 chemokine rantes (Scys6) gene, complete cds
7836	20784	34067	2.97	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
8387	21291		0.47	4.1E-01	M84594.1	NT	Homo sapiens aromatic decarboxylase gene, exon 4
8813	21544	34885	1.69	4.1E-01	BF574604.1	EST_HUMAN	602133281F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4288238 5'
9638	22562	35932	1.34	4.1E-01	675592.1	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slbpcc-pending), mRNA
10094	22944		0.84	4.1E-01	AF160597.1	NT	Volavio gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for
10756	23842		1.52	4.1E-01	AF139076.2	NT	Campylobacter jejuni NCTC1168 complete genome; segment 3/8
10895	23780	37207	1.13	4.1E-01	AV849579.1	EST_HUMAN	AV849579 GLC Homo sapiens cDNA clone GLOCVD12 3'
10895	23869	37297	0.68	4.1E-01	P18684	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK69)
10895	23869	37298	0.68	4.1E-01	P18684	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK69)
11051	23935		1.01	4.1E-01	BF345382.1	EST_HUMAN	CM2-HT0137-200989-010-e08 HT0137 Homo sapiens cDNA
11277	24189	37651	80.3	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
11830	23865	37400	2.12	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12803	25912		2.53	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
148	15867		3.81	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-280999-012-d10 CT0201 Homo sapiens cDNA
1065	14108	27046	0.97	4.0E-01	8404856	NT	Laqueus rubellus mitochondrial, complete genome
1367	14399	27353	1.49	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmation (dm1) mRNA, complete cds
1503	14534		5.87	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2852	13247	26165	1.48	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recognin (Ubr1), mRNA
3008	16061	28894	1.35	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3008	16061	28895	1.35	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3760	18792	29683	2.47	4.0E-01	AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3901	16930	29808	4.68	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3901	16930	29809	4.68	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4931	17930		11.38	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6130	19189	32325	1.08	4.0E-01	AW070610.1	EST_HUMAN	EST382691 MAGE sequences, MAGK Homo sapiens cDNA
							STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
6706	19742	32944	0.75	4.0E-01	P27285	SWISSPROT	E2 AND E1; 6 KD PEPTIDE]
8507	21438	34778	0.51	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-160900-202-g02 TN0110 Homo sapiens cDNA
8590	21521	34866	1.1	4.0E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9558	22485	35845	1.27	4.0E-01	AA323289.1	EST_HUMAN	EST260688 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
12001	24843		2.28	4.0E-01	BF030262.1	EST_HUMAN	601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
12143	24983		2.52	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12506	26785		1.58	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
1404	14435	27391	1.88	3.9E-01	AF208618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2590	15694	28683	3.5	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2755	15746	28740	6.31	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2755	15746	28741	6.31	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3144	16194	28087	6.19	3.9E-01	AJ225898.1	NT	Shortholobium meliloti egl, syB2, cya3 genes and orf3
4188	17187	30080	1.82	3.9E-01	BF592611.1	EST_HUMAN	7161d01.x1 NCI_CGAP_B16 Homo sapiens cDNA clone IMAGE:3339169 3'
5112	18109	30854	1.59	3.9E-01	BE728607.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:38933699 5'
6157	19215	32355	4.8	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6532	18576	32758	0.56	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8532	21463	34803	1.02	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9420	22348	35713	0.83	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170898-004-b08 CT0105 Homo sapiens cDNA
9428	22356		0.76	3.9E-01	BF348634.1	EST_HUMAN	602019944F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155322 5'
9776	22700	36086	1.93	3.9E-01	AW195898.1	EST_HUMAN	xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O84821
10074	22989	36384	1.68	3.9E-01	AB97337.1	EST_HUMAN	O94821 KIAA0713 PROTEIN;
10390	23279	36700	3.46	3.9E-01	M19879.1	NT	wp76a02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to
10662	23548	36982	0.7	3.9E-01	D89722.1	NT	SW:RFX5 HUMAN P48382 BINDING REGULATORY FACTOR.;
10840	23725	37149	1.14	3.9E-01	BF361856.1	EST_HUMAN	Human clabrin 27 gene, exons 10 and 11, and L1 and Alu repeats
10840	23726	37150	1.14	3.9E-01	BF361856.1	EST_HUMAN	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
11088	23952	37387	0.55	3.9E-01	M18440.1	NT	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
11259	24182		2.64	3.9E-01	AV695974.1	EST_HUMAN	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
12170	25006	38609	1.64	3.9E-01	AV702623.1	EST_HUMAN	Human beta-52-crystallin (B2-1) gene, exon 4, partial cds
12305	25851		3.39	3.9E-01	AF304354.1	NT	Human beta-52-crystallin (B2-1) gene, exon 4, partial cds
12888	25490		1.63	3.9E-01	11433335	NT	AV695974 GKX Homo sapiens cDNA clone GKCBQC11 5'
170	13271		3.69	3.8E-01	7019488	NT	AV702623 ADB Homo sapiens cDNA clone ADBDBE06 5'
528	13597		4.86	3.8E-01	AB029291.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
1893	14814		1.11	3.8E-01	AE003870.1	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
							Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
							Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
							Xylella fastidiosa, section 16 of 229 of the complete genome

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2606	15004	28598	1.22	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2679	15030	28673	5.44	3.8E-01	6878002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3046	16098		22.67	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 08SE-MP1213)
3095	16146	28044	2.06	3.8E-01	AF043383.1	NT	Pleuroctes americanus aminopeptidase N (ampN) gene, partial cds
3542	16580	29483	10.02	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3599	16636		0.69	3.8E-01	AJ807219.1	EST_HUMAN	wf38b12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3614	16638		1.21	3.8E-01	AJ807219.1	EST_HUMAN	wf38b12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3820	16850	29734	1.38	3.8E-01	BE154080.1	EST_HUMAN	PMD-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3890	17017	28906	0.98	3.8E-01	6754085	NT	Mus musculus general transcription factor II I (GTF2), mRNA
5804	18876	31983	1.03	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6596	19637		0.5	3.8E-01	S46825.1	NT	prion protein [mink, Genomic, 2446 nt]
6614	19944	33163	4.65	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
7065	20271	33527	4.54	3.8E-01	AJ374601.1	EST_HUMAN	tas44f11.x1 Scores_total_fetus_Nb2HF9_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
7270	20178	33421	1.15	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7922	20845	34150	4.03	3.8E-01	AA626274.1	EST_HUMAN	zu88c05.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:745064 3'
7939	20861		4.31	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
8189	21096	34427	0.63	3.8E-01	V00683.1	NT	Yeast mitochondrial gene for ATPase (genes oil-2 and oil-4)
9120	22048	35407	3.24	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
9185	22113	35471	0.82	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9376	22304	35665	1.45	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10090	22883		5.51	3.8E-01	T06413.1	EST_HUMAN	ye43h06.r1 Scores_fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains
10190	23081	36482	0.54	3.8E-01	7305518	NT	Alu repetitive element/contains PTR5 repetitive element;
11235	24161		1.72	3.8E-01	AV755814.1	EST_HUMAN	Mus musculus Sp1/PU.1 interaction partner (Sp1), mRNA
11965	24808		3.55	3.8E-01	BE716219.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
12117	24958	38461	2.41	3.8E-01	R42550.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
12117	24958	38462	2.41	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Scores_infant brain 1NIB Homo sapiens cDNA clone IMAGE:30288 3'
12492	25233		2	3.8E-01	AE001124.1	NT	yf92h11.s1 Scores_infant brain 1NIB Homo sapiens cDNA clone IMAGE:30288 3'
12609	25870		1.71	3.8E-01	U94788.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12720	25368		1.88	3.8E-01	BE828256.1	EST_HUMAN	Human p53 (TP53) gene, complete cds
2504	15505	28507	10.48	3.7E-01	AB037831.1	NT	QV3-ET0063-190700-271-e05 ET0063 Homo sapiens cDNA
3521	16559	29461	12.37	3.7E-01	AF056336.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3938	18967	29850	0.64	3.7E-01	AA319482.1	EST_HUMAN	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
							EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4329	17343	30209	12.09	3.7E-01	A1218707.1	EST_HUMAN	ok39cd07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4429	17437	30297	1.66	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT007-080300-104-b02 OT007 Homo sapiens cDNA
4498	17507	30373	2.68	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5971	19037	32158	1.22	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6175	19232	32379	1	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6788	19821	33033	0.96	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6809	19842		0.89	3.7E-01	L10353.1	NT	Mus saxicola heptoglobin mRNA, complete cds
7503	20442	33725	5.21	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7828	20757	34061	0.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3866652 5'
7828	20757	34062	0.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3866652 5'
8263	21168	34502	0.66	3.7E-01	T66802.1	EST_HUMAN	ye50a07.r3 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:06324 5'
8249	21254	34589	0.48	3.7E-01	AW511326.1	EST_HUMAN	hd45d05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2612457 3' similar to contains Alu repetitive element; contains L1.12 L1 repetitive element;
8904	21834	35189	2.31	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8904	21834	35190	2.31	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8937	21867	36225	0.79	3.7E-01	AA902912.1	EST_HUMAN	ok43b11.s1 NCI_CGAP_La12 Homo sapiens cDNA clone IMAGE:1516701 3'
9743	22687		1.87	3.7E-01	AJ271366.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
10688	23552		0.55	3.7E-01	K00891.1	NT	mouse Ig germline alpha membrane exons region
10706	23592	37019	4.2	3.7E-01	A1336411.1	EST_HUMAN	q46b07.x1 Soares_fetal_lung_Nbr-L19W Homo sapiens cDNA clone IMAGE:1950997 3'
11291	24211	37660	1.8	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11471	24384	37832	5.03	3.7E-01	A1297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11471	24384	37833	5.03	3.7E-01	AJ267957.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11898	23898	37436	2.46	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12100	24941	38444	2.93	3.7E-01	D79348.1	EST_HUMAN	HUM230A068 Human aorta polyA+ (Tfujiwara) Homo sapiens cDNA clone GEN-230A06 5'
12126	24967		1.9	3.7E-01	AA973540.1	EST_HUMAN	oo48d03.s1 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1609221 3' similar to gb:M77698 TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12182	25018		3.09	3.7E-01	6977078	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12388	25164		4.15	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12470	25216		1.98	3.7E-01	D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds
12813	25435		2.7	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K076.j1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K076 5'
12876	25475	31762	2.36	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
280	13374	26289	0.75	3.6E-01	AJ008609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1023	14072		6.82	3.6E-01	U89241.1	NT	Human mlbp gene, partial cds
1340	14373	27326	4.1	3.6E-01	T80255.1	EST_HUMAN	yc03e05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1340	14373	27326	4.1	3.6E-01	T80266.1	EST_HUMAN	y03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5'
1932	14953	27929	5.21	3.6E-01	AW590194.1	EST_HUMAN	hg33102.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2947419 3'
1932	14953	27930	5.21	3.6E-01	AW590194.1	EST_HUMAN	hg33102.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2947419 3'
1966	14984	27968	4.68	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2288	15296		1.66	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2413	15417		2.44	3.6E-01	X76725.1	NT	P. Irregularis (P3804) gene for actin
2497	15499	28499	1.31	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2497	16499	28500	1.31	3.6E-01	L05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2510	15511	28514	1.77	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2677	15673	28671	1.69	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE)
2942	18409		10.87	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (suc3) mRNA, complete cds
3530	16568	29471	1.92	3.6E-01	X76758.1	NT	H. sapiens serodinin transporter gene, exons 9 and 10
3530	16568	29472	1.92	3.6E-01	X76758.1	NT	H. sapiens serodinin transporter gene, exons 9 and 10
4514	17523	30388	1.24	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4854	17856	30721	0.8	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
5131	18127	30989	3.83	3.6E-01	AW339383.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872586 3'
5240	18227	31075	0.68	3.6E-01	BE067699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5567	18645	31523	0.75	3.6E-01	AJ008569.1	NT	Homo sapiens lipo gene intron 5
6323	19373	32541	0.92	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6752	19786	32998	1.56	3.6E-01	Y10186.1	NT	Homo sapiens PHEX gene
7508	20447		3.84	3.6E-01	R94080.1	EST_HUMAN	x694h12.x1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:275987 5'
7682	20596	33895	1.47	3.6E-01	AW027174.1	EST_HUMAN	w072c10.x1 Soares thymus_NHFT Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR.O16117
8270	21175	34510	0.47	3.6E-01	AW079100.1	EST_HUMAN	O15117 FYN BINDING PROTEIN. [1];
8802	21732	35081	0.74	3.6E-01	P98167	SWISSPROT	x694h12.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574503 3' similar to contains element
8855	21785	35134	8.06	3.6E-01	AL161583.2	NT	SCO-SPONDIN
						NT	Amblyopsis thalassina DNA chromosome 4, contig fragment No. 79
9530	22457	35819	0.57	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9530	22457	35820	0.57	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
9554	22481	35940	3.22	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9554	22481	35841	3.22	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9734	22659	36042	1.47	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9935	22840	36228	1.05	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9935	22840	36229	1.05	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
10002	22819		0.7	3.6E-01	X62825.1	NT	C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
10377	23266	36888	20.27	3.6E-01	Q53194	SWISSPROT	PROBABILE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
11383	24299	37745	1.94	3.6E-01	BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11550	24459	37922	3.81	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11877	23977	37415	2.68	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12260	23970		4.08	3.6E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
12340	25135		7.58	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12478	25222		3.44	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12819	25439		1.81	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) (Drosophila) homolog), translocated to, 10 (AF10), mRNA
119	13227	26139	1.45	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
222	13321	26237	2.31	3.5E-01	6878033	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
701	13760	26677	4.76	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
748	13805	26730	1.48	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
748	13805	26731	1.48	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
806	13862	26787	3.87	3.5E-01	BF129798.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053851 3'
1642	14673	27638	1.06	3.5E-01	BF310688.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1686	14698	27656	0.95	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2302	15310	28316	0.99	3.5E-01	P06799	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2848	15929	28543	1.14	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Striatogene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
3873	16902		0.91	3.5E-01	AA642138.1	EST_HUMAN	mf60d03.s1 NCJ_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4362	17376	30239	2.6	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5044	18041	30897	4.88	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5328	18312	31161	1.47	3.5E-01	J112094.1	EST_HUMAN	ym11h12.e1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:478113
5517	18596	31444	1.21	3.5E-01	Q86687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5517	18596	31445	1.21	3.5E-01	Q86687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5741	18814	31910	1.31	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6485	19530		1.02	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-e11 SN0012 Homo sapiens cDNA
6673	19710	32805	0.59	3.5E-01	AA431833.1	EST_HUMAN	zw75f03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935
6721	19757	32884	0.64	3.5E-01	U37150.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6958	19987	33211	0.92	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7409	20108		2.9	3.5E-01	X98505.1	NT	S. sacchari mRNA for CD31 protein (PECAM-1)
7971	20893	34205	0.65	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7971	20893	34208	0.55	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8214	21118	34452	0.54	3.5E-01	X06091.1	NT	E. coli L-arabinose transport operon with genes araF, araG and araH
8649	21580		2.72	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8652	21583	34918	0.69	3.5E-01	BF358871.1	EST_HUMAN	RC4-ET0024-280600-014-d07 ET0024 Homo sapiens cDNA
9036	21985		0.79	3.5E-01	AF051561.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9482	22410	35771	1.34	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10256	23146	36554	1.99	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
10398	23287	36709	5.09	3.5E-01	Z28825.1	NT	X. laevis gene for albumin including HPI enhancer
10473	23361	36775	0.89	3.5E-01	BE174794.1	EST_HUMAN	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11175	24102	37548	3.66	3.5E-01	XG1084.1	NT	C. griseus rhodopsin gene for opsin protein
11462	24377	37826	2.05	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11462	24377	37827	2.05	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11953	24797	38297	1.51	3.5E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
12022	24884	38365	1.58	3.5E-01	N77597.1	EST_HUMAN	y250h12.r1 Soares multiple sclerosis_2N5HNSP Homo sapiens cDNA clone IMAGE:290375 5'
12044	24885		1.74	3.5E-01	M82885.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
12109	24950	38453	1.62	3.5E-01	L05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12351	25873		2.69	3.5E-01	AF297468.1	NT	Schistosoma mansoni strain NIMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
12413	26182		4.57	3.5E-01	XG4565.1	NT	B. taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12559	25271		1.93	3.5E-01	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13094	25827	31488	2.82	3.5E-01	H80814.1	EST_HUMAN	ys64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
13094	25827	31487	2.82	3.5E-01	H80814.1	EST_HUMAN	ys64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
730	19788		1.78	3.4E-01	AJ242958.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1002	14051	26995	5.28	3.4E-01	Y07998.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial traA gene
1004	14053	26997	21.9	3.4E-01	AW380120.1	EST_HUMAN	Q13-HT0261-241199-019-g10 HT0261 Homo sapiens cDNA
1354	14386	27339	1.3	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2423	18427	28428	2.47	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3044	16098	28998	0.72	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3044	16096	28999	0.72	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3191	16240	29135	0.98	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3204	16252	29148	7.69	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3392	16435	29338	0.94	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3593	16630	29834	5.01	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3855	16884		1.31	3.4E-01	BF449010.1	EST_HUMAN	Tn94a01.x1 NCL_CGAP_Ovd18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4136	17157		1.62	3.4E-01	AA584196.1	EST_HUMAN	nc11b10.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4614	17622	30485	1.13	3.4E-01	AF16834.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4755	17760	30822	2.1	3.4E-01	BE069812.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4771	17776	30844	1.42	3.4E-01	BF314689.1	EST_HUMAN	601901632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130935 5'
5067	18084		6.1	3.4E-01	AI240673.1	EST_HUMAN	q195cd5.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1667208 3' similar to contains Alu repetitive element
5256	18242		0.66	3.4E-01	AA587031.1	EST_HUMAN	nm73g04.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1089558 3' similar to gb:M68776_mn1 KERATIN, TYPE II CYTOSKELETAL 1 (HUMAN);
5373	18355	31195	1.16	3.4E-01	AW002545.1	EST_HUMAN	wu10d12.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2816687 3' similar to TR:Q13537 Q13537
5882	18951	32067	2.72	3.4E-01	AL161594.2	NT	SIMILAR TO POGO ELEMENT. ;
6022	19084		4.43	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6239	19293		2.27	3.4E-01	L02971.1	NT	zrt12d11.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
6263	19314	32479	0.83	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6346	19398	32562	2.27	3.4E-01	AW204605.1	EST_HUMAN	60157181T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838626 3'
6346	19398	32562	2.27	3.4E-01	AW204605.1	EST_HUMAN	U14JBR1-1e1e-12-0111.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2710682 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6482	18527	32705	1.82	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249.1 761 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:249365 5'
7047	20073		1.3	3.4E-01	N05225.1	EST_HUMAN	z53a12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
					tm63g05.x1 NCJ_CGAP_Bm25	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
7279	20232	33482	1.22	3.4E-01	AI469082.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7413	20112	33346	0.48	3.4E-01	BF678702.1	EST_HUMAN	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
7886	20812	34118	0.41	3.4E-01	BE971689.1	EST_HUMAN	601651613R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934947 3'
8485	21416		0.61	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
	8814	35092	0.77	3.4E-01	Y14930.1	NT	Homo sapiens TORAV28 gene, allele A4, partial
9056	21985		2	3.4E-01	AA337063.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
9128	22054	35414	1.25	3.4E-01	L04690.1	NT	Orcetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9411	22339	35703	1.9	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
9753	22677	36061	4.32	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9753	22677	36062	4.32	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9955	22860		0.63	3.4E-01	AB017610.1	NT	Ephydra fluvialis mRNA for PLC-gamma8, complete cds
9979	21337	34672	5.71	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9979	21337	34673	5.71	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
10218	23109	36510	0.93	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
10401	23290	36713	1.51	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10956	23840		0.74	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
							Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 149) of the complete genome
11455	24371		4.38	3.4E-01	AE000881.1	NT	PROBABLE E4 PROTEIN
11491	24403	37854	3.01	3.4E-01	P06925	SWISSPROT	
11534	24444	37805	2.43	3.4E-01	AF045681.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11729	24631	38111	1.62	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11729	24631	38112	1.62	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11930	24775	38273	2.47	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerol/MUC18, complete cds
11938	24801	38299	3.9	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12192	25027	38528	1.84	3.4E-01	BF061948.1	EST_HUMAN	7k69d12.x1 NCJ_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480646 3'
12242	25068		2.46	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12344	25137		1.49	3.4E-01	Z21621.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
12433	25733		1.82	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
12541	25261		12.67	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12668	25758		3.15	3.4E-01	BE218652.1	EST_HUMAN	h42h08.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12620	25847		2.91	3.4E-01	9838361	NT	PTR5 repetitive element:
12725	25370	31801	1.9	3.4E-01	AJ287131.1	NT	Beta vulgaris mitochondrion, complete genome
12921	26930		1.46	3.4E-01	AJ288948.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
13002	25554						Glossidium cellubryticum partial spoIVB gene and spoOA gene, strain ATCC 35319
13101	25616						Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) Q11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes. >
15	13130	26016	2.08	3.4E-01	AF019413.1	NT	Naegleria gruber mitochondrion, complete genome
109	13130	26016	1.62	3.4E-01	11468174	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
470	13541	26464	5.42	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
656	13718	26620	4.93	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1228	14265	27209	0.93	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1333	14387	27317	2.53	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1628	14658	27621	3.64	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
2428	15432		4.03	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dgtr5), mRNA
2891	16043	28947	1	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS), mRNA
3060	16112		4.56	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Yeo3-12 complete genome
3103	16154	29050	1.96	3.3E-01	Q02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P36)
3554	16592	29497	0.72	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3877	16906	29787	0.99	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3889	16918	29786	1.71	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
4048	17075	29967	2.5	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4087	17112	29980	1.01	3.3E-01	AF161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4389	17403		1.57	3.3E-01	AF200448.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4474	17485		1.92	3.3E-01	4759025	NT	Homo sapiens RAS protein activator like 1 (GAP1 like) (RASAL1) mRNA
4800	17801		1.1	3.3E-01	D31862.1	NT	Rattus norvegicus DNA for regulatory, partial cds
4952	17850	30808	1.79	3.3E-01	AI539114.1	EST_HUMAN	tp78p12.x1 NC1 CGAP_U18 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
			1.4	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3354	18337		0.97	3.3E-01	AF038547.2	NT	Bacillus stearothermophilus beta-1,4-mannanase (manF), esterase (esA), transcription regulator (repA), and alpha-galactosidase (galA) genes, complete cds
5507	18586	31434	2.28	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5507	18586	31435	2.28	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5777	18849	31954	0.97	3.3E-01	P39055	SWISSPROT	DYNAMIN
5777	18849	31955	0.97	3.3E-01	P39055	SWISSPROT	DYNAMIN
6097	19062	32190	0.84	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6171	19228	32373	1.45	3.3E-01	BE618650.1	EST_HUMAN	601472768T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
6171	19228	32374	1.45	3.3E-01	BE618650.1	EST_HUMAN	601472768T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875753 3'
6271	19322	32487	49.51	3.3E-01	P06691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
7101	20307	33568	0.89	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7101	20307	33567	0.89	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7216	20216	33462	4.71	3.3E-01	AI628131.1	EST_HUMAN	ty64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element
7216	20216	33463	4.71	3.3E-01	AI628131.1	EST_HUMAN	ty64h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element
8256	21161	34494	1.95	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
9126	22053	35413	21.18	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
9288	22216	35574	0.62	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9320	22248	35611	0.54	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9320	22248	35612	0.54	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9658	22584	35955	0.88	3.3E-01	Q82925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9917	22905	36293	1.28	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9917	22905	36294	1.28	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
10042	22942	36330	3.15	3.3E-01	N69868.1	EST_HUMAN	za87h01.s1 Soares fetal_lung NBHL19W Homo sapiens cDNA clone IMAGE:297649 3'
10081	22874	36262	2.52	3.3E-01	BF376745.1	EST_HUMAN	IC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10497	23385		1.56	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG-C) gene, exons 1-3, complete cds
11164	24062	37539	2.42	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11164	24062	37540	2.42	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11466	24379		2.27	3.3E-01	BF528469.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
11680	24584	38061	8.39	3.3E-01	BE219351.1	EST_HUMAN	hw51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'

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Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11785	24707	38199	4.62	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
12140	24980		3.98	3.3E-01	AA806821.1	EST_HUMAN	ab71g22.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338860 3'
12159	13130	26016	1.87	3.3E-01	X07590.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
12995	25549		25.89	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-644000 nt. position (277)
479	13550		1.75	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
741	13799		1.34	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
1189	14228	27167	15.88	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1308	14341	27289	2.22	3.2E-01	Z50202.1	NT	P.vulgaris arc5-1 gene
1417	14448	27402	5.67	3.2E-01	Q48924	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1659	14889		0.98	3.2E-01	AF206730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1789	14825	27793	1.19	3.2E-01	Z36041.1	NT	S cerevisiae chromosome II reading frame ORF YBR172c
1808	14834	27804	4.71	3.2E-01	AW957194.1	EST_HUMAN	EST369284 IMAGE resequences, MAGD Homo sapiens cDNA
1808	14834	27805	4.71	3.2E-01	AW957194.1	EST_HUMAN	EST369284 IMAGE resequences, MAGD Homo sapiens cDNA
1868	14890	27870	1.33	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2173	15185	28190	2.66	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111612 5'
2572	15570		2.76	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2759	15750	28746	1.72	3.2E-01	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3671	16704		1.03	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for ankyrin N-acetyltransferase
4501	17511	30377	1.77	3.2E-01	M18618.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4587	17595	30453	0.74	3.2E-01	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4619	17627	30491	1.69	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4850	17852		6.43	3.2E-01	BF633617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
5153	18148	30991	0.94	3.2E-01	BE792748.1	EST_HUMAN	601485591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868789 5'
5454	18535	31377	3.04	3.2E-01	BE173994.1	EST_HUMAN	CMD-HT0569-060300-289-f10 HT0569 Homo sapiens cDNA
6183	19240	32367	1.24	3.2E-01	L27221.1	NT	Glardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6477	19522	32699	0.52	3.2E-01	BE383518.1	EST_HUMAN	601297331F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627462 5'
6477	19522	32700	0.52	3.2E-01	BE383518.1	EST_HUMAN	601297331F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627462 5'
6558	19600	32786	0.76	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P85), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6981	19911	33127	0.67	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FHTA Homo sapiens cDNA clone FHTAABH101 5'
7037	20063		1.44	3.2E-01	AB002399.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8439	21371	34712	0.57	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8750	21680	35023	1.69	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8842	21772	35119	0.56	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat, map NOS-D12W.ox1
8939	21869	35227	15.44	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8942	21872	35232	15.29	3.2E-01	BF311635.1	EST_HUMAN	801897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
9030	21959		1.7	3.2E-01	AL181574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
9087	21998	35349	1.42	3.2E-01	BF248771.1	EST_HUMAN	801855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
9097	21998	35350	1.42	3.2E-01	BF248771.1	EST_HUMAN	801855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
9136	22084	35424	1.47	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
9229	22157	35510	0.85	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9229	22157	35511	0.85	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
9919	22545	35918	0.62	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9925	22551		2.39	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9993	22618	35995	0.82	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9993	22618	35998	0.82	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10499	23387	36797	3.21	3.2E-01	U44914.1	NT	Borrelia burgdorferi plesmid op32-2, erpC and erpD genes, complete cds; and unknown genes
10895	23581	37011	0.69	3.2E-01	BE326230.1	EST_HUMAN	h99f05.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3181599 3'
10800	23588		3.96	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11112	24042	37487	3.28	3.2E-01	T06913.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#936208) Homo sapiens cDNA clone HFBZ21
12365	25872		4.56	3.2E-01	L07288.1	NT	Drosophila melanogaster laritinin A (Lam-A) mRNA, complete cds
12844	25458		3.57	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12934	25716		1.71	3.2E-01	AF157825.1	NT	Bos taurus Inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
12977	25837		1.49	3.2E-01	L36874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
13024	25904	31364	1.48	3.2E-01	BE385776.1	EST_HUMAN	801275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2720	15713	28712	3.72	3.1E-01	R18051.1	EST_HUMAN	ye90h06.r1 Soares fetal liver spleen 'NFLS' Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:U64241 QM PROTEIN (HUMAN);
2748	15862	28733	3.75	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174). mRNA
2748	15862	28734	3.75	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174). mRNA
2900	15954		1.33	3.1E-01	AW829036.1	EST_HUMAN	h146h08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3216	16264		4.39	3.1E-01	AB028089.1	NT	Mus musculus gene for Ser/Thr Kinase KIAMRE, exon 8
3981	17009	28897	0.95	3.1E-01	AJ251886.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5034	18031	30888	0.89	3.1E-01	S68245.1	NT	carbonic anhydrase IV [rats, Sprague-Dawley, lung, mRNA, 1205 nt]
5078	18073	30922	0.66	3.1E-01	AE003984.1	NT	Xylaria fastidiosa, section 130 of 229 of the complete genome
5184	18176	31021	0.95	3.1E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
5666	18740	31649	10.28	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5794	18866	31974	0.87	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN HI1238
5785	18867	31975	0.85	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141W
5806	18878		0.89	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5980	19045	32168	2.26	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6537	26650	32764	0.53	3.1E-01	R94322.1	EST_HUMAN	Y44104.1 Scars fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:188367 5'
6739	19773	32984	1.41	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6812	19846	33055	0.98	3.1E-01	A1284458.1	EST_HUMAN	q39401.x1 NCI CGAP_C88 Homo sapiens cDNA clone IMAGE:1874883 3'
6978	20006	33238	0.82	3.1E-01	X71887.1	NT	H. sapiens gene for Immunoglobulin kappa light chain variable region A8 and A9
7071	20277		1.1	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT0222-281099-005-h05 CT0222 Homo sapiens cDNA
7307	25625	31297	2.34	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
8132	21042	34372	0.71	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8230	21135	34467	0.45	3.1E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naiip6) gene, complete cds, and Naiip3 gene, exons 2-9 and 11-16
8408	21311	34642	0.5	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271089-022-E03 CT0219 Homo sapiens cDNA
8408	21311	34643	0.5	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271089-022-E03 CT0219 Homo sapiens cDNA
9207	22135	35492	0.91	3.1E-01	R46318.1	EST_HUMAN	Y94610.1 st Scars Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35839 3'
10589	23455	36875	1.21	3.1E-01	BF688839.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10589	23455	36876	1.21	3.1E-01	BF688839.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10628	23514	36947	2.28	3.1E-01	A1244001.1	EST_HUMAN	q16161.x1 NCI CGAP_K183 Homo sapiens cDNA clone IMAGE:1863880 3' similar to gb:S55700
							HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10782	23678		0.54	3.1E-01	T55325.1	EST_HUMAN	y647h08.s1 Strata gene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:74387 3' similar to similar to gb:M91036_m22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11384	24300	37746	1.42	3.1E-01	AL021127.2	NT	Mus musculus chromosome X conf1a; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 195
11967	24810	38305	2.2	3.1E-01	7882291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
12508	25242		1.44	3.1E-01	AF304162.1	NT	Sitosterolemia vitreum 40S ribosomal protein S11 mRNA, partial cds
12848	25322		4.24	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12983	25542		4.75	3.1E-01	AF199779.1	NT	Homo sapiens transcription factor GCM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
13011	25900		1.53	3.1E-01	10946823	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrpl-pending), mRNA
75	15840	26100	7.93	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pike), mRNA
273	13368	26284	9.5	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1251	14287	27230	1.77	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.xt NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1627	14558	27518	5.53	3.0E-01	AJ006755.1	NT	Balanoptera physalus gene encoding atrial natriuretic peptide
2150	15162	28164	1.17	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3258	16305		1.65	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 <i>ajpG</i> gene for polyglutamate lyase, complete cds
3454	16495	29399	0.8	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
3933	16981	29844	1.83	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-281199-001-g01 ST0262 Homo sapiens cDNA
4634	17640	30503	2.9	3.0E-01	AJ006755.1	NT	Balanoptera physalus gene encoding atrial natriuretic peptide
4842	17843		1	3.0E-01	AF157835.1	NT	Bacteriophage APSE-1, complete genome
5297	18495	29399	0.75	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
5536	18615	31465	5.08	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3948794 5'
5617	18693	31559	0.48	3.0E-01	AF224668.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5621	18697	31594	0.92	3.0E-01	AF229247.1	NT	Centigalo orthopoxvirus hemagglutinin gene, complete cds
5694	18767	31691	3.73	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5694	18767	31692	3.73	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5731	18804	31898	5.41	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
7144	20252	33504	2.95	3.0E-01	D16313.1	NT	Mouse cyclokeratin 15 gene, complete cds
7182	18454	31324	0.82	3.0E-01	U02389.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7255	20164	33403	1.03	3.0E-01	AF229247.1	NT	Centigalo orthopoxvirus hemagglutinin gene, complete cds
7343	20339	33608	0.55	3.0E-01	X63941.1	NT	S. Cerevisiae GAC1
7480	20420	33699	0.88	3.0E-01	AL63206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7712	20644	33941	5.72	3.0E-01	10947007	NT	Mus musculus midline (Midn-pending), mRNA
7923	20846	34151	2.35	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL9 PspA (pspA) gene, partial cds
8505	21439	34777	1.19	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8945	21875		3.79	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9f), mRNA
9032	21961	35321	0.54	3.0E-01	Z70200.1	NT	H. sapiens gene for U5 snRNP-specific 200kD protein

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Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9045	21974	35332	1.63	3.0E-01	BE56033.1	EST_HUMAN	801339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681694 5'
9388	22316	35878	0.69	3.0E-01	AF141676.1	NT	Streptomyces sulfonfolaciens isopenicillin N synthase (pcbC) gene, partial cds
9429	22357		0.92	3.0E-01	7661685	NT	Homo sapiens DKFZP596M0122 protein (DKFZP596M0122), mRNA
9759	22063	36069	1.14	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
10102	22993	36388	0.61	3.0E-01	P76389	SWISSPROT	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
10474	23362	36776	0.86	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288338 5'
10882	23767	37192	2.27	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BiP, complete cds
12183	25019	38520	2.77	3.0E-01	H61029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:194107 5'
12183	25019	38521	2.77	3.0E-01	H61029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:194107 5'
12522	25247		1.64	3.0E-01	PS4660	SWISSPROT	PONTICULIN PRECURSOR
12762	25857		2.68	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13005	25998		6.68	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
2037	15054	28053	1.52	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2263	15273	28278	1.03	2.9E-01	AF222718.1	NT	Chrysodidymus synurideus mitochondrion, complete genome
3227	16275	29176	1.4	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3268	16343	29246	1.16	2.9E-01	AW764239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3298	16343	29247	1.16	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3966	16994	29878	0.92	2.9E-01	AI610836.1	EST_HUMAN	lp21a11.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
4173	17194		0.71	2.9E-01	AW002902.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element; w02f10.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2490395 3'
4599	17807	30464	1.16	2.9E-01	AA284488.1	EST_HUMAN	z557d12.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element
4803	17811	30470	0.79	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4803	17811	30471	0.79	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
5132	18128	30970	1.1	2.9E-01	7662169	NT	Homo sapiens KIAA0537 gene product (KIAA0537), mRNA
5367	18349		1.11	2.9E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
5439	18521		1.63	2.9E-01	R37485.1	EST_HUMAN	yt7e12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5580	20184	33428	0.82	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5972	19038	32169	5.29	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,29,30 and levanase
5972	19038	32160	5.29	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,29,30 and levanase
5986	19050	32175	4.94	2.9E-01	6679662	NT	Mus musculus Eph receptor A8 (EphA8), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6291	19342	32510	1.3	2.8E-01	AA418145.1	EST_HUMAN	z87b12.r1 Soares_NIHIMPu_S1 Homo sapiens cDNA clone IMAGE:767115'
6533	19577	32759	0.93	2.9E-01	AI797128.1	EST_HUMAN	w827cd5.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1 repetitive element;
6592	19623	32808	2.55	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6728	19764	32971	0.43	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6728	19764	32972	0.43	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7022	20048		0.53	2.9E-01	Z60156.1	NT	D discoideum gene for 34 kD actin binding protein
7184	20184	33428	0.59	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7327	18495	31270	1.57	2.9E-01	AF142328.1	NT	Mus musculus Filin protein (Filin) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7455	20395	33688	2.87	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7521	20460	33746	1.76	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; BING1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1,3-galactosyl tr-
8498	21429	34769	1.78	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8498	21429	34770	1.78	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8728	21658	35004	0.55	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8728	21658	35005	0.55	2.9E-01	AJ237937.1	NT	Bos taurus partial stat5A gene, exons 5-19
8740	21870		1.12	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
9167	22085	35444	0.77	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9481	22409	35770	1.11	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonylea receptor-like protein mRNA, complete cds
9584	22511	35874	0.88	2.9E-01	M22452.1	NT	Bahoon lymphocyte homing/adhesion receptor mRNA, complete cds
9768	22752	36133	0.89	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9788	22752	36134	0.89	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11332	24251	37688	1.76	2.9E-01	AF128943.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11802	24511	37978	2.08	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11802	24511	37979	2.08	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
12013	24855	38355	1.9	2.9E-01	AA935373.1	EST_HUMAN	ny35h02.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
12017	24859	38359	3.68	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
12030	24872	38375	1.53	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12030	24872	38376	1.53	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12704	25359	31796	1.55	2.9E-01	AW005671.1	EST_HUMAN	w28f05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER29 repetitive element;
12785	25414	31787	2.61	2.9E-01	AF092453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12823	25442		1.55	2.9E-01	BE788198.1	EST_HUMAN	601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
580	13658		1.3	2.8E-01	U57136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
595	13662		0.72	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1110	14152	27083	2.47	2.8E-01	AF108050.1	NT	Gulra gulra oocyte maturation factor Mos (c-mos) gene, partial cds
1303	14336	27283	1.41	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1303	14336	27284	1.41	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1317	14350	27298	0.91	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1757	14784	27755	1.69	2.8E-01	AW66020.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
2025	15043	28037	1.41	2.8E-01	ALD47020.1	EST_HUMAN	DKFZp586i2321_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586i2321
2145	15158	28160	1.16	2.8E-01	AW511195.1	EST_HUMAN	Id44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2494	15496	28496	2.51	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2494	15496	28497	2.51	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2578	15577		2.16	2.8E-01	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2714	15708	28703	1.07	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
3011	16063		1.52	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
3012	16084	28967	2.41	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3012	16064	28968	2.41	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3436	16477	29083	0.98	2.8E-01	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
4082	17107	28985	2.65	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4220	17238		0.88	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PAO1, section 11 of 529 of the complete genome
4284	17308		2.98	2.8E-01	AI060868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4568	17574	30437	1.22	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Mage9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4571	17578	30441	3	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L. PROTEIN)
4936	17935	30792	1.11	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 80 (SZNAE12) polyprotein precursor, gene, partial cds
4943	17942	30800	3.99	2.8E-01	AF030194.1	NT	Bovine adenovirus 3 complete genome
4971	17969	30828	1.41	2.8E-01	BF528188.1	EST_HUMAN	602042801F1 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4180129 5'
4994	17993	30850	3.14	2.8E-01	AI272669.1	EST_HUMAN	q159c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
5408	18389	31227	0.91	2.8E-01	AI805266.1	EST_HUMAN	test3c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2087618 3' similar to TR:O60392
5408	18389	31228	0.91	2.8E-01	AI805266.1	EST_HUMAN	test3c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2087618 3' similar to TR:O60392

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5494	25628	31419	23.22	2.8E-01	AA346997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5800	18872	31980	2.93	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
6028	19090		0.85	2.8E-01	AW092583.1	EST_HUMAN	CM7-BN0024-150200-1718-g12 BN0024 Homo sapiens cDNA
6143	19202	32339	0.54	2.8E-01	AA705286.1	EST_HUMAN	ae01d06.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 F(K506-BINDING PROTEIN (HUMAN);
6163	19220		0.61	2.8E-01	AA404576.1	EST_HUMAN	z41f01.r1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6417	25976		0.83	2.8E-01	M36688.1	NT	Bovine 680 bp repeated unit of 1,723 satellite DNA
6462	19507	32682	1.52	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6462	19507	32683	1.52	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
7035	20061	33295	9.12	2.8E-01	BF511215.1	EST_HUMAN	U1-H-B14-act-f-04-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7349	20345	33612	0.83	2.8E-01	U65300.1	NT	Orthogeomys heterodus cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7746	20876	33974	0.47	2.8E-01	BE881455.1	EST_HUMAN	601490157F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3882142 5'
7945	20772		1.02	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
8412	19220		0.53	2.8E-01	AA404576.1	EST_HUMAN	z41f01.r1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
8671	21602	34941	1.53	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCI CGAP_Co8 Homo sapiens cDNA clone IMAGE:1826289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8671	21602	34942	1.53	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCI CGAP_Co8 Homo sapiens cDNA clone IMAGE:1826289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8787	21717	35065	2.55	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
9080	22009	35365	0.83	2.8E-01	AA911629.1	EST_HUMAN	af02h05.s1 NCI CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419893 3' similar to gb:M87789 (G
9151	22079		9.22	2.8E-01	BF347847.1	EST_HUMAN	GAMMA-1 CHAIN C REGION (HUMAN);
9999	22816	36205	1.29	2.8E-01	U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scon-2) gene, complete cds
10233	23124		1.24	2.8E-01	L13654.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
10400	23289	36711	1.44	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10400	23289	36712	1.44	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10457	23345	36762	0.71	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10562	23445	36870	5.21	2.8E-01	7706163	NT	Homo sapiens hypochelical protein (LOC51319), mRNA
10802	23688		1.17	2.8E-01	9626154	NT	Fujinami sarcoma virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11184	24110	37557	2.81	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11184	24110	37558	2.81	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11211	24137	37587	2.98	2.8E-01	BF665970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
11317	24236	37681	2.21	2.8E-01	AF051662.1	NT	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11724	24626		3.63	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273863 5'
12222	25056	38555	2.52	2.8E-01	R22890.1	EST_HUMAN	Yh21H1.1 r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130437 5' similar to contains LTR3 repetitive element ;
12738	25378		12.34	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12834	25449	31776	6.3	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-e07 HT0606 Homo sapiens cDNA
499	13569	26487	4.49	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
636	13697	26602	2.7	2.7E-01	AA450061.1	EST_HUMAN	Z39B10.s1 Soares, total fetus, Nb2HF8, gw Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1288	14321	27267	1.38	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1644	14675		1.92	2.7E-01	X79815.1	NT	G.lambia SR2 gene
1759	14786	27756	2.77	2.7E-01	W58067.1	EST_HUMAN	zd22h10.r1 Soares, fetal, heart, NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1801	14827	27795	1.34	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2149	15917		2.21	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2390	15395	26397	6.89	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT C088P1U (M89), partial
2479	15481	28482	3.93	2.7E-01	AK310858.1	EST_HUMAN	te43c11.x2 NCL CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046636 3' similar to contains element L1 repetitive element ;
2941	15994	28896	1.32	2.7E-01	AF251276.1	NT	Mus musculus serine protease inhibitor 14 (Spi14) mRNA, complete cds
3026	16078		0.81	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3899	18928	29806	0.86	2.7E-01	AJ290443.1	NT	Corynebacterium glutamicum metK gene, ORF1 (partial) and ORF2 (partial)
4097	17122	29999	2.56	2.7E-01	AJ928015.1	EST_HUMAN	wo92e11.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4108	17132	30006	0.78	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4108	17132	30007	0.78	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4113	17136	30010	2.67	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4177	17197	30067	1.06	2.7E-01	AI701406.1	EST_HUMAN	we26f0.5.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342629 3' similar to TR:Q13638 Q13638 ORF2 FUNCTION UNKNOWN ;
5000	17899	30856	3.23	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs68) gene, complete cds
5171	18163		4.27	2.7E-01	AW856131.1	EST_HUMAN	RC1-GT0286-230200-016-e03 GT0286 Homo sapiens cDNA
5191	18183	31026	0.92	2.7E-01	AI827753.1	EST_HUMAN	wf11g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360324 3'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5449	18530	31258	2.42	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4)
5678	18752		1.39	2.7E-01	AB033171.1	NT	Astreporea myrophthalma mitochondrial cyto gene for cytochrome b, partial cds
6599	19640	32820	0.71	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6599	19640	32820	0.71	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6897	19927	33143	1.08	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6897	19927	33144	1.08	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
7086	20292	33552	1.99	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7361	20355	33625	0.5	2.7E-01	U15987.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
7405	20104		0.46	2.7E-01	AF040070.1	EST_HUMAN	td08008.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2076103 3'
7746	20677	33975	0.76	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7994	20912	34227	0.94	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7994	20912	34228	0.94	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
8141	21050	34381	2.24	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8141	21050	34382	2.24	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8203	21109	34439	0.9	2.7E-01	AA351121.1	EST_HUMAN	EST168740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
8203	21109	34440	0.9	2.7E-01	AA351121.1	EST_HUMAN	EST168740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
8283	21188	34528	0.51	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8445	21377	34718	0.71	2.7E-01	AA013147.1	EST_HUMAN	ze35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element
8604	21535		0.63	2.7E-01	AF048820.1	NT	Cerassulus auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8714	21645	34991	0.57	2.7E-01	AW868503.1	EST_HUMAN	MR1-SN0082-100500-002-d09 SN0082 Homo sapiens cDNA
8764	21694	35036	0.64	2.7E-01	R39257.1	EST_HUMAN	yc91f06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8867	21797	35151	0.86	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
9318	22245	35608	0.76	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9578	22505	35869	0.59	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9873	22789	36178	9.77	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)

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9873	22788	36179	9.77	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9875	22790		2.78	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10317	23208	36617	0.8	2.7E-01	D89680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10563	23469	36895	1.14	2.7E-01	AF091848.1	NT	Oryzodagus cuticularis calgranulin C mRNA, partial cds
10618	23504	36938	0.86	2.7E-01	AF097434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10743	23629	37060	1.07	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10743	23629	37061	1.07	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
11010	23894		0.62	2.7E-01	AB011679.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
11251	24175	37622	1.55	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11251	24175	37623	1.55	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11261	24184	37633	3.26	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12987	25545		2.8	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
492	16875	26480	1.46	2.6E-01	P78411	SWISSPROT	IROQUOIS-GLASS HOMEODOMAIN PROTEIN IRX-2
503	13574		1.31	2.6E-01	D76459.1	NT	Bos taurus mRNA for mb-1, complete cds
1420	14451	27405	1.41	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912345 5'
1456	14488	27448	0.9	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1814	14835	27911	4.79	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1814	14835	27912	4.79	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2105	15119		9.35	2.6E-01	AW733152.1	EST_HUMAN	bb04d10.x1 NIH_MGC 14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2167	15179	28185	1.13	2.6E-01	MT1844.1	NT	Human prealbumin gene, complete cds
2877	16976		11.89	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2860043 5'
3841	16977	29575	1.02	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(edentine-N) methyltransferase (dam) gene, complete cds
3711	16743	29633	2.18	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4190	17210	30076	0.71	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4252	17268	30137	17.02	2.6E-01	BE080508.1	EST_HUMAN	QV1-BT0630-040400-132-003 BT0630 Homo sapiens cDNA
4468	17477	30336	1.42	2.6E-01	AF175283.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4611	17619	30481	0.72	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4611	17619	30482	0.72	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds

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4664	17669	30539	1.47	2.6E-01	AA457617.1	EST_HUMAN	ea89d07.r1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4757	17762	30624	1.03	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lha3*) mRNA, complete cds
4828	17829	30697	1.22	2.6E-01	AF142703.1	NT	Ophiostoma radiocosa maturation-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5092	18089	30939	4.99	2.6E-01	H04858.1	EST_HUMAN	y51a05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5258	18244	31085	1	2.6E-01	P08503	SWISSPROT	ACYL-CoA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD)
5525	18604		1.14	2.6E-01	AB035972.1	NT	Paramedium caudatum gene for PAP, complete cds
5634	18710	31610	0.88	2.6E-01	M96060.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds
5763	18838		0.81	2.6E-01	A1862398.1	EST_HUMAN	td16a03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element
5983	19048	32172	0.67	2.6E-01	AF207550.1	NT	MER35 repetitive element ; Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, plm-2 protooncogene homolog plm-2h, and eha-hypo potassium channel genes, complete cds; JM12 protein and transcription factor (GHM enhancer 3 genes, partial cds; and unknown g>
6306	25975		2.34	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
6442	19488	32685	2.01	2.6E-01	A1582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6442	19488	32686	2.01	2.6E-01	A1582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6689	19725	32925	1.01	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 67
6864	19892	33219	0.65	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
6864	19892	33220	0.65	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7389	20382	33651	1.07	2.6E-01	A1914380.1	EST_HUMAN	wd48604.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPH-A-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7787	20716	34019	0.74	2.6E-01	BE148961.1	EST_HUMAN	CM0-HT0248-031189-085-f04 HT0248 Homo sapiens cDNA
7833	25677		1.75	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 416
7875	20802		0.62	2.6E-01	AA196149.1	EST_HUMAN	zp92e01.r1 Striatogene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:627672 5'
8204	21110	34441	1.63	2.6E-01	R10365.1	EST_HUMAN	y37a03.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to
8265	21170	34504	0.5	2.6E-01	Q09855	SWISSPROT	gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8346	21251		0.48	2.6E-01	AF314149.1	NT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C29E8.01 IN CHROMOSOME I
8432	21364	34703	1.41	2.6E-01	R02411.1	EST_HUMAN	Mus musculus telokin mRNA, complete cds
							y682a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'

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8483	21414	34751	1.35	2.0E-01	BE144331.1	EST_HUMAN	MRO-HTT0166-181199-003-d12 HTD166 Homo sapiens cDNA
8719	21650	34986	0.83	2.0E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8719	21650	34987	0.63	2.0E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8909	21839	35194	3.16	2.0E-01	BF343588.1	EST_HUMAN	G02014422F1 NC1 CGAP Bm84 Homo sapiens cDNA clone IMAGE:4150396 5'
8981	21911	35266	2.35	2.0E-01	Q10189	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
9252	22180	35533	4.07	2.0E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9252	22180	35534	4.07	2.0E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
10000	22817	36206	1.09	2.0E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
10259	23149		0.57	2.0E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10381	23270	36692	1.28	2.0E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10381	23270	36693	1.28	2.0E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10887	23573		0.71	2.0E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10987	23871		1.16	2.0E-01	Y10196.1	NT	Homo sapiens PHEX gene
11074	23958		0.56	2.0E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11855	24705	38196	1.81	2.0E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11856	24799		53.33	2.0E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12350	25142		1.61	2.0E-01	10190558	NT	Mus musculus jerky (Jrk), mRNA
12520	25963		3.66	2.0E-01	BE893491.1	EST_HUMAN	G01511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12580	25282	31841	3.08	2.0E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXD2) gene, complete cds, alternatively spliced
12894	25484		1.79	2.0E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12866	25531		1.95	2.0E-01	AE001713.1	NT	Thermoboga maritima section 25 of 136 of the complete genome
13038	25575		2.47	2.0E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
260	13357	26272	2.76	2.0E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
261	13357	26272	1.71	2.0E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
274	13369		3.59	2.0E-01	M28501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
857	13911	26854	1.33	2.0E-01	U09664.1	NT	Mus musculus (CRL/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1087	14131		1.24	2.0E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1148	14190	27129	7.22	2.0E-01	T89837.1	EST_HUMAN	ye11g07.1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1405	14436		0.93	2.0E-01	AB025343.1	NT	Olea europaea OEW mRNA for lipoel synthase, complete cds
1540	14570	27529	1.51	2.0E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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1758	14785		4.13	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2431	15435		9.17	2.5E-01	AE000875.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2518	15519		1.96	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.11 NC1 CGAP GC81 Homo sapiens cDNA clone IMAGE:594862 5'
2683	15677	28676	1.69	2.5E-01	X95310.1	NT	S. tauris mRNA for D-aspartate oxidase
3473	16513		4.87	2.5E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA
3608	16645	28544	8.3	2.5E-01	AL181517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4156	17177		1.54	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4423	17434		0.91	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4728	17733	30595	0.77	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds, and Naip3 gene, exons 2-9 and 11-16
4863	17865		1.6	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4869	17869	30733	4.63	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4895	17894	30760	2.98	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4918	17917		3.27	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4947	17948	30804	0.78	2.5E-01	BE86785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3622600 5'
5178	18170	31015	1.06	2.5E-01	AW873588.1	EST_HUMAN	h62f11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to WP:Y71F9A_294.D CE22858 ;
5242	18229	31078	0.94	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5242	18229	31079	0.94	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5509	18588	31437	10.94	2.5E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6185	19242	32389	0.59	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQ11 gene
6186	19243		0.75	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6649	19888	32880	0.68	2.5E-01	P22219	SWISSPROT	PROTEIN KINASE VPS15
6915	19945	33164	0.89	2.5E-01	AJ251973.1	NT	Homo sapiens partial steern-1 gene
7396	20095	33329	0.71	2.5E-01	8894138	NT	Rattus norvegicus rabn 3 (RABIN3), mRNA
7740	20671	33969	0.81	2.5E-01	U13992.1	NT	Feline calicivirus CF/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds, and unknown gene
7771	20701		1.49	2.5E-01	AF194119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
8037	20952	34267	0.63	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
8085	20997	34317	4.95	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8427	21359	34699	1.71	2.5E-01	BF109040.1	EST_HUMAN	757a03.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3625369 3'
8438	21370	34711	0.79	2.5E-01	BE980712.1	EST_HUMAN	601653391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'

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8804	21734	35083	2.25	2.5E-01	BF038695.1	EST_HUMAN	801469238F1 NIH_MGC 86 Homo sapiens cDNA clone IMAGE:3962809 5'
9195	22123	35479	4.58	2.5E-01	H53236.1	EST_HUMAN	y98407.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:202501 5'
9433	22361	35724	1.03	2.5E-01	M88628.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
10047	22983	36361	22.61	2.5E-01	U89951.2	NT	Homo sapiens matrix metalloproteinase MMP Ras1-1 gene, promoter region
10047	22963	36352	22.51	2.5E-01	U89951.2	NT	Homo sapiens matrix metalloproteinase MMP Ras1-1 gene, promoter region
10101	22950	36339	1.58	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10101	22950	36340	1.58	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10600	23486	36915	1.69	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-e07 S10186 Homo sapiens cDNA
10830	23716	37141	0.62	2.5E-01	11466862	NT	Porphyra purpurea chloroplast, complete genome
11020	23904	37343	1.77	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
11023	23907	37347	1.81	2.5E-01	X58491.1	NT	Mouse L1M LINE DNA
11516	24426	37884	4.42	2.5E-01	ID50314.1	NT	Human mRNA for KIAA0124 gene, partial cds
12075	24916		1.61	2.5E-01	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
12290	25101	38675	6.69	2.5E-01	AF200328.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
12316	25936		4.23	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
575	13043	28550	1.43	2.4E-01	AA093616.1	EST_HUMAN	on70d04.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
873	13926	26874	2.48	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4271678 5'
1330	14364	27312	12.06	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1330	14364	27313	12.06	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1411	14442	27395	1.04	2.4E-01	Y17283.1	NT	Homo sapiens FLJ-1 gene, partial
1873	14898		17.09	2.4E-01	AF267793.1	NT	Mesembryanthemum crystallinum pulvinate potassium channel protein Mkr1p mRNA, complete cds
1918	14939	27916	1.12	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2152	15164	28166	1.03	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2181	15192		1.15	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2279	15288	28296	1.94	2.4E-01	AE000680.1	NT	Aquifex seductus section 12 of 109 of the complete genome
2407	15412	28415	1.44	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2566	15565	28565	1.9	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A;
2612	15801	28800	2.72	2.4E-01	X71783.1	NT	D discoideum (AX3-K) pma gene
2834	15823	28819	4.96	2.4E-01	AF030154.1	NT	S pombe swi6 gene
						NT	Bovine adenovirus 3 complete genome
3177	16227		3.83	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3824	16854	29738	0.87	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5049	18048		1.32	2.4E-01	AL181589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5205	18198	31038	0.67	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5205	18198	31039	0.67	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5848	18722	31627	0.84	2.4E-01	A1925707.1	EST_HUMAN	w033d05.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5848	18722	31628	0.84	2.4E-01	A1925707.1	EST_HUMAN	w033d05.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5873	18747	31868	0.68	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5882	18923	32038	13.04	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5882	18923	32039	13.04	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5880	18949		0.67	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6106	25639		0.88	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (cam2 gene)
6113	19173	32305	2.65	2.4E-01	BF592336.1	EST_HUMAN	7154d04.x1 NCL CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
6215	19270	32423	2.36	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element
6327	19377	32544	2.06	2.4E-01	7661801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6381	19430	32598	1.07	2.4E-01	AV733787.1	EST_HUMAN	Homo sapiens HSPC142 protein (HSPC142), mRNA
6647	19686	32877	0.56	2.4E-01	AA398672.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cDAAD11 5'
6814	19847	33068	3.19	2.4E-01	A1698989.1	EST_HUMAN	z70d02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:7276883 3'
7398	20097	33331	0.47	2.4E-01	AF163863.1	NT	wc62e11.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
7729	20681	33959	10.49	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7927	20849	34155	0.46	2.4E-01	N48732.1	EST_HUMAN	Muscle vision tyrosine aminotransferase gene, complete cds
8185	21092		0.43	2.4E-01	U05013.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guce2) mRNA, complete cds
8187	21094	34425	0.96	2.4E-01	AF229644.1	NT	y55c11.1 Soares_multiple_sclerosis_2NbrMSP Homo sapiens cDNA clone IMAGE:277460 5'
8658	21589	34925	0.56	2.4E-01	X97252.1	NT	Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds
8658	21589	34926	0.56	2.4E-01	X97252.1	NT	Mus musculus DXImx48a protein (DXImx48a) mRNA, complete cds
8776	21706	35051	0.66	2.4E-01	AJ063397.1	NT	M.musculus path gene and promoter
8776	21706	35052	0.66	2.4E-01	AJ063397.1	NT	M.musculus path gene and promoter
8923	21853	35208	1.8	2.4E-01	AJ012585.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
9161	22089	35448	1.27	2.4E-01	BF242794.1	EST_HUMAN	Streptococcus pneumoniae r08 and h08 genes; two component system 08
9679	22602	35975	0.59	2.4E-01	AL139077.2	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
9676	22602	35976	0.59	2.4E-01	AL139077.2	NT	601877679F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4106288 5'
							Campylobacter jejuni NCTC11168 complete genome; segment 4/6
							Campylobacter jejuni NCTC11168 complete genome; segment 4/6

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10092	22885	36269	6.68	2.4E-01	AI693515.1	EST_HUMAN	w443a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
10226	23117	36518	0.68	2.4E-01	AF220087.1	NT	MER22 b1 TAR1 repetitive element;
10228	23117	36519	0.68	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
10919	23804	37231	1.74	2.4E-01	Q03692	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
11208	24132	37580	2.55	2.4E-01	AL181494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11276	24197	37650	2.16	2.4E-01	AF030199.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11615	24523	37981	1.63	2.4E-01	BE286917.1	EST_HUMAN	Mus musculus type 1 sigma receptor gene, complete cds
11615	24523	37992	1.63	2.4E-01	BE286917.1	EST_HUMAN	801176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631843 5'
11647	24553		2.11	2.4E-01	Z21047.1	NT	801176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631843 5'
12373	25747		1.94	2.4E-01	AF004213.1	NT	Parvovirus mosaic virus genomic RNA
13034	25572		5.21	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
410	13483	26403	1.54	2.3E-01	S75898.1	NT	Homo sapiens chromosome 21 segment HS21C081
660	13722		2.97	2.3E-01	U39713.1	NT	aromatase [Psephila guttata=zabara finches, ovary, mRNA, 3188 nt]
690	13751	26666	21.44	2.3E-01	U67598.1	NT	Mycoplasma genitalium, section 35 of 51 of the complete genome
962	14012	26954	3.47	2.3E-01	BE311893.1	EST_HUMAN	Methanococcus jannaschii section 138 of 150 of the complete genome
1630	14660	27620	1.07	2.3E-01	Y10887.2	NT	801142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1656	14686	27649	2.08	2.3E-01	Y10887.2	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
2059	15076		1.73	2.3E-01	AJ235353.1	NT	Mus musculus cdh5 gene, exon 1, partial
2470	15473	28472	1.69	2.3E-01	BE287718.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2700	15984	28668	1.34	2.3E-01	M11319.1	NT	801176562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631015 5'
2872	14445	27369	2.23	2.3E-01	AB015033.1	NT	Human erythropoietin gene, complete cds
3004	16056	28960	1.3	2.3E-01	AA601379.1	EST_HUMAN	Mariellabilla agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
3133	16183		7.86	2.3E-01	R21732.1	EST_HUMAN	no16d06.s1 NCI_OGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu
3428	18469	29378	1.45	2.3E-01	H68836.1	EST_HUMAN	repetitive element; contains element THR repetitive element;
3912	16941	29820	0.99	2.3E-01	S82821.1	NT	y121b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
4011	17038		6.59	2.3E-01	7662133	NT	y121b10.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:213283 5'
4469	17470	30327	0.91	2.3E-01	R82252.1	EST_HUMAN	(GSTA5-glutathione S-transferase Yc2 subunit [5' region, intron 1] (rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3)
4506	17516		2.08	2.3E-01	L78789.1	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4561	17569	30431	1.04	2.3E-01	D90899.1	NT	y1701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148017 5'
4601	17608	30467	2.01	2.3E-01	AF092635.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4669	17674	30544	8.59	2.3E-01	5031984	NT	Synchoecysis sp. POC6803 complete genome, 1/27, 1-133859
							Homo sapiens mitogen-activated protein kinase p38delta (PRKN13) mRNA, complete cds
							Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5179	18171	31016	0.8	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5289	18283	31134	0.89	2.3E-01	BF574804.1	EST_HUMAN	602132210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5'
5487	18567	31413	2.37	2.3E-01	AB040845.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5614	18690	31585	2.08	2.3E-01	BF088381.1	EST_HUMAN	7130606.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV
5720	18793	31885	4.78	2.3E-01	X96887.1	NT	P03330 GAG POLYPEPTIDE [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]. ;
5846	18917	32145	1.14	2.3E-01	L39112.1	NT	C.familiaris rom1 gene
5958	19025	32145	3.24	2.3E-01	S60371.1	NT	Vitellogenin cornu small subunit ribosomal RNA gene
6166	19223	32366	1.86	2.3E-01	AI708840.1	EST_HUMAN	23S rRNA [Leuconostoc carnosum, Genomic, 2895 nt]
6168	19223	32387	1.86	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6849	19978	33201	0.75	2.3E-01	AF198089.1	NT	CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7204	20204	33449	4.52	2.3E-01	AI718148.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
7470	20410	33688	0.85	2.3E-01	8923323	NT	CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7667	20601	33959	0.75	2.3E-01	AF000227.1	NT	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
7818	20745	34050	2.81	2.3E-01	AF175389.1	NT	CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7819	20748	34052	2.15	2.3E-01	AF175389.1	EST_HUMAN	Oryctolagus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for
7819	20748	34053	2.15	2.3E-01	AF175389.1	EST_HUMAN	mitochondrial product
8052	20865	34266	3.54	2.3E-01	6754779	NT	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to contains Alu
8057	20970	34266	1.55	2.3E-01	BE888071.1	EST_HUMAN	repetitive element;
8219	21124	34506	2.88	2.3E-01	N80983.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
8267	21172	34506	0.84	2.3E-01	11416821	NT	Secale cereale omega tectalin gene, complete cds
8267	21172	34507	0.84	2.3E-01	11416821	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
8410	21313	34845	0.55	2.3E-01	AF177946.1	NT	AV719681 GLC Homo sapiens cDNA clone GLCDG808 5'
8434	21366	34706	0.72	2.3E-01	AL161558.2	NT	AV719681 GLC Homo sapiens cDNA clone GLCDG808 5'
8573	21504	34848	1.85	2.3E-01	M68831.1	NT	Mus musculus myosin XV (Myo15), mRNA
9332	22260	35624	0.57	2.3E-01	AW090541.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
9445	22873	35738	0.55	2.3E-01	AW098446.1	EST_HUMAN	2a12a08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:292358 5'
9683	22809	35982	0.83	2.3E-01	AA372184.1	EST_HUMAN	Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
							Homo sapiens protocadherin alpha cluster (LOC63960), mRNA
							Streptomyces coelicolor A3(2) phosphoenolpyruvate carboxylase (ppc) gene, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
							Oxytricha nova macronuclear telodierne-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
							xc90e06.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2691554 3'
							EST376633 IMAGE resequences, MAGH Homo sapiens cDNA
							EST84081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9883	22809	35983	0.63	2.3E-01	AA372164.1	EST_HUMAN	EST184081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (c3b:X63368)
10110	23001	36397	0.74	2.3E-01	6879318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA
10249	23140	36546	0.81	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2068739 5'
10301	23181	36802	0.94	2.3E-01	AW584480.1	EST_HUMAN	EST376633 IMAGE resequences, MAGH Homo sapiens cDNA
10347	23236	36854	1.53	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HindIII restriction-modification system (HindIII methyltransferase (EC 2.1.1.72) and HindIII endonuclease (EC 3.1.21.4))
10380	23269	36891	0.89	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0038-281289-001-404 DT0038 Homo sapiens cDNA
10443	23332	36749	3.13	2.3E-01	BE173060.1	EST_HUMAN	MFR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10498	23386	36796	2.6	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10923	23808	37238	0.95	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10933	23818	37818	6.03	2.3E-01	BF133577.1	EST_HUMAN	601646159R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102082 3'
11453	24369	37810	1.7	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11634	24540	38012	2.07	2.3E-01	AJ250189.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11834	24540	38013	2.07	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11780	24712	38203	3.1	2.3E-01	AE002167.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
12208	25041		1.55	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
12359	25148		3.55	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12436	25194		42.5	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT28M8 Homo sapiens cDNA clone HCOE44 5'
12516	25875	31474	3.19	2.3E-01	AW303623.1	EST_HUMAN	x021d07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q9Z175
12552	25916	31370	0.63	2.3E-01	BE882464.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR8.b2 TAR1 repetitive element;
12597	25293		1.91	2.3E-01	BF663319.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3808689 5'
12645	25321		1.8	2.3E-01	AJ006519.1	NT	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12736	25321		1.6	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12868	25533		1.91	2.3E-01	BF475811.1	EST_HUMAN	Rattus norvegicus mRNA for acid gated ion channel
92	13205	26118	0.78	2.2E-01	AJ052190.1	EST_HUMAN	hac39h12.x1 Lysyl oxidase, nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
1585	14616	27578	2	2.2E-01	AF167850.1	NT	MER38 repetitive element;
2101	15115	28120	2.24	2.2E-01	M34640.1	NT	oz14a10.x1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
2425	15429	28430	5.5	2.2E-01	BF677538.1	EST_HUMAN	TR-Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN 1;
2627	15625	28618	1.92	2.2E-01	BE618258.1	EST_HUMAN	Homo sapiens PPAR delta gene, promoter region
							Fresh-water sponge Emf1 alpha collagen (COLF1) gene
							602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249989 5'
							601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2827	15825	28619	1.92	2.2E-01	BE18258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866180 5'
2924	15977	28875	5.61	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-412 HT0353 Homo sapiens cDNA
2924	15977	28876	5.61	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-412 HT0353 Homo sapiens cDNA
2863	16015		2.07	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3451	16492		3.7	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3816	16846	29731	0.66	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS2(C085
3884	16913		1.11	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4308	17322		1.03	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4316	17330	30194	6.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4363	17377	30240	2.9	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds
4363	17377	30241	2.9	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds
4455	17475	30334	1.18	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4455	17475	30335	1.18	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4939	17938		1.66	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4945	17944	30802	1.72	2.2E-01	AA211216.1	EST_HUMAN	zq87cd5.r1 Stratagene INT neuron (#837233) Homo sapiens cDNA clone IMAGE:848988 5'
5088	18085	30936	1.06	2.2E-01	M86524.1	NT	Human dystrophin gene
5173	18165		1.2	2.2E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
5283	18289	31117	1.18	2.2E-01	H60548.1	EST_HUMAN	y42h09.r1 Soares fetal liver spleen cDNA clone IMAGE:208001 5' similar to
5402	18384	31224	1.59	2.2E-01	5835974	NT	gb:Z14116 .rna1 CD69 GLYCOPROTEIN PRECURSOR (HUMAN);
5403	18385	31225	1.32	2.2E-01	AL163300.2	NT	Vicia cracca mitochondrion, complete genome
5951	19018	32138	1.79	2.2E-01	5803002	NT	Homo sapiens chromosome 21 segment HS21C100
5952	19023		3.45	2.2E-01	D64000.1	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 166, mRNA
6231	19285	32443	0.76	2.2E-01	U67087.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6231	19285	32444	0.76	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
7003	20030	33261	0.59	2.2E-01	AB039490.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
7105	20311	33572	0.45	2.2E-01	AA490108.1	EST_HUMAN	Homo sapiens gene for fukutin, complete cds
7105	20311	33573	0.45	2.2E-01	AA490108.1	EST_HUMAN	ab02e09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839686 3'
7372	20366	33636	8.36	2.2E-01	AV756238.1	EST_HUMAN	ab02e09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839686 3'
7489	20429	33708	1.58	2.2E-01	AF082738.1	NT	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
							Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsa) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7489	20429	33709	1.58	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7671	20605	33903	1.87	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7671	20605	33904	1.87	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7906	20831	34134	0.66	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
8165	21062	34393	0.61	2.2E-01	AF287067.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
8191	21068	34428	0.62	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8599	21530		2.43	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8667	21598	34838	0.75	2.2E-01	Z48933.1	NT	E. coli sepaA and sepaB genes
9115	22043	35399	0.63	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
9439	22367	35728	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9439	22367	35729	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9453	22381	35743	4.92	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
9473	22401	35763	0.6	2.2E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
9573	22600		2.97	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
9659	22685	35958	2.61	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Dera1), mRNA
9740	22684	36049	1.46	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
9828	22735	36117	1.49	2.2E-01	W02988.1	EST_HUMAN	z0408.11 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:291591 5'
9847	22955	36345	17.3	2.2E-01	P49634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9890	22805	36193	0.81	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (klp3)
9901	22889	36273	0.95	2.2E-01	7657423	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9915	22903	36280	4.25	2.2E-01	M89943.1	NT	Brechenia reio epandymin beta and gamma chains (Epd) gene, complete cds
10147	23038	36437	0.68	2.2E-01	Q90980	SWISSPROT	CYCLOC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10331	23220	36634	3.89	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CP-HSP21) mRNA, complete cds; nuclear gene for chloroplast product
10460	23348	36765	2.15	2.2E-01	BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10673	23659	36991	1.18	2.2E-01	9625671	NT	Human herpesvirus 5, complete genome
10857	23743	37166	0.54	2.2E-01	AF068264.1	NT	Pseudomonas aeruginosa quinoxaline ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinone quinone synthesis A (pqoA) genes, complete cds; and pyrroloquinone
10824	23809		0.7	2.2E-01	AF071001.1	NT	Mus musculus PH-R1 (Phr1) gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10988	23852	37277	0.59	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10988	23852	37278	0.59	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11652	24558	38028	1.46	2.2E-01	AB021083.1	NT	TT virus ORF1 gene, isolate TS4-II, partial cds
11854	24704	38195	5.43	2.2E-01	X01818.1	NT	Drosophila 68C glue gene cluster
11893	23993	37432	3.94	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12293	25104		2.1	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
12392	25926						Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12468	25214		4.39	2.2E-01	U82871.2	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12567	18428	31352	3.91	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12618	25305	31815	1.89	2.2E-01	11428873	NT	Homo sapiens zinc finger protein 220 (ZNF220), mRNA
13042	25921		2.38	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAH802 5'
997	14047	26891	1.65	2.1E-01	AA889289.1	EST_HUMAN	nm31e11.s1 NCI CGAP Lip2 Homo sapiens cDNA clone IMAGE:1061804
1000	14049	26993	1.18	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1151	14192		2.58	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1226	14263	27205	1.16	2.1E-01	6764299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1226	14263	27206	1.16	2.1E-01	6764299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1531	14561	27521	1.32	2.1E-01	AJ248995.1	NT	Mus musculus mas proto-oncogene and Ig12r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1830	14851	27927	1.7	2.1E-01	AA908824.1	EST_HUMAN	oK73502.s1 NCI CGAP_G04 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2170	15182	28188	2.31	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2503	15925	28505	1.01	2.1E-01	H73988.1	EST_HUMAN	602083128F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2503	15925	28506	1.01	2.1E-01	H73988.1	EST_HUMAN	yu0407.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2596	15594	28578	0.96	2.1E-01	AF022814.1	NT	yu0407.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:232837 3'
2967	16019	28916	2.34	2.1E-01	6912445	NT	Fugu rubripes transcription factor (SLP-1) and heme-oxygenase genes, complete cds
3874	16903		7.46	2.1E-01	9838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
4199	17160	30036	1.04	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
4199	17160	30037	1.04	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4348	17362		1.11	2.1E-01	AF124526.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4483	17494		1.74	2.1E-01	AB033041.1	NT	Oroshia cavinana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4691	17696	30562	2.64	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
							Homo sapiens pshsp47 gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4748	17751	30809	0.66	2.1E-01	X93161.1	NT	P.falciparum mRNA for small GTPase rab11
5156	18149	30895	1.7	2.1E-01	D13567.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
5395	18377	31219	1.12	2.1E-01	4557484	NT	Homo sapiens ceruloplasmin (ferroxidase) (CP) mRNA
5414	18395	31232	0.76	2.1E-01	BE157836.1	EST_HUMAN	MR2-HT0377-070100-011-g08 HT0377 Homo sapiens cDNA
5484	18565	31408	6.2	2.1E-01	BF072895.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
7214	20214	33461	1.1	2.1E-01	AJ223392.1	NT	Doto fragilis mitochondrial 16S rRNA gene, partial
7226	20135	33376	2.05	2.1E-01	U04842.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7805	20734	34038	0.67	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7806	20734	34037	0.67	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7818	20747		2.13	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
8165	21072	34402	1.76	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT19) gene, complete cds
8218	21123	34455	1.3	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8218	21123	34456	1.3	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8285	21189		0.45	2.1E-01	T87354.1	EST_HUMAN	YCB3501.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114793 5'
8650	21581		1.26	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b), mRNA
							Haemophilus influenzae hmcD, putative haemodin processing protein (hmcC), putative ABC transporter (hmcB), putative haemodin structural protein (hmcA), and haemodin immunity protein (hmcI) genes, complete cds
9069	21998	35352	3.85	2.1E-01	U68399.1	NT	DKFZp434H0814.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0814 5'
9355	22283	35044	0.94	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0814 5'
9355	22283	35045	0.94	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0814 5'
9589	22515	35877	6.8	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YEL025w
10035	22835	36323	0.7	2.1E-01	N42538.1	EST_HUMAN	Y11e10.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270854 5'
10035	22835	36324	0.7	2.1E-01	N42538.1	EST_HUMAN	Y11e10.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270854 5'
10044	22960	36348	2.89	2.1E-01	X97378.1	NT	A.thaliana mRNA for AFRABP1b protein
10144	23035	36433	0.97	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10818	23704	37132	1.48	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10846	23732	37155	2.12	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10853	23739	37162	0.84	2.1E-01	BF574264.1	EST_HUMAN	(80 KD) DIACYLGLYCEROL KINASE
11918	24765		1.7	2.1E-01	A141875.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11896	24838		2.83	2.1E-01	11036647	NT	qa6508.x1 Soares_fetal heart NbH19W Homo sapiens cDNA clone IMAGE:1691751 3'
12011	24853	36354	2.01	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
							RC3-HT0622-040500-013-511 HT0622 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12230	25524		2.08	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12713	26364		1.45	2.1E-01	AF217490.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12956	26517		1.97	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916675 5'
13067	26593	31725	1.51	2.1E-01	BE672330.1	EST_HUMAN	7a59e02.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3223034 3'
213	13312	26230	1.93	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
557	13626		2.34	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
723	13781	26703	0.89	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VH42
836	13891	26828	1.97	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1039	14085	27024	0.79	2.0E-01	D90905.1	NT	Synechocystis sp. POC8803 complete genome, 7/27, 781 449-920915
1152	14193	27131	2.56	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1282	14315	27264	1.45	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1334	14368	27318	1.4	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1479	14510		1.16	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1505	14538	27499	9.31	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1574	14604	27564	1.95	2.0E-01	AB007974.1	NT	Homo sapiens tRNA, chromosome 1 specific transcript KIA0505
1578	14609	27670	1.13	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1723	14751	27719	1.33	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1748	14773		1.69	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1782	14808		2.69	2.0E-01	U67625.1	NT	Methanococcus jannaschii section 87 of 150 of the complete genome
2370	15376		1.69	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2932	15985		1.05	2.0E-01	AF074890.1	NT	Homo sapiens full length insert cDNA YH85A11
3546	16584	29489	0.86	2.0E-01	P46807	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3628	16884		1.19	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI_CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3770	16802	29689	0.84	2.0E-01	P34641	SWISSPROT	MER21 repetitive element;
4038	17065	29955	0.98	2.0E-01	Z49909.1	NT	GED-11 PROTEIN
4114	17137	30011	0.85	2.0E-01	X83997.1	NT	Sus scrofa
4536	17547	30408	0.66	2.0E-01	AF242431.1	NT	C.parasitica capC gene
4681	17686		7.99	2.0E-01	BE826165.1	EST_HUMAN	Mus musculus neuronal apoptosis inhibitory protein 6 (Nalpe6) gene, complete cds; and Nalpe3 gene, exons 2-6 and 11-18
5154	18147	30992	0.81	2.0E-01	AA861824.1	EST_HUMAN	QV4-EN0032-180500-223-c03 EN0032 Homo sapiens cDNA
5154	18147	30993	0.81	2.0E-01	AA861824.1	EST_HUMAN	ak35h08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407995 3'
6170	18162	31010	8.09	2.0E-01	8922080	NT	ak35h08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407995 3'
							Homo sapiens hypothetical protein ASH1 (ASH1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5201	16584	29489	0.66	2.0E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5244	18231	31081	0.95	2.0E-01	Y18218.1	NT	Homo sapiens putative psihbD pseudogene for hair keratin, exons 1 to 9
5358	18341		1.34	2.0E-01	A1274530.1	EST_HUMAN	q10-02.x1 NCI_OGAP_K48 Homo sapiens cDNA clone IMAGE:1981178 3' similar to gb:M16967
5630	18706	31605	2.4	2.0E-01	X56600.1	NT	COAGULATION FACTOR V PRECURSOR (HUMAN);
5944	19011	32130	2.06	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
6054	19116	32245	0.78	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6295	19346	32514	6.16	2.0E-01	U16300.1	NT	F. rubripes DNA encoding for vav-1-RNA synthetase
6415	19463		0.61	2.0E-01	M75967.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
6536	19581	32765	0.59	2.0E-01	P02467	SWISSPROT	Human hepatocyte growth factor gene, exon 1
6697	19733	32834	4.07	2.0E-01	X61033.1	NT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6808	19841	33052	3.82	2.0E-01	AW360885.1	EST_HUMAN	Mauratus mu class diathione transferase gene
7565	20502	33791	0.54	2.0E-01	U39724.1	NT	PM1-C10247-141099-001-g08 CT0247 Homo sapiens cDNA
7674	20608	33907	1.19	2.0E-01	AF250371.1	NT	Mycoplasma genitalium section 46 of 51 of the complete genome
7849	20776	34077	0.77	2.0E-01	P54422	SWISSPROT	Mus musculus phosphofructokinase-1 C isozyme (Pfkfb) gene, exons 3 through 7
8248	21153	34488	0.64	2.0E-01	V00726.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8369	21273	34606	5.19	2.0E-01	AK024427.1	NT	Mouse germ line gene coding for beta-globin (Y2)
8531	21462		7.24	2.0E-01	AF028026.1	NT	Homo sapiens mRNA for FLJ00016 protein, partial cds
8779	21709	35055	3.52	2.0E-01	X91151.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
9889	22804	36192	1.26	2.0E-01	U82511.1	NT	M. musculus scp2 gene exon 14
9927	22832	36219	0.69	2.0E-01	U71122.1	NT	Dictyostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds
10085	22878		5.64	2.0E-01	AE001278.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
10266	23166	36568	0.53	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
10403	23292		2.26	2.0E-01	AF146992.1	NT	DAUGHTERLESS PROTEIN
10544	23430	36851	2.07	2.0E-01	AF086907.1	SWISSPROT	DAUGHTERLESS PROTEIN
10544	23430	36851	2.07	2.0E-01	AF086907.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
10664	23550	36983	0.8	2.0E-01	AF157814.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10664	23550	36984	0.8	2.0E-01	AF157814.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10710	23596		0.65	2.0E-01	X78388.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10890	23775	37201	1.03	2.0E-01	X97121.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
11278	24200	37652	2.76	2.0E-01	D88088.1	NT	D. melanogaster DNA mobile element (hoppe)
11278	24200	37653	2.76	2.0E-01	D88088.1	NT	R. norvegicus mRNA for NTR2 receptor
							Salvelinus pluvius mRNA for transferrin, complete cds
							Salvelinus pluvius mRNA for transferrin, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12213	25047		1.44	2.0E-01	P24873	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6
12223	25057	38556	45.65	2.0E-01	AA559191.1	EST_HUMAN	nl68c12.s1 NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1045846 similar to gb.M81105 MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (HUMAN);
12691	26349		1.92	2.0E-01	AF206637.2	NT	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12872	25773		1.86	2.0E-01	AF302773.1	NT	Homo sapiens nifedipine-Lm isoform (nifedipine) mRNA, complete cds
12885	25704	31661	2.56	2.0E-01	AW975297.1	EST_HUMAN	EST387405 IMAGE resequences, MAGN Homo sapiens cDNA
12920	26530	31748	3.46	2.0E-01	AI023692.1	EST_HUMAN	ov80a10.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12941	25508		15.98	2.0E-01	AF078184.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
114	13222		5.83	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
372	13459	26374	5.6	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
679	13741	26655	1.15	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
679	13741	26656	1.15	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
686	13748	26663	4.55	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
687	13748	26663	6.39	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo sapiens cDNA
1013	14052		3.84	1.9E-01	7305180	NT	Mus musculus Interleukin 2 receptor, gamma chain (Il2rg), mRNA
1131	14173	27111	5.97	1.9E-01	AA353813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1397	14428	27382	1.72	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1455	14487		3.57	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rpb-2) gene, complete cds
2404	15409	28412	6.5	1.9E-01	8922633	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2965	16017	28914	4.62	1.9E-01	U68068.1	NT	Sigmoidon hispidus p83 gene, partial cds
2980	16031		8.17	1.9E-01	J00922.1	NT	Galus gallus ovalbumin (Y) gene, complete cds
3045	16097	29000	0.97	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
							Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
3441	16462	29390	0.82	1.9E-01	5803065	NT	
3455	16496	29400	8.52	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3539	16577	29481	6.95	1.9E-01	R19467.1	EST_HUMAN	J42F10.r1 Soares fetal liver spleen 1NFILS Homo sapiens cDNA clone IMAGE:129547 5'
3872	16901	29784	0.75	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4078	17104	29983	4.85	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4171	17192	30064	2.05	1.9E-01	AW754108.1	EST_HUMAN	GM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4231	17247		0.98	1.9E-01	AE001912.1	NT	Deinoceratus radiodurans R1 section 49 of 229 of the complete chromosome 1
4331	17345	30210	1.12	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA
4581	17589	30450	0.76	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4885	17884	30750	0.84	1.9E-01	Z69780.1	NT	Fugu rubripes genes encoding carbanoyl phosphate synthetase III, myosin light chain, MAP2
5134	18130		1.22	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5798	18870		4.81	1.9E-01	AW130149.1	EST_HUMAN	x129a07.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2819444 3' similar to gb:M73779 RETINOIC
5841	18912	32028	6.81	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
6053	19115	32244	0.63	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
6102	19163		2.78	1.9E-01	AU133116.1	EST_HUMAN	Mus musculus Wrm protein (Wrm) gene, complete cds
6187	19244		0.54	1.9E-01	AE001299.1	NT	AU133118 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6584	19625	32809	0.94	1.9E-01	A762391.1	EST_HUMAN	Chlamydia trachomatis section 26 of 87 of the complete genome
6651	19690	32883	0.88	1.9E-01	AW148452.1	EST_HUMAN	wf54h02.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394099 3'
7311	18479	31302	1.77	1.9E-01	R43212.1	EST_HUMAN	x14c08.x1 NCL CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP
7315	18483	31307	0.57	1.9E-01	X68216.1	NT	SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7341	20337	33602	0.83	1.9E-01	AF034920.1	NT	yg08a12.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31863 3' similar to contains MER13
7341	20337	33603	0.83	1.9E-01	AF034920.1	NT	P. sativum PS-IAA4/5 gene
7633	20568	33863	0.59	1.9E-01	U73846.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7888	20814	34120	0.54	1.9E-01	U93688.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7913	20837	34140	1.13	1.9E-01	U80922.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7986	20888	34188	2.71	1.9E-01	AF072724.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tst), enterotoxin (ent), and integrase (int) genes, complete cds
8565	21496	34839	1.72	1.9E-01	AL161657.2	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPPB) gene, complete cds
9244	22172	35526	13.86	1.9E-01	AB033024.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
9500	22428	35790	1.56	1.9E-01	M14568.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9500	22428	35791	1.56	1.9E-01	M14568.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
10387	23278	36697	0.93	1.9E-01	AA912486.1	EST_HUMAN	Marasupial cat beta-globin gene mRNA, partial cds
10736	23622	37053	0.91	1.9E-01	BE830353.1	EST_HUMAN	Marasupial cat beta-globin gene mRNA, partial cds
10736	23622	37054	0.91	1.9E-01	BE830353.1	EST_HUMAN	oB9g10.s1 NCL CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu
11088	24020	37481	2	1.9E-01	AL161503.2	NT	repetitive element;
11088	24020	37462	2	1.9E-01	AL161503.2	NT	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
11196	24121	37567	2.99	1.9E-01	AF223391.1	NT	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
11936	24780	38276	1.55	1.9E-01	M22253.1	NT	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
12147	24987	38488	2.14	1.9E-01	AJ243213.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
12169	25005	38508	1.58	1.9E-01	L07344.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							Rattus norvegicus sodium channel 1 mRNA, complete cds
							Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
							Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
33	13149	28038	2.65	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
279	15871	26288	1.29	1.8E-01	AB022090.1	NT	Mus musculus Ccig gene for chaperonin containing TCP-1 gamma subunit, partial cds
391	13475	28895	1.58	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
770	13827	26768	0.81	1.8E-01	AB021480.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1009	14098	27000	0.8	1.8E-01	AB12212.1	EST_HUMAN	wb71f02.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1118	14159	27097	1.46	1.8E-01	AF000580.1	NT	Dicotyledon discoidium plasmid Ddp5, complete genome
1315	14348	27295	7.91	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1889	14910		1.15	1.8E-01	AI733708.1	EST_HUMAN	qg2d10.x5 NC1 CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;
1931	14962	27928	1.64	1.8E-01	AB061897.1	NT	Mus musculus Scya6, Scya9, Scya18-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2742	15735		2.61	1.8E-01	AW935723.1	EST_HUMAN	QV3-DT0018-087299-038-g04 DT0018 Homo sapiens cDNA
2940	15993		1.88	1.8E-01	AF184589.1	NT	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds
2947	15999	28901	1.18	1.8E-01	AW182300.1	EST_HUMAN	x41a03.x1 Soares NFL T_GBC S1 Homo sapiens cDNA clone IMAGE:2659759 3'
3169	16219	29109	1.07	1.8E-01	AW995178.1	EST_HUMAN	QVQ-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3423	16464	29371	0.89	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3687	16720	29812	0.86	1.8E-01	H03389.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3687	16720	29812	0.86	1.8E-01	H03389.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4345	17359	30224	1.01	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4441	17462		0.99	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DOB), complete cds
4671	17675	30545	6.57	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4886	17885	30751	2.43	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya18-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5177	18169	31014	1.77	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-157299-112-g06 ST0203 Homo sapiens cDNA
5230	18213	31065	1.04	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5259	18245	31096	1.16	1.8E-01	AI439881.1	EST_HUMAN	ti57e04.x1 NC1 CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2194590 3'
5324	18308	31158	0.71	1.8E-01	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
5481	18562	31406	0.56	1.8E-01	BE082626.1	EST_HUMAN	RC6-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA
6019	18931	32207	1.05	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90

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6149	19209	32347	0.88	1.8E-01	N28629.1	EST_HUMAN	y38108.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:284063 5'
6388	19417	32582	1.05	1.8E-01	6678428	NT	Mus musculus Trnf receptor-associated factor 8 (Traf8), mRNA
6398	19417	32583	1.05	1.8E-01	6678428	NT	Mus musculus Trnf receptor-associated factor 8 (Traf8), mRNA
6790	19823	33035	1.39	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6839	19871		2.26	1.8E-01	N04853.1	EST_HUMAN	y62102.r1 Soares_multiple_sclerosis_2NblmSP Homo sapiens cDNA clone IMAGE:278163 5'
7186	20186		0.48	1.8E-01	11430157	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
7350	20346	33613	1.04	1.8E-01	AB018661.1	NT	Citullus lanatus mRNA for vsus, complete cds
7350	20346	33614	1.04	1.8E-01	AB018661.1	NT	Citullus lanatus mRNA for vsus, complete cds
7410	20109	33343	0.67	1.8E-01	BE961363.1	EST_HUMAN	601648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
7850	20777	34078	0.87	1.8E-01	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
9881	22793	36182	1.18	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9913	22901	36288	1.76	1.8E-01	9628232	NT	Bacteriophage Iike, complete genome
10024	22924		0.63	1.8E-01	AA493751.1	EST_HUMAN	rh02a05.01 NCL_CGAP_Thyl Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1 repetitive element;
10103	22994	36389	1.07	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
10103	22994	36390	1.07	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
10141	23032	36428	0.98	1.8E-01	M26019.1	NT	S.commune orotidine-5-phosphate decarboxylase (URA1) gene, complete cds
10141	23032	36429	0.98	1.8E-01	M26019.1	NT	S.commune orotidine-5-phosphate decarboxylase (URA1) gene, complete cds
10298	23189	36699	0.76	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10302	23192	36603	0.76	1.8E-01	U07548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10632	23518		0.84	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10855	23741	37164	1.52	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
11082	24014	37456	3.41	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
11121	24051	37496	5.92	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysis genes, complete cds
11177	20346	33613	3.11	1.8E-01	AB018661.1	NT	Citullus lanatus mRNA for vsus, complete cds
11177	20346	33614	3.11	1.8E-01	AB018661.1	NT	Citullus lanatus mRNA for vsus, complete cds
11178	24104	37551	5.51	1.8E-01	AF010107.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
11457	24372	37820	3.47	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11894	23994	37433	3.87	1.8E-01	X57033.1	NT	B. taurus mRNA for potassium channel
12178	25014	38519	2.19	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
12322	25123		2.09	1.8E-01	10085561	NT	Bovine ephemeral fever virus, complete genome
12804	25428		4.9	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12912	25495		20.38	1.8E-01	R24494.1	EST_HUMAN	Y44810.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12951	25514		2.7	1.8E-01	Y11114.1	NT	E-dispar mRNA for hexokinase (hbk1)
589	13656	26568	2.03	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615788 5'
831	13886	26824	2.18	1.7E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
987	14038		1.61	1.7E-01	P35516	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1085	14129	27066	0.82	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1085	14129	27067	0.82	1.7E-01	AF081810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1839	14882	27844	0.92	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
1898	15018		2.77	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2902	15956	28855	2.06	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL VIBCO gene, partial cds
2902	15956	28856	2.06	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL VIBCO gene, partial cds
2969	16021	28919	1.83	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3040	16092	28994	1.2	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3040	16092	28995	1.2	1.7E-01	AJ238736.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3152	16202	29093	2.18	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3422	16493	29370	0.78	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3507	16545	29445	2.08	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3672	16705	29697	1.11	1.7E-01	AJ224877.1	NT	Homo sapiens hsp1 gene, complete CDS
3692	16725		1.11	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
4015	17042	29932	6.68	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4675	17690		1.86	1.7E-01	X62938.1	NT	Schistosoma gregaria alpha repetitive DNA
4953	17951	30809	1.75	1.7E-01	AJ247635.1	EST_HUMAN	q157409.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element;
5288	18282	31132	1.57	1.7E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
5288	18282	31133	1.57	1.7E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
5313	18297	31150	0.7	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827187 5'
5593	18639	31547	1.9	1.7E-01	AA470686.1	EST_HUMAN	net13802.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:381066 3' similar to gb:M17888 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							net13a02.s1 NCLCGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17889 60S
5593	18889	31548	1.9	1.7E-01	AA470886.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5787	18859	31967	0.75	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6686	19627	32810	16.24	1.7E-01	H72118.1	EST_HUMAN	ysd2g06.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:213658 3'
6615	19658		0.49	1.7E-01	AJ235270.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4
6650	19689	32881	0.69	1.7E-01	AJ370876.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6650	19689	32882	0.69	1.7E-01	AJ370876.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
7172	18444	31313	0.61	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
7206	20208		2.1	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OV) gene, complete cds
7344	20340		0.63	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7589	20525	33814	1.46	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7677	20611	33910	10.88	1.7E-01	BE734179.1	EST_HUMAN	601556022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7900	20826	34130	1.25	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLFO PROTEIN)
7918	25679	34144	0.88	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
8341	21246	34580	0.41	1.7E-01	BF326962.1	EST_HUMAN	QV3-BN0047-020800-284-d08 BN0047 Homo sapiens cDNA
8341	21246	34581	0.41	1.7E-01	BF326962.1	EST_HUMAN	QV3-BN0047-020800-284-d08 BN0047 Homo sapiens cDNA
8367	21271	34605	0.44	1.7E-01	AL114556.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8443	21375	34715	1.47	1.7E-01	AF000573.1	NT	Homo sapiens homogenilase 1,2-dioxygenase gene, complete cds
8541	21472	34813	0.84	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8853	21783	35130	6.01	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8853	21783	35131	6.01	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9255	22183	35538	0.54	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-01-a10 BN0032 Homo sapiens cDNA
9287	22215	35573	2.31	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9403	22331	35693	1	1.7E-01	AF217413.1	NT	Homo sapiens neurotrophin 3 isoform gene, complete cds, alternatively spliced
9403	22331	35694	1	1.7E-01	AF217413.1	NT	Homo sapiens neurotrophin 3 isoform gene, complete cds, alternatively spliced
9549	22476	35834	0.56	1.7E-01	R77002.1	EST_HUMAN	y66g02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144242 5'
10118	23009	36405	10.51	1.7E-01	AP001508.1	NT	Bacillus helveticus genomic DNA, section 2/14
10220	23111	36512	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 MAGe resequences, MAGO Homo sapiens cDNA
10220	23111	36513	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 MAGe resequences, MAGO Homo sapiens cDNA
10237	23128	36531	2.6	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
10324	23213	36625	0.92	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10728	23814		2.47	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10880	23765	37190	1.28	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10881	23766	37181	1.66	1.7E-01	AA827872.1	EST_HUMAN	ng60a07.s1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081 TRANSFORMING PROTEIN RHOC (HUMAN);
11123	24053	37486	7.92	1.7E-01	BE390835.1	EST_HUMAN	601286547c1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11245	24189	37816	2.42	1.7E-01	AA814617.1	EST_HUMAN	af49a03.s1 NCL CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
11552	24461	37924	9.7	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11552	24461	37925	8.7	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11636	24542	38016	2.25	1.7E-01	Y08391.1	NT	S.pombe pop1+ gene
11814	24735	38228	2.11	1.7E-01	AA883375.1	EST_HUMAN	ak45f09.s1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
12134	24975		1.42	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12166	25002	38503	1.49	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRL LARGE SUBUNIT P61 PRECURSOR (FCRL) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12166	25002	38504	1.49	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCRL LARGE SUBUNIT P61 PRECURSOR (FCRL) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12235	25084	38586	3.57	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12607	25737		1.47	1.7E-01	AB24404.1	EST_HUMAN	b68g05.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12880	25477	31763	8.17	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
13097	25850		1.48	1.7E-01	AJ011763.1	NT	Bos taurus prostacyclin receptor gene, 5'UTR
130	13234	26151	1.48	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
703	15846	26879	1.14	1.6E-01	R31497.1	EST_HUMAN	yh76f12.r1 Soares placenta Nb24-P Homo sapiens cDNA clone IMAGE:135599 5'
1523	14594	27515	1.52	1.6E-01	AA549863.1	EST_HUMAN	nk26c12.s1 NCL CGAP_Go11 Homo sapiens cDNA clone IMAGE:1014839 3'
1544	14574	27534	3.98	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1639	14980	27938	1.56	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2001	15019		1.11	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2408	15923	28416	1.13	1.6E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2516	15517	28521	1.85	1.6E-01	AB037728.1	NT	Homo sapiens mRNA for KIAA1908 protein, partial cds
2934	15987	28886	16.49	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2934	15987	28887	16.49	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3408	16450	28357	0.98	1.6E-01	AF062843.1	NT	Danio rerio Plm1 mRNA, complete cds
3657	15019		1.22	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
3700	16732	29622	1.11	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3700	16732	29623	1.11	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3840	16859	29763	1.5	1.6E-01	AE000862.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4086	17111		2.69	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4117	17140	30013	0.98	1.6E-01	AF084456.1	NT	Citridia fasciculata trypanoxin 1 (bmi) gene, complete cds
4396	17409		1.11	1.6E-01	U62771.1	NT	Lymnaea stagnalis octopamine receptor type 1 (Lym oar1) mRNA, complete cds
4436	17447	30307	15.13	1.6E-01	AF179880.1	NT	Homo sapiens apelin gene, complete cds
4567	17575		3.62	1.6E-01	AW968601.1	EST_HUMAN	EST380677 MAGE resequences, MAG.1 Homo sapiens cDNA
4576	17583		6.22	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cdc3), mRNA
4816	17817	30694	0.74	1.6E-01	AF100154.1	NT	Rattus norvegicus kynurenine aminotransferase/glutamine transaminase K (Kat) gene, complete cds
4816	17817	30685	0.74	1.6E-01	AF100154.1	NT	Rattus norvegicus kynurenine aminotransferase/glutamine transaminase K (Kat) gene, complete cds
5035	18032	30889	0.74	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPEPTIDE (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
5059	18058	30908	1.69	1.6E-01	AA088343.1	EST_HUMAN	zB4h09.s1 Stratiogene color (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
5086	18083	30933	1.39	1.6E-01	AJ006336.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.;
5086	18083	30934	1.39	1.6E-01	AJ006336.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5161	18154	31001	0.95	1.6E-01	BE018707.1	EST_HUMAN	Lycopodium esculentum RsaI fragment 2, satellite region
5192	18184	31027	1.02	1.6E-01	A017141.1	EST_HUMAN	bb83h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048023 5' similar to gb:M61715
5572	18350	31528	0.86	1.6E-01	L40808.1	NT	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE);
5712	18785	31715	2.52	1.6E-01	AW197498.1	EST_HUMAN	o34005.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639208 3'
5712	18785	31716	2.52	1.6E-01	AW197498.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5724	18797	31889	2.17	1.6E-01	AF034716.1	NT	xm43101.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2686989 3' similar to TR:O75984 O75984
6261	19312	32477	0.86	1.6E-01	BE925803.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
6505	19549	32728	0.55	1.6E-01	BF183584.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
6505	19549	32729	0.55	1.6E-01	BF183584.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN;
6696	19732	32932	1.77	1.6E-01	AL161588.2	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6696	19732	32933	1.77	1.6E-01	AL161588.2	NT	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
7090	20299	33556	0.57	1.6E-01	AA398047.1	EST_HUMAN	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
7110	20314	33577	0.7	1.6E-01	AB046786.1	NT	601809725R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
7162	20269		0.54	1.6E-01	BF683630.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7300	18469	31291	4.25	1.6E-01	AW291215.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7680	20614	33913	0.57	1.6E-01	Z49632.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84

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8250	21155	34489	1.28	1.6E-01	AW246359.1	EST_HUMAN	2822248.5pTime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8298	21200	34536	0.65	1.6E-01	6753237	NT	Mus musculus Ca<2+>-dependent activator protein for secretion (Cadps), mRNA
8311	21215		0.48	1.6E-01	AU136525.1	EST_HUMAN	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5'
8450	21382	34724	1.68	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
8603	21534		0.75	1.6E-01	BE244087.1	EST_HUMAN	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8696	21827		0.75	1.6E-01	U38243.1	NT	Bacteroides vulgatus beta-lactamase (cfxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
9191	22119	35475	1.12	1.6E-01	Z99719.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
9385	22313	35875	1.03	1.6E-01	R13673.1	EST_HUMAN	yf80h08.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
9488	22416		0.78	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9523	22450	35873	2.14	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001W
9655	22581		0.77	1.6E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10177	23068		2.24	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-H01 ST0200 Homo sapiens cDNA
10178	23070	36469	2.26	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001W
10213	23104		1.17	1.6E-01	BE155684.1	EST_HUMAN	PM2-HT0353-270100-004-F11 HT0353 Homo sapiens cDNA
11100	24031	37476	3.05	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11434	24350	37798	8.89	1.6E-01	O14847	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11434	24350	37797	8.89	1.6E-01	O14847	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11439	24355	37803	1.52	1.6E-01	BE259649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:316183 5'
11555	24464		3.89	1.6E-01	AF106084.1	NT	Pisum sativum falciptarum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11847	24697	38188	8.03	1.6E-01	6871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12086	24927	38431	2.17	1.6E-01	X07471.1	NT	Human small polydisperse circular DNA (Hspc-64)
12086	24927	38432	2.17	1.6E-01	X07471.1	NT	Human small polydisperse circular DNA (Hspc-64)
12130	24971		1.56	1.6E-01	BF527237.1	EST_HUMAN	602039465F2 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177073 5'
12355	25145	38169	5.34	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12634	25315	31818	1.58	1.6E-01	L14833.1	NT	Rat convertase PC5 mRNA, 5' end
12661	25332		1.97	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12754	25718		9.25	1.6E-01	AB045310.1	NT	Osuntia sativus KS mRNA for anti-leucine synthase, complete cds
12903	25490		2.43	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12984	25543		4.75	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13000	25592	31766	2.07	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
267	13362	26277	1.36	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
267	13362	26278	1.36	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
608	15845		2.06	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
809	13865	26800	1.13	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1119	14181	27089	2.41	1.5E-01	AJ009735.1	NT	Oryzias latipes mRNA for EGG522 myosin heavy chain, 3'UTR
1124	14186	27103	1.83	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1140	14182		1.54	1.5E-01	L36126.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1244	14280	27222	0.68	1.5E-01	AW195516.1	EST_HUMAN	xn39d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1302	14335	27281	2.86	1.5E-01	D26536.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
1302	14335	27282	2.88	1.5E-01	D26536.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
1500	14531	27496	1.54	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
2956	16008		1.21	1.5E-01	AW572516.1	EST_HUMAN	xw56a02.x2 NCI_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb.X55072_ma1
3082	16133	28029	4.76	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3100	16151	28047	0.68	1.5E-01	OT8687	SWISSPROT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3401	16443	28350	5.96	1.5E-01	AA935049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3426	16487	28375	0.79	1.5E-01	Z23104.1	NT	oo68d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb.M11433
3426	16487	28376	0.79	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
							L. stagnalis mRNA for G protein-coupled receptor
							L. stagnalis mRNA for G protein-coupled receptor
3488	16527	29426	1.01	1.5E-01	AW612237.1	EST_HUMAN	hh29802.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2856539 3' similar to contains element
							MER16 repetitive element;
3819	16849	29733	2.52	1.5E-01	U09084.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3835	16884	29747	0.77	1.5E-01		NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDH-K1), nuclear gene encoding mitochondrial protein, mRNA
3935	16983	29849	2.77	1.5E-01	AW695983.1	EST_HUMAN	h10f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
4134	17165	30033	0.86	1.5E-01	AW386699.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4188	17208	30073	0.72	1.5E-01	Z12628.1	NT	B. napus mitochondrion DNA for ORF158
4279	17293	30159	12.39	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4838	17839	30709	1.6	1.5E-01	BF687665.1	EST_HUMAN	602067152F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4894	15732	28748	2.4	1.5E-01	BF69381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4903	17802	30770	1.13	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4903	17802	30771	1.13	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5120	18117	30859	2.4	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5437	18519	31244	2.14	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5487	18548	31388	0.72	1.5E-01	AF256652.1	NT	Caiman crocodilus MHC class II beta chain (hclbeta) gene, complete cds
5511	18590		5.58	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5728	18801	31894	4.9	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-180200-064-F10 CT0219 Homo sapiens cDNA
5771	18844	31946	6.93	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5771	18844	31947	6.93	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
6127	19185	32321	0.57	1.5E-01	4506810	NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN8A) mRNA
6237	19291	32450	1.69	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6237	19291	32451	1.69	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6278	19329	32495	2.15	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6436	19483	32658	3.09	1.5E-01	BE27658.1	EST_HUMAN	601504322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6495	19539		2.03	1.5E-01	4506306	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6601	19642	32824	1.74	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6779	25654	33024	1.7	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6810	19843	33053	5.41	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (OSORF3), mRNA
6821	19854	33066	1.87	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6871	19902	33117	2.03	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6981	20008	33239	1	1.5E-01	AA714760.1	EST_HUMAN	rw30d10 st NCI CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
7010	20037	33270	1.67	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7319	18487	31310	6.54	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGE Homo sapiens cDNA
7363	25669		0.71	1.5E-01	AA811545.1	EST_HUMAN	0573f02.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element
7583	20519		2.21	1.5E-01	AF210842.1	NT	LTR2 repetitive element ;
7743	20674	33972	0.51	1.5E-01	AJ233986.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7788	20717	34020	1.69	1.5E-01	AB73157.1	EST_HUMAN	Leucophaea maderae mRNA for lipocalin, Lma-P22
8030	20946	34282	1	1.5E-01	AF298073.1	NT	wf52a08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
8030	20946	34283	1	1.5E-01	AF298073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
8042	20956	34270	1.48	1.5E-01	AW500611.1	EST_HUMAN	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
8042	20956	34271	1.48	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
8205	21111	34442	0.64	1.5E-01	U46560.1	NT	UI-HF-BN0-akk-d-05-q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
8336	21597	34904	1.1	1.5E-01	P21303	SWISSPROT	Saccharomyces cerevisiae weak multicopy suppressor of lost-1 (SOL3) gene, complete cds
							MEROZOITE RECEPTOR PK68 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8768	21728	35077	1.24	1.5E-01	AA970317.1	EST_HUMAN	cc85g12.x1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8887	21817		0.97	1.5E-01	BE884769.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8970	21900		16.06	1.5E-01	CT6900.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
9002	21931	35287	1.58	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#8672) Homo sapiens cDNA clone GEN 629109 5'
9155	22083	35441	1.73	1.5E-01	D84476.1	NT	Pangasinanodon gigas growth hormone (GH) mRNA, complete cds
9174	22102		0.75	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9398	22324	35687	1.62	1.5E-01	4601972	NT	WNT-10A PROTEIN PRECURSOR
9649	22575	35946	2.57	1.5E-01	NT4228.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9735	22600	36043	1.62	1.5E-01	BF585495.1	EST_HUMAN	za59e09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286866 3' similar to
9742	22686		2.45	1.5E-01	AV754819.1	EST_HUMAN	PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9885	21343	34878	7.35	1.5E-01	U00455.1	NT	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
10332	23221	36635	0.76	1.5E-01	M77144.1	NT	AV754819 TP Homo sapiens cDNA clone TPAH12 5'
10432	23321	36738	7.83	1.5E-01	AF007570.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
10432	23321	36739	7.83	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10689	23585	37014	2.61	1.5E-01	X98852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10798	23684	37113	3.32	1.5E-01	AB14046.1	EST_HUMAN	Aplysia californica carboxypeptidase D mRNA, complete cds
10798	23684	37114	3.32	1.5E-01	AB14046.1	EST_HUMAN	P leniussculus mRNA for Integrin beta subunit
10875	23761	37188	1.92	1.5E-01	U40932.1	NT	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
11018	23902	37340	1.49	1.5E-01	AJ011984.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
11018	23902	37341	1.49	1.5E-01	AJ011984.1	NT	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
11139	24068	37513	1.84	1.5E-01	BE088492.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
11139	24068	37514	1.84	1.5E-01	BE088492.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
11263	24186	37634	5.36	1.5E-01	AL163280.2	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds
11263	24186	37635	5.36	1.5E-01	AL163280.2	NT	Claviceps purpurea ps1 gene
11515	24425	37883	1.58	1.5E-01	AW841915.1	EST_HUMAN	Claviceps purpurea ps1 gene
11607	20717	34020	1.49	1.5E-01	AB79157.1	EST_HUMAN	CM2-BT0888-210300-122-f11 BT0888 Homo sapiens cDNA
12050	24891		1.57	1.5E-01	AI193704.1	EST_HUMAN	CM2-BT0888-210300-122-f11 BT0888 Homo sapiens cDNA
12315	25766		41.76	1.5E-01	BF700582.1	EST_HUMAN	CM2-BT0888-210300-122-f11 BT0888 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens chromosome 21 segment HS21C080
							IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
							wr52c08.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3'
							q972e01.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:174536 3' similar to
							gb:M17987 EOS ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
							602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12680	25331		2.53	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12702	25357		1.67	1.5E-01	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12721	25783		3.83	1.5E-01	R83077.1	EST_HUMAN	y987a04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
12801	25803		3.37	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
12802	25722	31697	7.76	1.5E-01	AL193074.2	NT	Campylobacter jejuni NC1C11168 complete genome; segment 1/6
13082	25603	31732	6.57	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
319	13411		1.38	1.4E-01	AF098663.1	NT	Homo sapiens T cell receptor beta locus, TORBV85P to TORBV21S2A2 region
935	13987		3.3	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1286	14319		1.33	1.4E-01	T91864.1	EST_HUMAN	y454c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1774	14800		1.35	1.4E-01	6678980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1778	14802	27770	1.31	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1923	14944		1.06	1.4E-01	AW135741.1	EST_HUMAN	U1-P-B11-act-a-99-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714008 3'
2002	15020		11.07	1.4E-01	AA720816.1	EST_HUMAN	y72a07.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1283821 3'
2496	15498	28498	1.35	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2840	15929	28826	3.98	1.4E-01	A1933496.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3349	16395	29286	1.03	1.4E-01	R66395.1	EST_HUMAN	y990a10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:40848 5'
3988	16986	29880	1.25	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3988	16986	29881	1.25	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4269	17285	30152	10.37	1.4E-01	A1699094.1	EST_HUMAN	b56a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4269	17285	30153	10.37	1.4E-01	A1699094.1	EST_HUMAN	b56a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4337	17351	30214	4.49	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4518	17527		0.98	1.4E-01	AA776287.1	EST_HUMAN	q50b01.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057.maf1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4980	17978	30838	0.98	1.4E-01	AV689659.1	EST_HUMAN	AV689659 GKC Homo sapiens cDNA clone GKCDUG09 5'
5489	18569	31415	4.8	1.4E-01	T90677.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5512	18591	31438	4.32	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5512	18591	31439	4.32	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6562	19594	32782	3.04	1.4E-01	BE326801.1	EST_HUMAN	h67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6757	19781	33004	4.3	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6757	19791	33005	4.3	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6853	19885	33059	4.04	1.4E-01	AW082766.1	EST_HUMAN	x67d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6867	19899		1.6	1.4E-01	BE266596.1	EST_HUMAN	801193523.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6891	19921	33136	2.17	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
7486	20426		1.03	1.4E-01	AL118588.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7782	20711		1.8	1.4E-01	AW016373.1	EST_HUMAN	U1-H-B10-aat-c-09-0-J1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7810	20739	34042	0.62	1.4E-01	F08745.1	EST_HUMAN	HSC1D8011 normalized infant brain cDNA Homo sapiens cDNA clone c-1db01
7866	20793		0.68	1.4E-01	A1762827.1	EST_HUMAN	w04f12.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN P49862 CASPASE-4 PRECURSOR;
7869	20796		0.43	1.4E-01	T53770.1	EST_HUMAN	ya90f11.12 Stragene placenta (#937225) Homo sapiens cDNA clone IMAGE:68973 5' similar to contains Alu repetitive element
8059	20982	34099	1.21	1.4E-01	U85945.1	NT	Oryctolagus cuniculus fructose 1,6, biphosphate aldolase (AldB) gene, complete cds
8220	21125	34457	1.69	1.4E-01	A1805192.1	EST_HUMAN	q100b12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8553	21484		0.65	1.4E-01	BF310258.1	EST_HUMAN	601894760F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124199 5'
9044	21973		1.55	1.4E-01	AV650047.1	EST_HUMAN	AV650047 GLC Homo sapiens cDNA clone GLCFSH08 3'
9343	22271		0.57	1.4E-01	AK436093.1	EST_HUMAN	h02b12.x1 Soares_NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:O02710 O02710 GAG POLYPROTEIN;
9470	22398	35761	5.31	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9545	22472	35830	0.76	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9667	22593	35967	1.2	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9667	22593	35968	1.2	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9728	22653	36036	8.78	1.4E-01	BF310959.1	EST_HUMAN	601895466F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9815	22721	36104	1.39	1.4E-01	W93411.1	EST_HUMAN	zd94a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
9885	22800	36186	0.51	1.4E-01	X73283.1	NT	M. variellii genes rpoH, rpoB and rpoA
9885	22800	36187	0.51	1.4E-01	X73283.1	NT	M. variellii genes rpoH, rpoB and rpoA
9896	22811	36200	1.26	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9896	22811	36201	1.26	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9882	21340	34676	1.58	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase la (IAL), and zinc finger protein (DNZ1) genes, complete cds
10321	23210	36622	0.74	1.4E-01	X68092.1	NT	C. parvifrons ORF for putative membrane transport protein
10493	23381	36794	1.11	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10590	23476	36903	0.73	1.4E-01	AW021908.1	EST_HUMAN	df28h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10590	23476	36904	0.73	1.4E-01	AW021908.1	EST_HUMAN	df28h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10750	23636	37068	0.7	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-a08 ST0218 Homo sapiens cDNA
10750	23636	37069	0.7	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-a08 ST0218 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11151	24080		1.76	1.4E-01	AA811480.1	EST_HUMAN	oes9a03.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
11280	24202	37654	3.28	1.4E-01	R53400.1	EST_HUMAN	y70c05.11 Soares breast 2Nth-Hst Homo sapiens cDNA clone IMAGE:154088 5'
11469	24382	37828	1.52	1.4E-01	AW104982.1	EST_HUMAN	xd73e10.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'
11637	24447	37908	1.51	1.4E-01	T98102.1	EST_HUMAN	ye47g10.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'
11637	24447	37909	1.51	1.4E-01	T98102.1	EST_HUMAN	ye47g10.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'
11639	24449	37912	1.5	1.4E-01	P08848	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F)(VLA-5) (CD49E)
11738	24640	38120	1.77	1.4E-01	X68092.1	NT	C.perfringens ORF for putative membrane transport protein
11773	20711		1.65	1.4E-01	AW015373.1	EST_HUMAN	UI-H-BIO-aat-o-09-0-UI.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11901	24001	37440	2.09	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11957	24800		1.44	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
12160	24998	38499	1.51	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; IPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFTZ7 (PFTZ7) gene, complete cds; and H5AR (H5ar) gene, complete cds
12802	25298	31813	4.54	1.4E-01	X74773.1	NT	P.salina plastid gene secY
12814	25305		2.27	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA
12859	25943		2.04	1.4E-01	BE513902.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12747	25386		6.48	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12825	25961		5.22	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
13019	25784		3.23	1.4E-01	D82883.1	NT	Mus musculus mRNA for prolidase, complete cds
13106	25922		3.39	1.4E-01	U01337.1	NT	Human Ser/Thr protein kinase (A-RAF-1) gene, complete cds
342	13432	26346	2.17	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
342	13432	26347	2.17	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
552	13621	26529	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
659	13721	26632	1.24	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
659	13721	26633	1.24	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
869	13922	26968	0.84	1.3E-01	X53330.1	NT	P.dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
919	13971	26918	1.37	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1053	14097	27035	1.24	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1154	14195		2.28	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1243	14279	27221	1.32	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1482	14493		0.95	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1882	14903	27887	1.13	1.3E-01	6680967	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
1973	14891	27874	2.21	1.3E-01	AL117078.1	NT	Batrachoseps chinea strain T4 cDNA library under conditions of nitrogen deprivation
2183	15194		0.93	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum acidiphila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF181
2309	15317		1.15	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-012 ST0173 Homo sapiens cDNA
2403	15408		2.79	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2625	15623	28616	2.68	1.3E-01	M86918.1	NT	Cerastium auratus keratin type I mRNA, complete cds
3410	16452	28358	0.66	1.3E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3512	16550	28450	1.1	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyol transacylase mRNA, complete cds
3786	16817	28704	0.78	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3786	16817	28705	0.78	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3870	16899	28783	0.67	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4074	17100		1.57	1.3E-01	AL161681.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4135	13721	26632	0.77	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4135	13721	26633	0.77	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4288	17252		1.13	1.3E-01	AF020713.1	NT	Bacteriophage SPB2 complete genome
4255	17271		4.13	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-003 DT0018 Homo sapiens cDNA
4283	17279	30148	2.18	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4282	17298	30182	26.88	1.3E-01	AW273741.1	EST_HUMAN	h23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4387	17401	30289	1.05	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4387	17401	30270	1.08	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4419	17430		1.93	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4592	17600	30437	0.88	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyol transacylase mRNA, complete cds
4650	17656	30522	2.2	1.3E-01	BE272330.1	EST_HUMAN	601126006F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2690063 5'
5059	18096		1.01	1.3E-01	AU136618.1	EST_HUMAN	AU136618 PLACE1 Homo sapiens cDNA clone PLAGE1004693 5'
5152	18143		0.74	1.3E-01	BF091980.1	EST_HUMAN	RC4-TN0077-180900-012-005 TN0077 Homo sapiens cDNA
5255	18241	31093	1.2	1.3E-01	AJ432531.1	EST_HUMAN	h33c10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3'
5288	18264	31103	0.66	1.3E-01	L76979.1	NT	Schizosaccharomyces pombe HMG-CoA reductase (hmg1+) gene, complete cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5377	18359	31198	0.92	1.3E-01	8922835	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
5508	18587	31436	0.76	1.3E-01	AW46988.1	EST_HUMAN	ha07606.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1 b1 L1 L1 repetitive element;
5547	18625	31500	1.89	1.3E-01	AW804417.1	EST_HUMAN	QVQ-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5691	18764		0.81	1.3E-01	AF107763.1	NT	Emertella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5778	18850		22.2	1.3E-01	AF058880.1	NT	Hepatitis C virus 68 CL10 genome polyprotein gene, partial cds
5926	18983	32112	0.88	1.3E-01	BF210920.1	EST_HUMAN	601874691F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6216	19271	32424	0.68	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6216	19271	32425	0.68	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6758	19792	33008	17.04	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6850	19882	33096	1.91	1.3E-01	X88891.1	NT	C. jacchus Intron 4 of visual pigment gene (red allele)
7086	20302		0.74	1.3E-01	W26367.1	EST_HUMAN	263 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7148	20256	33508	0.55	1.3E-01	BE782926.1	EST_HUMAN	601465067F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7148	20256	33509	0.55	1.3E-01	BE782926.1	EST_HUMAN	601465067F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869079 5'
7359	20354		0.73	1.3E-01	BF525660.1	EST_HUMAN	602044345F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7637	20572		1.85	1.3E-01	H48664.1	EST_HUMAN	y33d02.r1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:207075 5'
8262	21167		0.45	1.3E-01	BF681616.1	EST_HUMAN	602166843F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297334 5'
8537	21468		0.87	1.3E-01	BE273339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8551	21482	34823	1.67	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
8582	21513	34857	1.28	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8850	21760	35127	0.7	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8919	21848		4.33	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL054c
8957	21887		5.17	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
9092	22021	35378	2.2	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
9503	22430	35792	0.88	1.3E-01	R11172.1	EST_HUMAN	y39g11.1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN;
9503	22430	35793	0.88	1.3E-01	R11172.1	EST_HUMAN	y39g11.1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN;
9760	22684	36070	0.78	1.3E-01	11038003	NT	Plutella xylostella granulovirus, complete genome
9760	22684	36071	0.78	1.3E-01	11038003	NT	Plutella xylostella granulovirus, complete genome
10005	22822	36210	4.26	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
10554	23440		1.09	1.3E-01	8393840	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd14), mRNA
10628	23515	36948	1.21	1.3E-01	AW851598.1	EST_HUMAN	MR2-CT0222-201099-001-601 CT0222 Homo sapiens cDNA
10879	25695	37199	1.15	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	24010		2.71	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-H08 BT0358 Homo sapiens cDNA
11301	24220	37689	1.62	1.3E-01	H01883.1	EST_HUMAN	y92d09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150449 5'
11540	24450	37813	1.66	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11924	24931		1.68	1.3E-01	BF092708.1	EST_HUMAN	MR4-TN0112-120900-102-e08 TN0112 Homo sapiens cDNA
11897	24599		4.27	1.3E-01	6871745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11776	24675	38163	1.54	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4251346 5'
11778	24675	38164	1.54	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4251346 5'
12025	24667	38369	3.34	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504804 5'
12145	24985	38485	1.51	1.3E-01	BE618394.1	EST_HUMAN	601473369F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3876208 5'
12461	25208	31852	1.75	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3866003 5'
12587	25285		3.46	1.3E-01	AJ242790.1	NT	Gallus gallus scyc1 gene for lymphotactin, exons 1-3
12957	25618		1.79	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares Dieckgräfe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520877 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ; t39502.x1 NCI_CGAP_Brm23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1
404	13517	26438	6.68	1.2E-01	AK21744.1	EST_HUMAN	ANNEXIN V (HUMAN);
447	13114		1.08	1.2E-01	U66912.1	NT	Dictyostellium discoideum ORF DG1016 gene, partial cds
569	13637		2.5	1.2E-01	AF099442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1403	14434	27389	2.23	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1403	14434	27390	2.23	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1410	14441		2.04	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdAAJB11 5'
1528	14557		1.23	1.2E-01	AA897474.1	EST_HUMAN	ai48cd9.st Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1655	14685	27648	1.2	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1677	14707	27670	3.09	1.2E-01	AJ285402.1	EST_HUMAN	q09f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1980553 3'
1793	14819		14.19	1.2E-01	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2196	15207	28211	1.22	1.2E-01	BF248490.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2305	15313	28317	0.98	1.2E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2630	15628	28621	1.96	1.2E-01	AW996556.1	EST_HUMAN	QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
2776	15767	28762	1.09	1.2E-01	AI623388.1	EST_HUMAN	ts18g07.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive element ;
2888	15942	28844	1.24	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2946	15998	28900	6.32	1.2E-01	AI720470.1	EST_HUMAN	as80c09.x1 Barslead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
2977	16029	28931	5.06	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3048	16100	29003	0.87	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3277	16325	29231	3	1.2E-01	AW370668.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	16349		1.05	1.2E-01	U67600.1	NT	QV1-BT0259-261099-021-c05 BT0259 Homo sapiens cDNA
3404	16446	28354	1.03	1.2E-01	AW503374.1	EST_HUMAN	Methanococcus jannaschii section 142 of 150 of the complete genome
3538	16576		0.66	1.2E-01	Z99118.1	NT	UI-HF-BNO-ekw-a-10-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078427 5'
3582	16619	29522	0.95	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
3582	16619	29523	0.95	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3669	16576		1.11	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3833	16862		1.19	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
4278	17292	30157	2.81	1.2E-01	Z54255.1	NT	6018107866R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053668 3'
4278	17292	30158	2.81	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4417	17428	30290	0.74	1.2E-01	M15801.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4834	17835	30705	1.1	1.2E-01	Z48183.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4887	17886		0.73	1.2E-01	L32873.1	NT	L. esculentum mRNA for glycylase-1
4989	17988	30845	1.03	1.2E-01	BF311914.1	EST_HUMAN	Arabidopsis thaliana homeodomain protein (GLABRA2) gene, complete cds
5033	18030	30887	1.04	1.2E-01	AF134904.1	NT	601897754F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127004 5'
5214	18204		0.97	1.2E-01	P16466	SWISSPROT	Schistocerca gregaria semaphorin 2a mRNA, complete cds
5251	18237	31087	1.02	1.2E-01	AL163227.2	NT	HEMOLYSIN PRECURSOR
5251	18237	31088	1.02	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5415	18396	31293	0.85	1.2E-01	L31380.1	NT	Homo sapiens chromosome 21 segment HS21C027
5431	18513	31236	0.67	1.2E-01	AA744369.1	EST_HUMAN	Macaca mulatta vitamin K dependent protein S (PROS) mRNA, complete cds
5483	18564	31408	0.89	1.2E-01	AF223391.1	NT	ny63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5493	18573	31418	2.48	1.2E-01	W33035.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
5553	18631	31510	2.67	1.2E-01	Z98266.1	NT	z08d02.r1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:327699 5'
5695	18768	31693	0.93	1.2E-01	Z48234.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
6441	19487	32664	1.9	1.2E-01	BE620945.1	EST_HUMAN	M.danesticus Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6495	19540	32717	0.73	1.2E-01	P10842	SWISSPROT	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6553	19595	32783	2.24	1.2E-01	AW845276.1	EST_HUMAN	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6623	19663	32848	1.56	1.2E-01	M26925.1	NT	ILO-GT0031-221099-113-e04 GT0031 Homo sapiens cDNA
6699	19735	32937	0.68	1.2E-01	AA747635.1	EST_HUMAN	Mouse galactosyltransferase mRNA, complete cds
							ny65c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6939	19968	33191	1.13	1.2E-01	BF347985.1	EST_HUMAN	60203112F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158386 5'
7107	20312	33575	0.43	1.2E-01	AF295739.1	NT	JC virus agnoprotein, VP2, VP1, large T antigen, and small t antigen genes, complete cds
7358	20353	33622	0.71	1.2E-01	H47789.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
7358	20353	33623	0.71	1.2E-01	H47789.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:193759 5'
8039	20953	34268	0.64	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp70, drbp76 gamma, drbp76 alpha and ILF3)
8306	21210	34546	0.5	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8306	21210	34547	0.5	1.2E-01	D87458.1	NT	Human mRNA for KIAA0282 gene, partial cds
8472	21403		1.62	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-280300-002-f09 BN0137 Homo sapiens cDNA
8540	21471	34812	3.35	1.2E-01	AI913753.1	EST_HUMAN	wc9g03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
8586	21517	34861	0.66	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:
8884	21814	35165	0.74	1.2E-01	AI832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (Cl-B22)
8967	21897		10.92	1.2E-01	AW083652.1	EST_HUMAN	at1b10.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc49d07.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8987	21916						Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
9023	21952	35308	4.31	1.2E-01	AF053772.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
9023	21952	35309	1.07	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
9163	22091		0.92	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
9247	22175		1.72	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
9282	22210		0.85	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
10100	22949	36338	2.16	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
10510	23397	36809	1.47	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
11323	24242		2.68	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11504	24414		3.06	1.2E-01	BE992324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11587	24496		1.63	1.2E-01	BF314481.1	EST_HUMAN	601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11702	24604	38078	2.65	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNA11 (DNA11) gene, exon 17
11758	24659	38143	1.76	1.2E-01	R40249.1	EST_HUMAN	yr80cd2.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28880 3'
11845	24695	38185	1.43	1.2E-01	9994174	NT	Homo sapiens UDP-Galactose 4-epimerase beta 1,4-galactosyltransferase, polypeptide 4 (B4GALT4), mRNA
11940	24784		1.41	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12221	25055	38554	1.51	1.2E-01	BF368736.1	EST_HUMAN	CM2-E70016-310500-206-b11 ET0016 Homo sapiens cDNA

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12250	25072		1.82	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12570	25275		3.58	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
12847	25903	31363	2.74	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12753	25389		1.79	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12755	13637		22.79	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12846	25468		2.72	1.2E-01	X63981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12933	25502	31771	5.48	1.2E-01	A1299903.1	EST_HUMAN	q20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12854	25515		3.58	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12959	25845		6.55	1.2E-01	O96433	SWISSPROT	CYCLIN T
12985	25544	31752	1.63	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
686	13654	26569	0.78	1.1E-01	A1561003.1	EST_HUMAN	h18d08.x1 NCI_CGAP_Br25 Homo sapiens cDNA clone IMAGE:2167983 3'
638	13689	26605	2.48	1.1E-01	AA569006.1	EST_HUMAN	hmo8g11.x1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gbX06985_ma1
1061	14125	27063	1.8	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1112	14154		1.47	1.1E-01	AL161550.2	NT	602129847F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4286771 5'
1186	15894	27184	4.18	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1277	14311	27261	1.96	1.1E-01	D84004.1	NT	EST3B4142 IMAGE resequences, MAGI Homo sapiens cDNA
1542	14572	27531	2.28	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
2198	15209		0.99	1.1E-01	AJ006701.1	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2335	15343		3.98	1.1E-01	6755215	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2567	15860		0.91	1.1E-01	6978676	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
2602	15600		1.2	1.1E-01	AW821909.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
3080	16131	29027	0.67	1.1E-01	F03263.1	EST_HUMAN	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3390	16433		2.14	1.1E-01	6753231	NT	HSCIRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3482	16522	29421	3	1.1E-01	BE393186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3513	16551	29451	1.39	1.1E-01	X62135.1	NT	601308879F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3627088 5'
3550	16588	29494	0.82	1.1E-01	R06946.1	EST_HUMAN	G.reinhardtii nuclear gene on linkage group XIX
3644	16960	29577	0.98	1.1E-01	Y07695.1	NT	y462g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element;
3765	16797		1.08	1.1E-01	P97394	SWISSPROT	A.limmerus gene for transposase
3772	16804	29681	1.8	1.1E-01	X62708.1	NT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4204	17222	30096	1.03	1.1E-01	AW818412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5 MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA

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4204	17222	30087	1.03	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4210	17227		0.65	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Noich4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
4351	17365		11.07	1.1E-01	AF157068.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4384	17398	30286	0.69	1.1E-01	AW802058.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4683	17688	30555	0.8	1.1E-01	AF084564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4946	17945	30803	1.28	1.1E-01	Y07095.1	NT	A. limnerius gene for transposase
5143	18138		0.89	1.1E-01	AW028547.1	EST_HUMAN	ww14h02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2528555 3'
5148	17227		0.82	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Noich4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
5241	18228	31076	0.76	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
5241	18228	31077	0.76	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
5303	18287	31140	1.02	1.1E-01	P70281	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
5667	18938		1.53	1.1E-01	AA747216.1	EST_HUMAN	rx76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element: contains element MER35 repetitive element;
5942	19009	32128	1.26	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5952	19047	32171	0.81	1.1E-01	AL110365.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6017	19079	32204	0.76	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
6017	19079	32205	0.76	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
6049	19111	32240	1.96	1.1E-01	X68851.1	NT	S. pombe sts8 gene encoding protein kinase
6086	19147	32292	4.55	1.1E-01	M85533.1	NT	Providencia rettgeri penicillin G amidase gene
6259	19310	32474	1.59	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6281	19332	32498	1.8	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6301	19352	32521	8.23	1.1E-01	AW653999.1	EST_HUMAN	RC3-CT0284-280989-011-a01 CT0284 Homo sapiens cDNA
6682	19728	32928	0.61	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6700	19736	32938	1.43	1.1E-01	AF036746.1	EST_HUMAN	AF036746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6746	19780	32993	0.81	1.1E-01	A1216307.1	EST_HUMAN	qg76006.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1641099 3'
6894	19924	33139	4.03	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
7001	20028		3.2	1.1E-01	AF032922.1	NT	Homo sapiens syntrophin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
7103	20309	33570	2.17	1.1E-01	11492372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7400	20098	33333	0.61	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome

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7400	20099	33334	0.61	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 56 of the complete genome
7551	25981		0.89	1.1E-01	BF382768.1	EST_HUMAN	601876524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7665	25674	33919	0.98	1.1E-01	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7)
7963	20885	34195	8.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7963	20885	34196	8.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
8023	20839	34254	0.52	1.1E-01	AA989608.1	EST_HUMAN	ou44g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1629172 3'
8104	21018	34343	1.87	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
8149	21058		0.72	1.1E-01	Z14088.1	NT	B subtilis gene encoding hypothetical polypeptide synthase
8150	21059	34390	3.26	1.1E-01	AA788784.1	EST_HUMAN	ek31806.s1 Soares_papthyroid_tumor_NHHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
8327	21232	34567	0.63	1.1E-01	BE782280.1	EST_HUMAN	CHROMOGHRANIN A PRECURSOR (HUMAN);
8546	21477	34819	0.8	1.1E-01	U67492.1	NT	601470055F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873229 5'
8786	21716	35063	1.64	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8786	21716	35064	1.64	1.1E-01	AA493574.1	EST_HUMAN	rh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8830	21750	35106	1.42	1.1E-01	X91233.1	NT	rh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8870	21800		1.1	1.1E-01	AW817918.1	EST_HUMAN	H.sapiens IL15 gene
8925	21855	35211	1.96	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
8977	22305	35666	1.95	1.1E-01	U02482.1	NT	DKFZp547P194_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547P194 5'
9469	22397	35760	1.28	1.1E-01	AB07474.1	EST_HUMAN	Pedococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
9560	22487	35848	0.6	1.1E-01	AF050081.1	NT	Wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element
9595	22521	35884	2.84	1.1E-01	AA192153.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
9595	22521	35885	2.84	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9878	22604	35977	0.62	1.1E-01	Y12727.1	NT	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9708	22633	36013	4.43	1.1E-01	IT2675.1	EST_HUMAN	P.furiosus partial dph5 gene and argF gene
9733	22658		0.73	1.1E-01	BE693260.1	EST_HUMAN	yf19h03.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb.M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9856	22681		0.88	1.1E-01	BE142305.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
10029	22929		2.47	1.1E-01	BF083149.1	EST_HUMAN	GM3-HT0142-271099-028-g11 HT0142 Homo sapiens cDNA
10421	23310		0.64	1.1E-01	AL161543.2	NT	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10702	23598		1.49	1.1E-01	R80590.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10825	23711	37138	1.14	1.1E-01	U60529.1	NT	y96a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
11244	16131	23027	2.08	1.1E-01	F03265.1	EST_HUMAN	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
							HSC:IRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11359	24277		2.21	1.1E-01	AF168032.1	NT	Caressilus auratus activin beta A precursor, mRNA, complete cds
11481	24394	37844	3.65	1.1E-01	R23708.1	EST_HUMAN	yh35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131750 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11490	24402	37853	1.79	1.1E-01	6981351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (PFK), mRNA
11556	24562	38033	2.69	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lgt genes encoding RNA guanine transglycosylase and DNA ligase
11556	24562	38034	2.69	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lgt genes encoding RNA guanine transglycosylase and DNA ligase
11751	24652	38133	2.61	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
12099	24940		1.63	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12343	25136		1.84	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
12444	25189		1.89	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-603 NT0112 Homo sapiens cDNA
12676	25731		1.99	1.1E-01	BE974596.1	EST_HUMAN	601680551R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950604 3'
1229	14266		2.23	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1299	14332	27278	2.06	1.0E-01	AI995499.1	EST_HUMAN	wa08a01.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:246577 3' similar to contains MER7.f3 MER7 repetitive element;
1419	14450	27404	2.07	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2512	15513	28516	1.08	1.0E-01	AW451385.1	EST_HUMAN	UI-H-B13-alc-d-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3572	16509	29512	1.45	1.0E-01	BF033991.1	EST_HUMAN	601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
3783	16814	29701	0.98	1.0E-01	BF239818.1	EST_HUMAN	601900489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
4036	17063	29952	3.39	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-a05 NT0048 Homo sapiens cDNA
4513	17522	30387	1.05	1.0E-01	AE002265.2	NT	Chlamydomonas reinhardtii AR39, section 91 of 94 of the complete genome
4970	17675		0.76	1.0E-01	AI792349.1	EST_HUMAN	an32a04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4825	17826	30894	1.33	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5030	18027	30885	2.62	1.0E-01	AW952344.1	EST_HUMAN	EST1364414 MAGE resequences, MAGE Homo sapiens cDNA
5300	18284	31135	0.68	1.0E-01	BE389100.1	EST_HUMAN	601286989F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613552 5'
5504	18583		8.68	1.0E-01	W86490.1	EST_HUMAN	zh82h04.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5603	18679		0.84	1.0E-01	X54015.1	NT	X.campestris genes for sensor and regulator protein
5685	18758		0.43	1.0E-01	Q36860	SWISSPROT	Cytochrome C OXIDASE POLYPEPTIDE III
6095	19156		0.99	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6257	19309	32473	12.02	1.0E-01	AF274975.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6592	19633	32815	0.84	1.0E-01	AA481879.1	EST_HUMAN	zv41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:766258 3' similar to contains L1.3 L1 repetitive element;
6606	19647	32830	0.68	1.0E-01	AA406039.1	EST_HUMAN	zic7c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743082 3'
7369	20363		1.63	1.0E-01	R23821.1	EST_HUMAN	yh34h06.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8200	21106		2.05	1.0E-01	Y12488.1	NT	M.musculus wlm gene
8324	21228	34563	0.51	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8324	21229	34564	0.51	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8420	21323	34666	0.41	1.0E-01	BF128224.1	EST_HUMAN	601810459R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053494 3'
8512	21443	34785	0.69	1.0E-01	AA861091.1	EST_HUMAN	ek32g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8744	21674		0.6	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
9061	21990		1.28	1.0E-01	AW189797.1	EST_HUMAN	x109b01.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2875689 3' similar to gb:X17206 40S
9727	22652	36036	1.23	1.0E-01	AF102855.2	NT	RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element ;
10028	22928	36316	0.67	1.0E-01	R44993.1	EST_HUMAN	Rattus norvegicus synaptic SAPAP-interacting protein Synapmon mRNA, complete cds
10038	22938		2.14	1.0E-01	MT6728.1	NT	y933h04.s1 Soares Infant brain T1N1B Homo sapiens cDNA clone IMAGE:34549 3'
10079	22872		2.71	1.0E-01	AE001501.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
10093	22943	36331	0.77	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori strain J99 section 62 of 132 of the complete genome
10336	23225	36840	2.03	1.0E-01	BF240154.1	EST_HUMAN	z66810.s1 Soares fetal heart NBH-H19W Homo sapiens cDNA clone IMAGE:327282 3'
10444	23333	36750	9.79	1.0E-01	AB046799.1	NT	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10444	23333	36751	9.79	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10641	23527		1.21	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10646	23532	36964	0.56	1.0E-01	T51952.1	EST_HUMAN	EST336915 IMAGE resequences, IMAGE Homo sapiens cDNA
10820	23706	37133	1.27	1.0E-01	BE792760.1	EST_HUMAN	y029a06.s1 Strategene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
11101	24032		1.88	1.0E-01	AU159127.1	EST_HUMAN	601684604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5'
11472	24385	37834	2.34	1.0E-01	BF242946.1	EST_HUMAN	AU159127 THYR01 Homo sapiens cDNA clone THYR01000895 3'
11472	24385	37835	2.34	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11837	24688	38177	4.8	1.0E-01	BE790543.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
12430	25505		3	1.0E-01	BE537719.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836734 5'
12658	25530		1.89	1.0E-01	X00854.1	NT	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12909	25896		4	1.0E-01	U52691.1	NT	Drosophila melanogaster ftz gene
12937	25505		2.82	1.0E-01	BE537719.1	EST_HUMAN	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12996	25874		30.18	1.0E-01	U66834.1	NT	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13043	25578		8.63	1.0E-01	AP001607.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
2829	15818	28813	1.39	9.8E-02	AF274008.1	NT	Bacillus halodurans genomic DNA, section 1/14
2835	15824	28820	1.29	9.9E-02	BE645554.1	EST_HUMAN	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1I) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2835	15824	28821	1.29	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
3311	16358	29258	1.23	9.9E-02	AF098810.1	NT	Homo sapiens neurabin III-alpha gene, partial cds
4032	17059	29948	0.9	9.9E-02	AB21637.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740832 3'
7185	20185	33429	0.49	9.9E-02	BE613498.1	EST_HUMAN	601604262F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906084 5'
7309	18477	31299	8.22	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin 3 deaminase, complete cds
8494	21425	34765	0.52	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
8494	21425	34766	0.52	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
9789	22763	35148	1.86	9.9E-02	675511.1	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
585	13553		1.16	9.8E-02	X56338.1	NT	O.sativa RAMy3C gene for alpha-amylase
3188	16237	29131	4.99	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4323	17337	30201	9.42	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4323	17337	30202	9.42	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7802	20827		0.93	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9788	22760		1.08	9.8E-02	M81943.1	NT	Human laminin B1 chain gene, exon 26
11882	23992	37431	2.03	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3804287 5'
12402	25174		1.7	9.8E-02	8393761	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1378	14411	27386	1.33	9.7E-02	AB005808.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds
1608	14638		0.99	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (spondyloplasia, thanatophoric dwarfism) (FGFR3) mRNA
2278	15287	28295	2.33	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
4088	17094		4.75	9.7E-02	Q89795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5529	18608	31456	0.93	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5529	18608	31457	0.93	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6247	19300	32480	1.38	9.7E-02	AW954476.1	EST_HUMAN	EST366546 MAGE sequences, MAGEC Homo sapiens cDNA
7879	20513	33912	3.3	9.7E-02	Z69119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
8562	21493	34835	1.62	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8562	21493	34836	1.62	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9408	22336	35700	1.25	9.7E-02	A1953984.1	EST_HUMAN	wk78006.x1 NCI_CGAP_OV38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_m1
11642	24548		2.11	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); Mus musculus ligatin (Lgtn) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2029	15046	28041	1.01	9.6E-02	A1080721.1	EST_HUMAN	0247d111.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2029	15046	28042	1.01	9.6E-02	A1080721.1	EST_HUMAN	0247d111.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4454	17464	30321	8.84	9.6E-02	Z32886.2	NT	Proteus mirabilis fibrillar operon, strain H14320
5122	18118	30960	1.47	9.6E-02	AW966230.1	EST_HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
5296	18281	31131	0.74	9.6E-02	BE061728.1	EST_HUMAN	RC5-BT0254-031099-011-e03 BT0254 Homo sapiens cDNA
6343	19393		2.9	9.6E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8402	21305		0.48	9.6E-02	6678783	NT	Mus musculus lymphocyte antigen 78 (Ly78), mRNA
8947	21877		0.6	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
10073	22988	36383	2.18	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
10394	23273		1.71	9.6E-02	BE894865.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10542	23428	36848	1.69	9.6E-02	A1243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10542	23428	36849	1.69	9.6E-02	A1243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 65
10620	23506	36940	0.64	9.6E-02	BF671270.1	EST_HUMAN	602066769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250669 5'
10648	23634	36966	2	9.6E-02	AB013985.1	NT	Anthrithum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10648	23634	36967	2	9.6E-02	AB013985.1	NT	Anthrithum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10751	23637	37070	4.05	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
11183	24109	37556	6.87	9.6E-02	Z19702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102162
12141	24981	38481	1.43	9.6E-02	AA625765.1	EST_HUMAN	z181g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
12974	25538		1.87	9.6E-02	H14599.1	EST_HUMAN	ym19h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48663 3'
13103	25618		3.56	9.6E-02	A1300197.1	NT	Xenopus laevis mRNA for dickkopf2 (dkk2 gene)
4192	17212	30079	2.37	9.5E-02	AW962395.1	EST_HUMAN	CM2-BN0023-050200-087-F12 BN0023 Homo sapiens cDNA
5852	18933	32052	0.88	9.5E-02	P51854	SWISSPROT	TRANSETOLASE 2 (TK 2) (TRANSETOLASE RELATED PROTEIN)
7694	20618	33918	4.96	9.6E-02	AF003473.1	NT	Trimeresurus flaviviridis DNA for phospholipase A2 inhibitor, complete cds
8001	20919	34286	7.98	9.6E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
8152	18933	32052	0.88	9.5E-02	P51854	SWISSPROT	TRANSETOLASE 2 (TK 2) (TRANSETOLASE RELATED PROTEIN)
8460	21391	34732	2.46	9.5E-02	BF035861.1	EST_HUMAN	601453942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8460	21391	34733	2.46	9.5E-02	BF035861.1	EST_HUMAN	601453942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
11122	24052	37497	2.86	9.5E-02	BF035861.1	EST_HUMAN	601453942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
11122	24052	37498	2.86	9.5E-02	BF035861.1	EST_HUMAN	601453942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12226	25060	38558	1.83	9.5E-02	U37070.1	NT	Human transforming growth factor-beta type II receptor (TGF-beta RI), promoter region
13031	25570		1.79	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1857	14879	27868	3.42	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291617 5'
3949	16977	29861	6.79	9.4E-02	Z33059.1	NT	M. capricornus DNA for CONTIG MC073
5182	18174	31019	0.71	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Cdbp), mRNA

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6572	19613	32799	0.82	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8036	20951	34266	0.62	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vcl genes, complete cds, and p85 gene, partial cds
9182	22090		1.8	9.4E-02	Z40863.1	NT	Acinetobacter sp. oysD, cobQ, sodM, lysS, rubA, rubB, esbB, oxyR, ppk, mlgA, ORF2 and ORF3 genes
11372	20951	34266	2.5	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vcl genes, complete cds, and p85 gene, partial cds
12298	25814		7.24	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13096	25612	31735	2.36	9.4E-02	U27699.1	NT	Human pethBGT-1 betaine-GABA transporter mRNA, complete cds
3031	16083		2.22	9.3E-02	4808280	NT	Homo sapiens BA11-associated protein 3 (BA1AP3) mRNA
3075	16127		7.87	9.3E-02	6912526	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3301	16348	29263	1.91	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4245	17261	30127	1.3	9.3E-02	BE543175.1	EST_HUMAN	601069147F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455435 5'
4250	17265	30133	3.6	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4250	17265	30134	3.6	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4948	17849		2.35	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAU06 5'
5136	18132	30974	1	9.3E-02	AF115443.1	NT	HIV-1 isolate B112 from Brazil gag protein (gag) gene, partial cds
5859	18930		1.09	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8374	21278	34610	0.4	9.3E-02	M75984.1	NT	Human hepatocyte growth factor gene exon 18, 3' end
8391	21295	34626	0.61	9.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8923	21763	35099	0.67	9.3E-02	AW566007.1	EST_HUMAN	EST69 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
8989	22595		0.52	9.3E-02	AL113179.1	NT	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
10232	23123	36525	2.62	9.3E-02	BE962631.2	EST_HUMAN	601655989F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10688	23574	37003	4.48	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10688	23574	37004	4.48	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10809	23696		4.05	9.3E-02	AW206117.1	EST_HUMAN	UHH-B11-ark-h-05-0-U1.st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12537	25748		2.76	9.3E-02	AJ248850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12879	25772		22.87	9.3E-02	AW468850.1	EST_HUMAN	h428h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
13059	25813		3.15	9.3E-02	AF100958.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; B1ng1 (B1NG1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), B1NG4 (B1NG4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
247	13345	26255	5.64	9.2E-02	U60315.1	NT	Malus domestica virus subtype 1, complete genome
247	13345	26256	5.64	9.2E-02	U60315.1	NT	Malus domestica virus subtype 1, complete genome
247	13345	26257	5.64	9.2E-02	U60315.1	NT	Malus domestica virus subtype 1, complete genome
2240	16260		2.02	9.2E-02	R64166.1	EST_HUMAN	y998f07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'
3222	16270	29169	4.67	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3351	16397	29297	1.11	9.2E-02	AA534354.1	EST_HUMAN	nt78901.s1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:928136 3'
3647	16883		1.21	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
4398	17352		1.5	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4412	17423		0.87	9.2E-02	BE298722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860176 5'
4750	17755	30615	1.81	9.2E-02	X96402.1	NT	G.gallus Mla-CK gene
8587	21518	34862	2.03	9.2E-02	T49920.1	EST_HUMAN	y499c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:565009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8755	21695	35028	2.03	9.2E-02	X85256.1	NT	H.vulgaris xylose isomerase gene
13045	25966		1.57	9.2E-02	11496872	NT	Podospore anserina mitochondrion, complete genome
446	13113	26000	3	9.1E-02	X77665.1	NT	O. curvulus k12 keratin gene
2440	15444	28444	1.27	9.1E-02	P78985	SWISSPROT	8-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)
3737	16769		1.41	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4598	17606	30463	2.1	9.1E-02	AL161564.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5932	18999	32119	1.65	9.1E-02	AF126756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G8c, G8d, G8e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7690	25982		0.45	9.1E-02	AF026308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7793	20712	34014	11.62	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
8128	21038	34307	0.87	9.1E-02	AF000061.1	NT	Aecopyrum pernix genomic DNA, section 47
8169	21076	34406	0.79	9.1E-02	U39073.1	NT	Mus musculus thymoprotein zeta mRNA, complete cds
8372	21276	34608	0.42	9.1E-02	AJ286537.1	NT	Welwitschia mirabilis partial phyN gene for phytochrome
9480	22408	35768	1.08	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10910	23795		1.58	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end
10938	23821	37248	0.93	9.1E-02	S74059.1	NT	Tg616=Cyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 5275 nt]
10954	23848	37274	0.88	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11608	24517	37897	3.28	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor mRNA, complete cds
12525	25249		2.31	9.1E-02	AF052695.1	NT	Rattus norvegicus cell cycle protein p50CDC gene, complete cds
12958	25767		10.65	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
768	13825	26755	2.93	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1680	14890	27650	5.44	9.0E-02	BE220482.1	EST_HUMAN	h39g10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2850	15839	28837	5.76	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2850	15839	28838	5.76	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3385	18428	29333	0.73	9.0E-02	AF276135.1	NT	Dictyostellium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4779	17784	30654	2.36	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
6227	19282	32437	13.23	9.0E-02	W56037.1	EST_HUMAN	zaf68a12.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:287694 5' similar to PIR:S52171 S52171 small G protein - human ;
7019	20045		0.93	9.0E-02	BF062651.1	EST_HUMAN	7n63a03.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element;
7072	20278	33532	0.61	9.0E-02	R62806.1	EST_HUMAN	yf11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
12811	25433		1.71	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1457	14489	27449	1.46	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5'
1457	14489	27450	1.46	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5'
2410	15414	28417	0.91	8.9E-02	BE155572.1	EST_HUMAN	PMO-HT0339-251199-003-401 HT0339 Homo sapiens cDNA
4265	17309		2.07	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFio2 protein (AtranFio2) gene, partial cds
6064	19123	32285	3.18	8.9E-02	AW452122.1	EST_HUMAN	U1-H-B13-ab-4-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6064	19123	32256	3.18	8.9E-02	AW452122.1	EST_HUMAN	U1-H-B13-ab-4-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6081	19142	32278	3.36	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7557	20494	33794	1.49	8.9E-02	P47259	SWISSPROT	FCID BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
7990	20909		1.78	8.9E-02	Z78021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA20F8
8628	21559	34897	1.01	8.9E-02	P28475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8707	21638	34985	0.85	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
8707	21638	34988	0.85	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285827 5'
9160	22088	35447	5.72	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
10146	23037	36435	1.02	8.9E-02	AI285627.1	EST_HUMAN	qu55005.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element ;
10146	23037	36436	1.02	8.9E-02	AI285627.1	EST_HUMAN	qu55005.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 MER10 repetitive element ;
10253	23143	36552	0.64	8.9E-02	AA339356.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
12432	25192		3.76	8.9E-02	BF696918.1	EST_HUMAN	602129882F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286180 5'
12582	25283		2.97	8.9E-02	6680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12860	25908		1.58	8.9E-02	AE001514.1	NT	Helicobacter pylori, strain J99 section 75 of 132 of the complete genome
1400	14431	27386	0.99	8.8E-02	QZ7474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3975	17003	29890	1.24	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4118	17141		6.33	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 195 KDA SUBUNIT (TAFII-195) (TAFII-190) (TAFII190)
4405	17417		0.8	8.8E-02	4530423	NT	Homo sapiens paired box gene 6 (airitidia, keratitis) (PAX6), isoform b, mRNA
7974	20895		0.7	8.8E-02	D17520.1	NT	Sheep mRNA for angiotensinogen, complete cds
9539	22468	35827	2.38	8.8E-02	AA151872.1	EST_HUMAN	zn99a05.s1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
11558	24467	37931	2.78	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11558	24467	37932	2.78	8.8E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11709	24611	38088	6.42	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
3759	16791	29681	4.71	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3759	16791	29682	4.71	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4820	17821	30690	1.35	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5155	18148	30984	0.66	8.7E-02	A1818839.1	EST_HUMAN	wk92802.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2422826 3'
5497	18576	31422	5.51	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5497	18576	31423	5.51	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
7161	20268	33524	0.7	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7161	20268	33525	0.7	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7394	20093	33327	0.69	8.7E-02	AF281342.1	NT	Oncohyndus mykiss TAT-binding protein 1 mRNA, partial cds
9081	22010	35366	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
9081	22010	35367	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
11154	24083		2.5	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11756	24657	38140	1.73	8.7E-02	AJ007763.1	NT	Glucobacter oxydans IRNA-11e and RNA-A1a genes
12487	25230		2.04	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12875	25339		2.57	8.7E-02	6670057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1280	14313	27262	4.96	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2259	15269	28275	2.28	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3231	16279	29179	3.01	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3713	16745		5.42	8.6E-02	AF153362.1	NT	Dictyostellum discoideum adenyl cyclase (acrA) gene, complete cds

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5306	18290	31143	1.83	8.6E-02	AF060174.1	NT	Rattus norvegicus synaptic vesicle protein 2C (SV2C) mRNA, complete cds
6331	19381	32549	4.7	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6634	19674	32861	1.53	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6634	19674	32862	1.53	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
8017	20933	34251	1.04	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8509	21440	34780	1.23	8.6E-02	5730066	NT	Homo sapiens Sfr2-related CBF activator protein (SRCAP) mRNA
8509	21440	34781	1.23	8.6E-02	5730066	NT	Homo sapiens Sfr2-related CBF activator protein (SRCAP) mRNA
8648	21679	34916	0.59	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006). mRNA
8708	21639		0.89	8.6E-02	U60188.1	NT	Dictyostellum discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
10257	23147	36585	1.3	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
10292	23182		0.67	8.6E-02	AW662153.1	EST_HUMAN	h20c08.x1 NCI_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2972846 3'
10650	23536	36959	0.71	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11395	24301	37747	1.89	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11395	24301	37748	1.89	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11695	24597	38074	2.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11695	24597	38075	2.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11872	23972	37409	6.04	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
12007	24849	39348	1.83	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BarFI methylase (Flm) and BsrFI restriction endonuclease (FIR) genes, complete cds
2419	15423	28424	3.2	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5866	18937	32055	0.7	8.5E-02	AA885491.1	EST_HUMAN	q483b07.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gbK01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5907	18976		1.89	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6244	19298	32456	5.44	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
9167	22095	35494	2.4	8.5E-02	6794779	NT	Mus musculus myosin XV (Myo15), mRNA
10351	23240	36639	3.24	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10351	23240	36680	3.24	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10849	23735	37158	0.57	8.5E-02	X76791.1	NT	V. armodyctas gene for armodyctoxin C
10963	23847	37273	0.89	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11596	24505		10.13	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11614	24522	37990	3.62	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12856	25713		2.03	8.5E-02	A1005586.1	NT	Anthrithum majus mRNA for MYB-related transcription factor

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12875	25871		2.65	8.5E-02	AF110403.1	NT	Bactrocera tryoni transposon Homer putative transposase gene, complete cds
13012	25559		2.28	8.5E-02	AA362384.1	EST_HUMAN	EST772736 Ovary II Homo sapiens cDNA 5' end
2716	15931	28706	3.67	8.4E-02	W69330.1	EST_HUMAN	zfd44e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5400	18382	31222	1.1	8.4E-02	AB042555.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
5495	18574	31420	9.5	8.4E-02	BE267153.1	EST_HUMAN	601180436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6986	20013	33244	1.74	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8607	21538	34880	5.64	8.4E-02	BE05074.1	EST_HUMAN	CM3-BT0790-260400-162-d05 BT0790 Homo sapiens cDNA
9401	22329	35691	0.81	8.4E-02	AF218890.1	NT	Homo sapiens atracilin precursor (ATRN) gene, exon 2
10848	23734	37157	1.86	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335942 3' similar to TR:O88312
3653	16689	29584	8.44	8.3E-02	P75334	SWISSPROT	O88312 GOB-4 ;
3685	16718	29609	0.82	8.3E-02	AI436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3685	16718	29610	0.82	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4404	17418		0.67	8.3E-02	M54964.1	NT	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6510	19554	32734	0.87	8.3E-02	AI942338.1	EST_HUMAN	C.thummi A2b region open reading frame, complete cds
6626	19568	32851	3.45	8.3E-02	AF052693.1	NT	wo79f11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
8560	21491	34832	3.01	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8591	21522		1.29	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds
8874	21804		1.57	8.3E-02	AA987873.1	EST_HUMAN	og88g08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.11 L1 L1 repetitive element ;
10087	22983	36374	1.33	8.3E-02	AW583503.1	EST_HUMAN	oc81f10.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1692779 3'
10080	22873		1.54	8.3E-02	AL161595.2	NT	la03h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
10829	23715		1.18	8.3E-02	AF020409.1	NT	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
1408	14437		7.8	8.2E-02	Y08170.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
1514	14645	27607	1.48	8.2E-02	AF167077.2	NT	Dicotyledonum discoidium DocA (docA) mRNA, complete cds
3122	16173		2.45	8.2E-02	AL163208.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
3669	16898		2.09	8.2E-02	AL161498.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
4382	17396	30261	7.87	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4382	17396	30262	7.87	8.2E-02	P48960	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4382	17396	30263	7.87	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5202	18193	31035	0.65	8.2E-02	AF240778.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5216	18208	31051	3.24	8.2E-02	U76009.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5518	18597	31446	1.73	8.2E-02	BE897030.1	EST_HUMAN	Mus musculus peptidogen F (PepT) mRNA, complete cds
							Mus musculus zinc transporter (ZnT-3) gene, complete cds
							601435576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7370	20364	33633	2.85	8.2E-02	AF308555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8106	21103		0.62	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 6'
8266	22194		0.65	8.2E-02	U29397.1	NT	Rattus norvegicus plasma membrane Ca ²⁺ -ATPase isoform 3 (PMCA3) gene, 5' flanking region
9331	22259	35623	3.87	8.2E-02	AW875128.1	EST_HUMAN	RC2-PT0004-031289-011-d05 PT0004 Homo sapiens cDNA
10126	23017	36412	6.21	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
10283	23173	36585	2.27	8.2E-02	BE264318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
11848	24554	38024	1.63	8.2E-02	9506428	NT	Rattus norvegicus B-cell translocation gene 3 (Bg3), mRNA
12507	25241	31865	4.43	8.2E-02	AE002246.2	NT	Chlamydomonas reinhardtii AR39, section 73 of 94 of the complete genome
12711	25363	31799	1.49	8.2E-02	AW862195.1	EST_HUMAN	QV4-CT0361-021289-049-b01 CT0361 Homo sapiens cDNA
12882	25703		3.81	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1513	14544	27506	1.22	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5961	19028	32149	1.02	8.1E-02	AE004006.1	NT	Xyella fastidiosa, section 152 of 229 of the complete genome
6840	19879	32889	0.87	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7561	20498		0.8	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8018	20834		1.45	8.1E-02	AI692681.1	EST_HUMAN	wd86108.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8914	21844	35197	0.69	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8914	21844	35198	0.69	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
10423	23312		1.79	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
11929	24774	38272	1.67	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	15864	26009	4.67	8.0E-02	AW954653.1	EST_HUMAN	EST3366723 MAGE resequences, MAGEC Homo sapiens cDNA
963	14013	26955	1.84	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1725	15908	27721	10.85	8.0E-02	D26535.1	NT	Human gene for dihydroilpoamide succinyltransferase, complete cds (exon 1-15)
1725	15908	27722	10.85	8.0E-02	D26535.1	NT	Human gene for dihydroilpoamide succinyltransferase, complete cds (exon 1-15)
1921	14942	27919	2.65	8.0E-02	BE087219.1	EST_HUMAN	PM3-B10347-170200-001-b08 BT0347 Homo sapiens cDNA
2493	15495		3.37	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075919 5'
2868	14160	27098	2.15	8.0E-02	M23449.1	NT	Dicystosium discoidum cyclic nucleotide phosphodiesterase gene, complete cds
2844	15966	28897	0.79	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3887	16916	29794	0.65	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGEC Homo sapiens cDNA
4159	17180		0.69	8.0E-02	4503034	NT	Homo sapiens CAMP responsive element binding protein-like 2 (CREBL2) mRNA
4928	17927		7.91	8.0E-02	X72784.1	NT	Molluscum contagiosum virus subtype 1, complete genome
5404	14013	26955	0.94	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
5945	18012	32131	0.49	8.0E-02	AW951139.1	EST_HUMAN	EST363209 MAGE resequences, MAGEC Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6108	19168	32300	3.19	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7644	19168	32300	1.49	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8704	21835	34981	2.63	8.0E-02	AL114983.1	NT	Bethyis chireea strain T4 cDNA library under conditions of nitrogen deprivation
9926	22831	36217	0.9	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9928	22831	36218	0.9	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10654	23540		0.51	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11232	24158	37607	2.52	8.0E-02	AF217798.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12638	25260	31835	4.67	8.0E-02	AJ005375.1	NT	Drosophila orena hunchback region
13056	17180		1.9	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2187	15198	28203	3.62	7.9E-02	BE250008.1	EST_HUMAN	600943191 F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
3020	16072	28974	15.45	7.9E-02	AI682029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173648 3' similar to gb:Z26876
3917	16945	29624	3.25	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3917	16945	29625	3.25	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4926	17925		1.21	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
5024	18021		0.99	7.9E-02	AV081738.1	EST_HUMAN	xb70a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581628 3'
6894	20021		1.11	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
8910	21541	34883	3.74	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Smt4p (SMT4) gene, complete cds
10531	23417	36831	6.09	7.9E-02	AI081644.1	EST_HUMAN	ou68b05.s1 NCL_CGAP_Bi2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
10531	23417	36832	6.09	7.9E-02	AI081644.1	EST_HUMAN	ou68b05.s1 NCL_CGAP_Bi2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
12967	25532		1.64	7.9E-02	AI761639.1	EST_HUMAN	CE088111
1238	14274	27216	1.32	7.8E-02	AI793275.1	EST_HUMAN	wg68h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
1238	14274	27217	1.32	7.8E-02	AI793275.1	EST_HUMAN	cc56d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
3812	16342		1	7.8E-02	BE250048.1	EST_HUMAN	cc56d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
4910	17909	30779	0.71	7.8E-02	BE866331.1	EST_HUMAN	cc56d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
5221	16942		3.56	7.8E-02	BE250048.1	EST_HUMAN	cc56d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
7431	20129	33370	1.19	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7431	20129	33371	1.19	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
9437	22365	35725	0.87	7.8E-02	X78344.1	NT	S. cerevisiae CAT8 gene
9605	22531	35898	0.84	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9605	22531	35899	0.84	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9899	22887	36271	1.13	7.8E-02	AA469354.1	EST_HUMAN	nc88b06.t1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:771731
10318	23207	36618	0.51	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 399281 to 4214814
11108	24039	37483	1.92	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12883	25479	31764	1.85	7.8E-02	U72847.1	NT	Homo sapiens envoplakin (EVPK) gene, exons 15 through 18
3648	16684		2.13	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5734	18807	31901	0.43	7.7E-02	AF062836.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
8413	21315	34647	0.61	7.7E-02	BE974473.1	EST_HUMAN	7e0403.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281501 3' similar to TR:O95415 O95415 I3 PROTEIN.;
8488	21419	34756	4.99	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.t1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
10350	23239	36658	5.01	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10630	23516	36949	1.09	7.7E-02	A1318662.1	EST_HUMAN	ta80p08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
10630	23516	36950	1.09	7.7E-02	A1318662.1	EST_HUMAN	ta80008.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
11449	24365	37814	5.97	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
12724	25780		1.61	7.7E-02	11438659	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3446	16487	29394	3.15	7.6E-02	BE514432.1	EST_HUMAN	601318428F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3468	16508	29409	1.18	7.6E-02	AA286447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
6334	18384	32552	0.7	7.6E-02	AJ061275.1	EST_HUMAN	en25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
6814	19655	32839	0.86	7.6E-02	BE378928.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9909	22897	36284	1.49	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10409	23298		1.74	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10715	23601	37028	0.59	7.6E-02	BE708002.1	EST_HUMAN	RC1-H10545-020800-017-406 HT0545 Homo sapiens cDNA
10836	23722		0.6	7.6E-02	BE959638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3830810 3'
11060	23944	37380	0.98	7.6E-02	X92656.1	NT	L. esculentum mRNA for triose phosphate translocator

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11080	23944	37381	0.98	7.6E-02	XQ2656.1	NT	L. esculentum mRNA for triose phosphate translocator
12102	24943	38446	2.23	7.6E-02	AW996645.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
811	13867	26802	1.05	7.5E-02		NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
811	13867	26803	1.05	7.5E-02		NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
4630	17636	30500	0.84	7.5E-02	AB015981.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
6068	19127	32258	1.45	7.5E-02	A1848714.1	EST_HUMAN	wq24h02.x1 NCL CGAP_K111 Homo sapiens cDNA clone IMAGE:2472257 3'
8913	21843	35198	1.49	7.5E-02	A1864367.1	EST_HUMAN	wf52b02.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
9074	22003	35357	1.4	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA100264 5'
10535	23421		0.58	7.5E-02	BF221730.1	EST_HUMAN	MEF27 repetitive element;
10971	23655	37282	0.87	7.5E-02	BF206809.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
11061	23945	37382	0.93	7.5E-02	X79460.1	NT	C.fiml DSM 20113 16S rDNA
500	13570	26488	1.17	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
2618	15616		0.98	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3655	16691	29587	0.81	7.4E-02	A1807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4817	17818	30886	1.15	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4909	17908	30778	3.04	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5054	18051	30304	1.65	7.4E-02	6678492	NT	Mus musculus ubiquitin C-terminal hydrolase related polypeptide (Uchrrp), mRNA
6366	18348	31191	1.05	7.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6771	18805		1.56	7.4E-02	R17477.1	EST_HUMAN	yg14g06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
6869	19801	33116	0.41	7.4E-02	AF030422.1	NT	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
7885	20811	34117	0.65	7.4E-02	AA605132.1	EST_HUMAN	no71d02.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
8481	21412	34749	1.33	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3895264 5'
9068	21997	35351	0.83	7.4E-02	U56089.1	NT	Human periodic tryptophan protein 2 (PW/P2) gene, exons 15 to 21, and complete cds
9709	22634	36014	1.1	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9709	22634	36015	1.1	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967861 5' similar to SW:SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
10330	23219	36633	1.02	7.4E-02	U62293.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
12179	25015		1.49	7.4E-02	U89282.1	NT	Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds
12171	25884		3.75	7.4E-02	AW379431.1	EST_HUMAN	CNM-HT0243-081198-037-d11 HT0243 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12854	25484	31781	2.43	7.4E-02	BF035096.1	EST_HUMAN	601453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
491	13562	26478	1.08	7.3E-02	BE984981.2	EST_HUMAN	601668738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
491	13562	26479	1.08	7.3E-02	BE984981.2	EST_HUMAN	601668738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
708	13767	26683	2.8	7.3E-02	AE001789.1	NT	Thermoloba maritima section 101 of 136 of the complete genome
1499	15802	27495	2.95	7.3E-02	AW900281.1	EST_HUMAN	CMD-NN1004-130300-284-q08 NN1004 Homo sapiens cDNA
1870	15812		16.74	7.3E-02	AL183302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4180	17200	30070	1.02	7.3E-02	AJ245944.1	NT	Homo sapiens NGB gene for neuroglobin, exons 1-4
5118	18115		1.64	7.3E-02	U12283.1	NT	Mus musculus NGB gene for neuroglobin, exons 8-10 and complete cds
6723	19759	32986	2.08	7.3E-02	AA779977.1	EST_HUMAN	224a02.s1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:102426 26S PROTEASE SUBUNIT 4 (HUMAN);
7882	20808	34113	3.2	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7882	20808	34114	3.2	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8293	21197		0.45	7.3E-02	BF316087.1	EST_HUMAN	601866047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125615 5'
8746	21678		1.48	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8972	21802	35257	0.55	7.3E-02	Y10887.2	NT	Mus musculus cdk5 gene, exon 1, partial
9751	22676		1.34	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11665	19759	32986	2.1	7.3E-02	AA779977.1	EST_HUMAN	224a02.s1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:102426 26S PROTEASE SUBUNIT 4 (HUMAN);
124	13230	26145	2.42	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
124	13230	26146	2.42	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1494	14525	27486	2.25	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1494	14525	27487	2.25	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2581	15680		3.69	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 2B reverse transcriptase (pol) gene, internal fragment, partial cds
3954	16982	29868	0.72	7.2E-02	AW298322.1	EST_HUMAN	UH-BW0-ajl-a-05-0-UJ.s1 NC1 CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2792049 3'
4455	17465	30322	3.42	7.2E-02	BF572307.1	EST_HUMAN	60207757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4806	17807	30673	0.71	7.2E-02	11468563	NT	Rhodomonas salina mitochondrion, complete genome
5470	18551	31393	2.77	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5471	18552	31394	8.49	7.2E-02	P11120	SWISSPROT	CALMODULIN
6356	19405		0.55	7.2E-02	BF217596.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7531	20470	33759	1.26	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7549	20487	33776	0.63	7.2E-02	AF221126.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative
7576	20512		1.44	7.2E-02	5834897	NT	zinc metalloprotease (zmpB) genes, complete cds
8766	21896	35039	0.69	7.2E-02	P05143	SWISSPROT	Strongylocentrotus purpuratus mitochondrion, complete genome
8766	21896	35040	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9616	22342		0.63	7.2E-02	Y17217.1	NT	PROLINE-RICH PROTEIN MP-3
10104	22895		0.67	7.2E-02	X16349.1	NT	Lactococcus lactis cspE gene
10138	23029	38426	2.37	7.2E-02	AV1712452.1	EST_HUMAN	Human gene for sex hormone-binding globulin (SHBG)
10279	23169	36582	4.17	7.2E-02	L14561.1	NT	AV1712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
10425	23314	36731	1.25	7.2E-02	BF125399.1	EST_HUMAN	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10508	23395	36807	2.45	7.2E-02	AW673187.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026438 5'
10889	23576	37006	0.62	7.2E-02	AA768204.1	EST_HUMAN	h24f11.x1 NCL_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340
							ATYPICAL PKC SPECIFIC BINDING PROTEIN :
							aa62e07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10839	23725	37148	2.26	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN)
10953	23837	37264	4.92	7.2E-02	BE565003.1	EST_HUMAN	genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10978	23860		3.94	7.2E-02	BE539214.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
11351	24269	37711	3.94	7.2E-02	AF049874.1	NT	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
12387	25165	31872	1.82	7.2E-02	AA773696.1	EST_HUMAN	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12471	25217		1.81	7.2E-02	AA584465.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12526	25250		4.57	7.2E-02	U82828.1	NT	nc03d08.s1 NCL_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1089839 3'
12540	25762		5.89	7.2E-02	AW900982.1	EST_HUMAN	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
							CIM4-NN1008-200300-116-c11 NN1008 Homo sapiens cDNA
1922	14943	27920	2.31	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2311	15319	28320	4.11	7.1E-02	BF208902.1	EST_HUMAN	601872281F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4092881 5'
8486	21417	34753	1.06	7.1E-02	A1125264.1	EST_HUMAN	gd92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
12280	25084		4.11	7.1E-02	BE304794.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
551	13620	26528	1.22	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1617	14548		1.24	7.0E-02	X96877.1	NT	Maritellia Micut-1 gene
1789	14812	27761	1.18	7.0E-02	AA056343.1	EST_HUMAN	z66f04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3076	16128	29026	2.02	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-UJ.st NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3967	16995	29879	1.54	7.0E-02	AA815438.1	EST_HUMAN	al66a12.s1 Soares testis NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
4128	17161	30026	1.29	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4237	17253		1.13	7.0E-02	AW792862.1	EST_HUMAN	QV4-B T0407-280100-090-e10 BT0407 Homo sapiens cDNA
4310	17324	30191	1.21	7.0E-02	AF077821.1	NT	CMD-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
5041	18038	30894	9.37	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5562	18640		0.82	7.0E-02	Y09143.2	NT	601816291F1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:4050071 5'
7799	20728	34030	0.88	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
8050	20863	34279	0.74	7.0E-02	Y19187.1	NT	AV689285 GKC Homo sapiens cDNA clone GKCAE06 5'
9643	22569	35940	1.23	7.0E-02	9628113	NT	Gallus gallus mRNA for partial acorzin, XL spliced variant (acz gene)
10124	23015	36411	1.57	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
10459	23347	36764	0.89	7.0E-02	U27268.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
11811	24732	38223	3.23	7.0E-02	AA724296.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
12980	25540	31750	1.68	7.0E-02	11421638	NT	ah99a05.s1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
537	13806	26514	9.27	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
537	13806	26515	9.27	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
						NT	Homo sapiens chromosome 21 segment HS21C010
						NT	Homo sapiens chromosome 21 segment HS21C010
1361	14392		1.08	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3857	16886	29770	1.36	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3857	16886	29771	1.36	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5253	18239	31090	0.93	6.9E-02	AA670269.1	EST_HUMAN	af25e08.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032710 3'
6141	19200		0.46	6.9E-02	AF161364.1	NT	Homo sapiens HSPC101 mRNA, partial cds
8062	20976		0.65	6.9E-02	AF164987.1	NT	Canine distemper virus strain A7517, complete genome
8630	21561		0.88	6.9E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
9116	22044	35400	0.96	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3683030 5'
9116	22044	35401	0.96	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3683030 5'
9664	22590	35963	0.7	6.9E-02	U22967.1	NT	Barbatte duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12415	25184		5.82	6.9E-02	X74315.1	NT	Xlaevis XFD2 mRNA for fork head protein
12571	25276		1.53	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOF6 HOMOLOG
12760	25409		5.15	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1924	14945	27921	4.83	6.8E-02	AF156673.1	NT	Homo sapiens putative hepatic transcription factor (WBSR14) gene, complete cds
1998	15014	28004	0.94	6.8E-02	BE263781.1	EST_HUMAN	601194141F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537708 5'
4247	17263	30129	0.87	6.8E-02	6879250	NT	Mus musculus phosphodiesterase 9A (Pde9a), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4668	17673		0.76	6.8E-02	BE141076.1	EST_HUMAN	MRO-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
6911	19941		0.66	6.8E-02	P20792	SWISSPROT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
7228	20137		1.21	6.8E-02	BE061890.1	EST_HUMAN	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA
7659	20593	33891	8.38	6.8E-02	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
8137	21046	34376	0.74	6.8E-02	U10858.1	NT	Dichosialium discoideum myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8865	21795	35147	5.72	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 576
8865	21795	35148	5.72	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 576
12234	25925		1.63	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Sirelagene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1
12354	25144		1.7	6.8E-02	AA756014.1	EST_HUMAN	ah6706.s1 Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
12338	25504		2.09	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1951	14982		2.6	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1911	14932	27609	1.47	6.7E-02	AI220285.1	EST_HUMAN	qg79e04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3781	16812	29698	5.04	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD-4 (CHOX-4)
4037	17064	28953	0.8	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
4037	17064	28954	0.8	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
8433	21365	34704	0.82	6.7E-02	X62895.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8433	21365	34705	0.82	6.7E-02	X62895.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)
10127	23018	36413	0.84	6.7E-02	AW137359.1	EST_HUMAN	U1-H-B1f-actr-g-01-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
10127	23018	36414	0.84	6.7E-02	AW137359.1	EST_HUMAN	U1-H-B1f-actr-g-01-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1377	14409	27363	0.91	6.6E-02	AI735509.1	EST_HUMAN	at12e09.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2354920 3' similar to
1398	14427	27381	0.96	6.6E-02	AF245116.1	NT	SW_LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG ;
2195	15206	28210	2.21	6.6E-02	AJ289241.1	NT	Drosophila melanogaster cactin mRNA, complete cds
3525	16563	29467	10.68	6.6E-02	R64306.1	EST_HUMAN	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3537	16575	29479	3.59	6.6E-02	7108357	NT	yf18b10.s1 Soares placenta NB21P Homo sapiens cDNA clone IMAGE:139579 3'
3637	16575	29480	3.69	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4167	17188	30061	1.93	6.6E-02	AF260225.1	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
5100	18097	30943	12.83	6.6E-02	Q61703	SWISSPROT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5100	18097	30944	12.83	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6868	19398	33114	3.37	6.6E-02	X08411.1	NT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6901	19931	33148	0.53	6.6E-02	P25159	SWISSPROT	P. vulgaris mRNA for chalcone synthase
6901	19931	33149	0.53	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
7108	19931	33148	0.65	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
7108	19931	33149	0.65	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7437	20134	33374	0.42	6.6E-02	AI243328.1	EST_HUMAN	qh41d01.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3'
8390	21284		0.48	6.6E-02	D14567.1	NT	Penicillium urticae mitochondrial rRNA (large rRNA) gene and its flanking region
8526	21457	34800	2.09	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
9043	21972	35331	0.99	6.6E-02	AF060055.1	NT	Dictyostelium discoideum darlin (darA) gene, complete cds
9477	22405	35764	1.14	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9477	22405	35765	1.14	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10458	23346	36763	0.54	6.6E-02	AF459752.1	EST_HUMAN	987g06.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2149498 3'
10589	23475	36902	1.44	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
10622	23508		0.81	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
11400	24316	37763	6.43	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0084-010800-006-a12 SN0084 Homo sapiens cDNA
12773	25402		2.22	6.6E-02	9937891	NT	Mus musculus DIPB gene (Dipb), mRNA
603	13669	26572	1.49	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954178 5'
1014	14064	27008	1.43	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1418	14449	27403	3.55	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1764	14790	27760	2.01	6.5E-02	AE000764.1	NT	Aquifex acidicus section 96 of 109 of the complete genome
5750	18823	31920	1.77	6.5E-02	AA443991.1	EST_HUMAN	zv48h12.e1 Soares ovary tumor Nb-HOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6822	18855	33067	0.89	6.5E-02	BF665340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7312	18480	31303	0.9	6.5E-02	U22861.1	NT	602118687F1 NIH_MGC 59 Homo sapiens cDNA clone IMAGE:4276029 5'
10451	23340	36756	0.66	6.5E-02	BE963200.2	EST_HUMAN	Azotobacter vinelandii ATCC 8046 negative regulator MucB (mucB) gene, partial cds
10451	23340	36757	0.66	6.5E-02	BE963200.2	EST_HUMAN	6016566817R1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3885637 3'
10944	23829	37255	0.61	6.5E-02	BF106300.1	EST_HUMAN	6016566817R1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3885637 3'
11084	24016	37457	6.78	6.5E-02	AA105648.1	EST_HUMAN	601823351F1 NIH_MGC 77 Homo sapiens cDNA clone IMAGE:4043138 5'
12252	25073		4.17	6.5E-02	M21496.1	NT	zr32g05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12578	25280		2.45	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
597	13664	26566	2.04	6.4E-02	X94549.1	NT	Nicotia glauca tobacco kinesin related protein 2 (KRP2) gene, complete cds
3059	18111	29018	0.97	6.4E-02	6969923	NT	A. carterae precursor of peridinin-chlorophyll-protein (PCP) gene
5005	18111	29016	1.01	6.4E-02	6969923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5237	18224	31073	1.56	6.4E-02	AL163247.2	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5635	18711	31611	1.05	6.4E-02	AI191958.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
6097	19158	32291	0.47	6.4E-02	7305186	NT	qe07b01.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3
6351	19400	32567	5.29	6.4E-02	AF052733.1	NT	LTR8 repetitive element;
6351	19400	32568	5.29	6.4E-02	AF052733.1	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
							Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
							Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6667	19705	32900	0.78	6.4E-02	AI672896.1	EST_HUMAN	we78g12.x1 Soares Dieckgraefe colon NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
7129	20333	33597	4.59	6.4E-02	BE974448.1	EST_HUMAN	601880425F2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
7865	20792	34095	0.46	6.4E-02	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 8/7
8911	21841		3.15	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
9223	22151	35503	4.58	6.4E-02	AA083305.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9672	22593	35971	0.75	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
10114	23005		0.61	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g08 OT0083 Homo sapiens cDNA
10239	23130	36533	1.88	6.4E-02	AB011128.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10754	23640	37073	0.88	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10754	23640	37074	0.88	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12131	24972	38475	2.01	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12131	24972	38476	2.01	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12483	25844		4.18	6.4E-02	AF107880.1	NT	Homo sapiens much 5B (MUC5B) gene, partial cds
12531	25254	31850	2.41	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1780	14806	27775	1.92	6.3E-02	AF105905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3658	16700		2.94	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
5084	18081	30930	1.09	6.3E-02	AI963769.1	EST_HUMAN	wr68g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492706 3'
5365	18347	31190	0.99	6.3E-02	D90912.1	NT	Synechocystis sp. PCC8803 complete genome, 14/27, 1718644-1848241
6378	18425	32591	1.14	6.3E-02	BF210738.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7612	20547		0.71	6.3E-02	X87869.1	NT	H. sapiens gene encoding Le autoantigen
9831	22737	36119	1.1	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominia gene, exons 1-3
10517	23404	36816	3.78	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: GMR-152
10764	23650		1.14	6.3E-02	AF698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
11158	19425	32591	3.33	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
4349	17363	30227	2.04	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4447	17458		1.05	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNP1) mRNA, complete cds
4448	18413		0.83	6.2E-02	U87594.1	NT	Methanococcus jannaschii section 128 of 150 of the complete genome

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4696	17701		7.74	6.2E-02	Q62191	SWISSPROT	92 KD RO PROTEIN (SUJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052)
6416	18397		1.07	6.2E-02	AF126399.1	NT	Arabidopsis thaliana werewolf (WER) gene, complete cds
7104	20310	33571	0.7	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
8075	20988	34305	0.86	6.2E-02	U41433.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8395	21298		0.6	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
8502	25990		0.86	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9882	22787	36183	0.54	6.2E-02	AA1778450.1	EST_HUMAN	af20a06.s1 Soares_t01a_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
10013	22913	36302	1.31	6.2E-02	6677898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
12342	25959		8.19	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12728	25371	31802	3.62	6.2E-02	BF112039.1	EST_HUMAN	7137108.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523816 3' similar to TR.Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
276	13370	26286	6	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
2737	15730	28725	1.52	6.1E-02	AA159188.1	EST_HUMAN	207765.s1 Stragelene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592929 3'
4077	17103		3.55	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKIC1) gene, complete cds
4765	17770	30635	1.14	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4765	17770	30636	1.14	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
6158	19216	32358	0.48	6.1E-02	7682463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6158	19216	32357	0.48	6.1E-02	7682463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
6352	19401		1.07	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
7510	20449	33733	0.45	6.1E-02	A1001497.1	NT	Homo sapiens AFG3L1 gene, exon 2
8839	21769	35115	4.28	6.1E-02	X69268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
9219	22147	35499	0.78	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
9219	22147	35500	0.78	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
11171	24099	37545	4.83	6.1E-02	BE178543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA
12302	25879		34.23	6.1E-02	X70569.1	NT	S. japonicum mRNA for serine-enzyme
12955	25516		6.39	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1289	14322	27268	1.14	6.0E-02	AE001777.1	NT	Thermidoga maritima section 89 of 136 of the complete genome
2724	15717	28714	1.5	6.0E-02	AW968848.1	EST_HUMAN	EST380924 MAGE resequencing, MAGJ Homo sapiens cDNA
2822	15811		1.83	6.0E-02	AB031288.1	NT	Mesocricetus card mitochondria DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2979	13213	26125	1.11	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragelene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2979	13213	26126	1.11	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragelene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3276	16324	28229	1.13	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Oolon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3276	16324	29230	1.13	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3702	16734		1.22	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5089	18086	30937	2.43	6.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5232	18220	31068	0.79	6.0E-02	AF146798.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
5583	18660		1.93	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011189-013-b04 BT0253 Homo sapiens cDNA
6460	19505	32880	1.03	6.0E-02	AI807637.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.11 L1 repetitive element;
7328	18498	31271	2.42	6.0E-02	5174898	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7328	18498	31272	2.42	6.0E-02	5174898	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7552	20489	33778	2.15	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049228 5'
7670	20804	33902	0.84	6.0E-02	BF210488.1	EST_HUMAN	601874710F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101074 5'
8133	21043	34373	1.78	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NIT Homo sapiens cDNA clone IMAGE:1754199 3'
9812	22718	36100	0.8	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:2237362 3'
9812	22718	36101	0.8	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:2237362 3'
9940	22845	36235	1.91	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
9940	22845	36236	1.91	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
10418	23305	36723	0.64	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
10418	23305	36724	0.64	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11778	24677		1.76	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565186 5' similar to gb:X69181.60S RIBOSOMAL PROTEIN L31 (HUMAN);
12893	25483		3.06	6.0E-02	AI809273.1	EST_HUMAN	wf63h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298 O60298 KIAA0551 PROTEIN;
248	13346	26258	4.63	5.9E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
3025	16077	28980	2.7	5.9E-02	AF190269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
7220	25665	33467	0.6	5.9E-02	AF145860.1	NT	Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds
9178	22104	35462	2.28	5.9E-02	9055249	NT	Mus musculus Iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
9983	21341		0.95	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
11224	24160		3.86	6.0E-02	6879870	NT	Mus musculus follistatin-like (Fst), mRNA
11459	24374	37822	1.5	5.9E-02	11433356	NT	Homo sapiens nihel (LOC61199), mRNA
11974	24817		1.7	5.9E-02	BF572939.1	EST_HUMAN	602076548F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4249834 5'
11988	24831		1.68	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
961	14011		4.6	5.8E-02	D60110.1	NT	Thiobacillus ferrooxidans marC, merA genes and URF-1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1687	14717	27678	1.07	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
3731	16763	28650	1.44	5.8E-02	AE001775.1	NT	Thermoboga maritima section 87 of 136 of the complete genome
4464	17475	30332	7.89	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4464	17475	30333	7.89	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4663	17663	30537	5.63	5.8E-02	A1247505.1	EST_HUMAN	qh5601.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb1M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4663	17663	30538	5.63	5.8E-02	A1247505.1	EST_HUMAN	qh5601.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb1M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4669	17694		2.93	5.8E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5262	18248	31098	1.1	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
5272	18258	31109	0.67	5.8E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5272	18258	31110	0.67	5.8E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6129	19188	32324	0.53	5.8E-02	AA190994.1	EST_HUMAN	zp88a11.s1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:627088 3'
8131	21041	34370	2.7	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8131	21041	34371	2.7	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
9224	22152	35504	0.54	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12431	25191		1.5	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12709	26949		4.96	5.8E-02	AA604269.1	EST_HUMAN	no75a11.s1 NCJ_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3105	16156	29061	0.88	5.7E-02	A081644.1	EST_HUMAN	cu63b05.s1 NCJ_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3119	16170	29065	1.56	5.7E-02	AF119117.1	NT	CE088111
3667	16996	29780	3.21	5.7E-02	AW968791.1	EST_HUMAN	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
6094	19155		0.75	5.7E-02	AF276948.1	NT	EST1378865 MAGE resequences, MAGI Homo sapiens cDNA
7879	20805	34108	0.55	5.7E-02	BE871911.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7879	20805	34109	0.55	5.7E-02	BE871911.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7868	20890	34201	0.78	5.7E-02	D78003.1	NT	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7868	20890	34202	0.78	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8793	21663	35008	1.59	5.7E-02	A126600.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
10364	23263	36673	0.72	5.7E-02	6681260	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
11633	24539	38010	3.77	5.7E-02	AF752885.1	EST_HUMAN	Mus musculus ecd2 oncogene (Ecd2), mRNA
							cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11833	24639	38011	3.77	5.7E-02	AF52685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11787	24709		1.75	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12925	25779		8.52	5.7E-02	D50320.1	NT	Pig DNA for SPAI-2, complete cds
12779	25403		1.59	5.7E-02	A1271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12837	25839		3.1	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12971	25935		5.5	5.7E-02	AF261280.1	NT	Pen tregoloytes epolipoprotein-E gene, complete cds
1549	14590	27540	1.35	5.6E-02	AF094455.1	NT	Hydrocotyle retundifolia ribosomal protein L18 (p116) gene, intron; chloroplast gene for chloroplast product
4752	17757	30617	1.08	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4809	17810	30676	1.14	5.8E-02	AA290599.1	EST_HUMAN	zs45001.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6954	19983	33207	4.17	5.6E-02	AW172708.1	EST_HUMAN	xp2c10.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O84979 O84979 KIAA0805 PROTEIN.;
7218	20218	33485	0.76	5.6E-02	AA866182.1	EST_HUMAN	cd47712.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7512	20451	33736	3.36	5.6E-02	BE080001.1	EST_HUMAN	QVQ-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA w234f05.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2559969 3' similar to gb:X06408 RAF
7525	20464	33752	0.58	5.6E-02	A1983738.1	EST_HUMAN	PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
8364	21268	34602	0.54	5.6E-02	A183583.1	EST_HUMAN	qd64g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9360	22288	35652	2.4	5.6E-02	BE542663.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9360	22288	35653	2.4	5.6E-02	BE542663.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10328	23217	36631	1.07	5.6E-02	AA482864.1	EST_HUMAN	nt43d107.s1 NCI_CGAP_AM1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.;
11897	24839		2.43	5.6E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2703	15997	28691	7.61	5.5E-02	X97869.1	NT	H. sapiens gene encoding Le autoantigen
3261	18309	29214	3.98	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (SH3d1B), mRNA
3882	16911		1.34	5.5E-02	BE968659.1	EST_HUMAN	601650078F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933859 5'
4312	17326	30192	1.48	5.5E-02	L41951.1	NT	Gallid herpesvirus mRNA fragment
4984	17883	30841	0.72	5.5E-02	AF161266.1	NT	Murray Valley encephalitis virus strain MVE-1-51, complete genome
5856	18927	32044	2.87	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6288	18927	32044	3.95	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7770	20700	34000	1.61	5.5E-02	6755902	NT	Mus musculus tufelin 1 (Tuf1), mRNA
8697	21628	34972	0.74	5.5E-02	AF170811.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8697	21628	34973	0.74	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10180	23071	36470	0.81	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10180	23071	36471	0.81	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10270	23160	36570	1.27	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
11458	24373	37821	7.83	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB);>
13099	25901	31362	1.82	5.5E-02	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
3065	16117		0.88	5.4E-02	AJ277468.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3483	18410		8.2	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
8702	21633		1.14	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395281 to 2613730
11085	24017	37458	1.76	5.4E-02	AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiens cDNA clone HEMBB1001630 5'
11142	24071	37517	2.53	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
12515	25770		2.17	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1080	14124	27061	1.35	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-062-a09 ST0213 Homo sapiens cDNA
1080	14124	27062	1.35	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021289-062-a09 ST0213 Homo sapiens cDNA
1525	14558	27517	10.63	5.3E-02	T94759.1	EST_HUMAN	y63712.1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01508 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2518	15520	28523	3.27	5.3E-02	AJ278408.1	NT	Pseudomonas putida tgsS gene
2984	16036	28339	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
2984	16036	28940	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3195	16243	29138	4.2	5.3E-02	AJ278408.1	NT	Pseudomonas putida tgsS gene
4721	17726	30589	1.05	5.3E-02	AJ011048.1	NT	Arabidopsis thaliana ell5 gene, exons 1-11
5223	18212	31058	9.91	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5502	18581	31429	1.88	5.3E-02	AE000627.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5502	18581	31430	1.98	5.3E-02	AE000627.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6340	19390	32559	1.11	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7211	20211	33456	4.08	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7451	20392	33662	1.47	5.3E-02	U92832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7752	20682		2.51	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8457	21318	34650	0.63	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SP011 INTERGENIC REGION
8978	21908		0.7	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cystatin C (cs8) gene, complete cds
9670	22596	35970	1.88	5.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-sen DNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10631	23517	36951	0.67	5.3E-02	AB022805.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10631	23517	36952	0.67	5.3E-02	AB022805.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10749	23635		0.88	5.3E-02	Y07907.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-18 hpf and postmitogenesis, 20-28 hpf)
10821	23707	37134	1.34	5.3E-02	X68432.1	NT	B. refo pou1c mRNA for transcription factor
2304	15312		246.31	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3160	16210	29100	2.51	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3160	16210	29101	2.51	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4018	17043	29833	0.89	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4376	17390	30253	3.69	5.2E-02	U07132.1	NT	Human steroid hormone receptor Npr-1 mRNA, complete cds
5322	18306	31156	0.72	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
6140	19199	32336	0.49	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6345	19395		1.19	5.2E-02	AB030965.1	EST_HUMAN	wf0e04.x1 NCI_COAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element:
7660	20584	33981	1.12	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8773	21703		2.58	5.2E-02	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10250	23141	36547	2.08	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
10250	23141	36548	2.08	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12748	23387		2.04	5.2E-02	Q03030	SWISSPROT	OXALACETATE DECARBOXYLASE ALPHA CHAIN
2387	15392		0.98	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_J1 547 (synonym: hbrf1) Homo sapiens cDNA clone DKFZp547D073 5'
4906	17905	30775	0.96	5.1E-02	AF085167.1	NT	Hordeum vulgare receptor-like kinase ARK1AS gene, partial cds
5126	18122		0.99	5.1E-02	AB031740.1	NT	Homo sapiens PBI gene for salivary proline-rich protein P-B, complete cds
5181	18173	31018	1.1	5.1E-02	BE957423.2	EST_HUMAN	601653565R2 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:3838361 3'
6969	19997	33225	0.74	5.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds
7180	18452	31321	1.46	5.1E-02	BF378826.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8828	21758	35102	1.08	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8828	21758	35103	1.08	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8921	21851	35206	1.65	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrocyclopropane 3beta-reductase
9442	22370	35733	0.84	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (OK 14)
9442	22370	35734	0.84	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (OK 14)
10325	23214	36626	8.81	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10878	23564	36994	2.93	5.1E-02	P40803	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
11269	24191	37940	2.49	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11269	24191	37641	2.49	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12756	25390		1.75	5.1E-02	AF062487.1	NT	Cucumis melo polygalacturonase precursor (MPC3) mRNA, complete cds
505	13576	26491	2.29	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1232	14268	27211	7.54	5.0E-02	Z89104.1	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
2007	15025	28016	4.26	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FIPF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2868	14063	27007	1.71	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3386	16429		1.67	5.0E-02	7305810	NT	Mus musculus Ume-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3656	16992		1.15	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3750	16782	29871	6.07	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
4934	17933		1.02	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
5087	18084	30935	0.91	5.0E-02	AF188530.1	NT	Homo sapiens ubiquitously tetrapeptide containing protein RoXan mRNA, partial cds
6370	19419	32585	0.73	5.0E-02	AF066264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6563	19604		1.09	5.0E-02	AJ242625.1	NT	Mus musculus Dimp-1 gene, exons 1-6
7329	18497	31273	0.82	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7967	20889	34200	10.25	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
8199	21105		0.49	5.0E-02	AV062464.1	EST_HUMAN	MRO-CT0064-100699-002-g10 CT0064 Homo sapiens cDNA
10866	23582	37012	1.55	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
11923	24768	38265	2.4	5.0E-02	U67800.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12312	25807		6.67	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
241	13338		17.96	4.9E-02	IM14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
390	13474	26393	2.19	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
390	13474	26394	2.19	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2917	15970	28867	0.76	4.9E-02	U32836.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3332	16378	29278	1.65	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3630	16668		0.72	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Striatagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632928 3' similar to
3652	16888	29582	0.88	4.9E-02	AA400914.1	EST_HUMAN	contains Alu repetitive element; contains element MSR1 repetitive element ;
3652	16888	29583	0.88	4.9E-02	AA400914.1	EST_HUMAN	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4320	17334	30196	1.06	4.9E-02	AF135438.1	NT	z178a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4320	17334	30197	1.06	4.9E-02	AF135438.1	NT	Danio rerio de novo DNA methyltransferase 3 (dnmt3) mRNA, partial cds
4391	17405		1	4.9E-02	M23626.1	NT	Danio rerio de novo DNA methyltransferase 3 (dnmt3) mRNA, partial cds
4954	17952	30810	1.55	4.9E-02	AW167821.1	EST_HUMAN	Drosophila melanogaster developmental protein (rough) gene, complete cds
4954	17952	30811	1.55	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5335	18319	31167	2.64	4.9E-02	7662616	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
5555	18633	31512	1.76	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5555	18633	31513	1.76	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7602	20441	33724	1.16	4.9E-02	AE000580.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
9175	22103		1.16	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
9314	22242	35604	0.86	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10782	23668	37097	0.88	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11839	24690	38179	3.68	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12881	25341		1.62	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC558884), mRNA
12924	25499		2.96	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
350	13438	26352	1.24	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
351	13438	26352	2.14	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
511	13582	26498	6.28	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2282	15300	28306	2.06	4.8E-02	W51983.1	EST_HUMAN	z049b02.s1 Soares senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3254	16302	29208	1.72	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
5278	18264	31114	0.86	4.8E-02	U91914.1	NT	Streptococcus constellatus D-ellantineD-ellantine ligase gene, partial cds
8716	21647	34993	1.33	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
9674	22600	35973	0.84	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9674	22600	35974	0.84	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
7143	20251	33503	3.42	4.7E-02	W01153.1	EST_HUMAN	yz27f02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element
7212	20212	33457	0.79	4.7E-02	BF886625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7212	20212	33458	0.79	4.7E-02	BF886625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7247	20158	33398	1.59	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8181	21088		0.52	4.7E-02	11431898	NT	Homo sapiens protein x 0001 (LOC51185), mRNA
8826	21756	35100	9.98	4.7E-02	X15543.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
9508	22435	35799	1.23	4.7E-02	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9527	22454		3.03	4.7E-02	AB026878.1	NT	Gallus gallus Wpckl-8 gene, complete cds
9768	22692	36078	6.73	4.7E-02	X15543.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
10173	23064	36461	0.53	4.7E-02	BF305237.1	EST_HUMAN	601892692F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
10255	23145		0.57	4.7E-02	A873042.1	EST_HUMAN	we78c10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11989	24832	38328	1.5	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11989	24832	38328	1.5	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12500	25951		1.89	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'
290	13384	26300	1.01	4.6E-02	BE153583.1	EST_HUMAN	PMO-H10339-251199-003-g05 HT0339 Homo sapiens cDNA
763	13620	26749	2.82	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1318	14351		0.83	4.6E-02	AI014255.1	EST_HUMAN	am50002.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P905533
1386	14417	27372	3.79	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA :contains element LTR1 repetitive element ;
2511	15512	28515	2.84	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTC8W C01 5'
2855	13384	26300	2.24	4.6E-02	BE153583.1	EST_HUMAN	xn2403.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
3378	16104	29008	0.67	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1 ;
3555	16104	29008	1.07	4.6E-02	BE153583.1	EST_HUMAN	PMO-H10339-251199-003-g05 HT0339 Homo sapiens cDNA
4219	17235		1.21	4.6E-02	AF220355.1	NT	PMO-H10339-251199-003-g05 HT0339 Homo sapiens cDNA
5836	19003	32122	1.49	4.6E-02	AF076982.1	NT	Mus musculus nucleolar RNA helicase II(Gu (dd21) gene, complete cds
6476	19521	32697	3.36	4.6E-02	X61624.1	NT	Heplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6476	19521	32698	3.36	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
7109	20313	33576	1.25	4.6E-02	AI149574.1	EST_HUMAN	C.reinhardtii atp2 (atpB) mRNA
8357	21282	34598	0.52	4.6E-02	6978720	NT	qc60b06.x1 Soares_placenta_8to8weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1 t3 L1 repetitive element ;
9214	22142	35497	3.8	4.6E-02	BE154006.1	EST_HUMAN	Rattus norvegicus Cathespin H (Cish), mRNA
11840	24691	38180	4.09	4.6E-02	AA913328.1	EST_HUMAN	PMO-H10339-060400-009-G12 HT0339 Homo sapiens cDNA
13016	25563		3.4	4.6E-02	X57808.1	NT	ci27h09.s1 Soares_NFL_T_G9C_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
469	13540	26463	2.77	4.5E-02	P22448	SWISSPROT	Human germline immunoglobulin lambda light chain gene
1246	14282	27224	0.8	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1246	14282	27225	0.8	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozalim VP35 gene, complete cds
1826	14849	27826	4.39	4.5E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozalim VP35 gene, complete cds
2122	15135	28141	1.85	4.5E-02	AE003984.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3787	16818	29706	5.68	4.5E-02	AL163278.2	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
						NT	Homo sapiens chromosome 21 segment HS21C078
						NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6478	19523	32701	1.5	4.5E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C080
6785	19818	33030	0.98	4.5E-02	AL163280.2	NT	Methanoscarcha frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
7205	20205	33450	0.64	4.5E-02	L28487.1	NT	

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7205	20205	33451	0.64	4.5E-02	L28487.1	NT	Methanoscina frisia carbon monoxide dehydrogenase large subunit (cdh1A) gene; carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8984	21894	35251	2.15	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10456	23344	36761	4.29	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' and similar to similar to neuro-D4 protein
10712	23598	37025	0.95	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12497	25237	31861	2.73	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFLP3), mRNA
12865	25846	31494	4.18	4.5E-02	AA191097.1	EST_HUMAN	zq43f11.1r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632483 5'
236	13334		4.12	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3335388 5'
2108	15122		5.72	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2513	15514	28517	1.86	4.4E-02	AW875475.1	EST_HUMAN	QV2-P70012-010300-070-g02 PT0012 Homo sapiens cDNA
3708	16740	29829	2	4.4E-02	AF159160.1	NT	Mycoplasma xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4740	17745	30605	1.51	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4740	17745	30606	1.51	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5399	18381	31221	1.05	4.4E-02	AF081575.1	NT	Petunia x hybrida flavonoid 3',5'-hydroxylase (Hf1) gene, complete cds
7477	20417	33695	4.16	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7477	20417	33696	4.16	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8273	21178	34514	0.42	4.4E-02	11525868	NT	Homo sapiens hypothetical protein PRO2492 (PRO2492), mRNA
8273	21178	34515	0.42	4.4E-02	11525868	NT	Homo sapiens hypothetical protein PRO2492 (PRO2492), mRNA
8312	22240	35601	2.47	4.4E-02	AA736969.1	EST_HUMAN	hw13f03.s1 NCL CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11510	24420	37875	3.67	4.4E-02	AF080689.1	NT	Hepatitis E virus strain HEVJUS2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11646	24552	38023	2.92	4.4E-02	AA496739.1	EST_HUMAN	ae33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12248	25071		2.67	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12416	25860		1.9	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4107418 5'
807	13863	28768	6.2	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2603	15601	28595	1.87	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBACH08 5'
3491	16530	29430	10.72	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3727	16759		1.33	4.3E-02	AF080588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5337	18321	31170	1.18	4.3E-02	AI075275.1	EST_HUMAN	oy8g05.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1671128 3' similar to contains Alu repetitive element; contains element MER3 repetitive element
6772	19806	33016	4.92	4.3E-02	P30427	SWISSPROT	PLECTIN
6772	19806	33017	4.92	4.3E-02	P30427	SWISSPROT	PLECTIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7036	20062	33296	0.92	4.3E-02	AA65286.1	EST_HUMAN	ns89c12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188866
8368	21272		0.44	4.3E-02	L15289.1	NT	Yeast para-aminobenzoate synthase gene, complete cds
8079	22008	35364	0.9	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DS-C3) gene, complete cds, alternatively spliced
9359	22287	35950	1.16	4.3E-02	X55372.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
9359	22287	35951	1.16	4.3E-02	X55372.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
847	13902	26842	2.57	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
891	13944		2.51	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
921	13973	26920	0.87	4.2E-02	AW003646.1	EST_HUMAN	w34g01.x1 NCI_CGAP_P141 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1749	14776		1.24	4.2E-02	AL445068.1	NT	L1 RETROPOSON, ORF2 MRNA ; contains L1, L3 L1 L1 repetitive element ;
3732	16764	29651	1.53	4.2E-02	P23061	SWISSPROT	Thermoplasma acidophilum complete genome, segment 4/5
4214	17231	30100	0.79	4.2E-02	BE262606.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
6812	18884	31893	0.73	4.2E-02	AF280107.1	NT	6011506933F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
5812	18884	31994	0.73	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7323	18491	31264	0.79	4.2E-02	BE268285.1	EST_HUMAN	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7950	20872	34183	4.63	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7976	20897	34210	0.72	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9369	22297	35660	4.41	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10660	23546	35880	1.74	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
11752	24653	38134	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-008-d10 BN0174 Homo sapiens cDNA
11752	24653	38135	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11938	24782	38279	1.69	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
12761	25889		3.73	4.2E-02	AI983494.1	EST_HUMAN	wf49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2610850 3'
533	13602	26513	0.67	4.1E-02	AF200629.1	NT	Homo sapiens HPST gene, intron 5
2725	15718	28715	1.05	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
3969	16997	29882	0.89	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
3969	16997	29883	0.89	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4585	17593		9.36	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-104-f06 NN0012 Homo sapiens cDNA
5839	18910	32025	0.94	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5839	18910	32026	0.94	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7209	20209		1.02	4.1E-02	X76881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7458	20398	33871	1.61	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7638	20858	34168	1.96	4.1E-02	7862347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
8045	20958	34273	0.66	4.1E-02	L02110.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
8234	21139	34471	2.85	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8785	21715	35062	0.72	4.1E-02	P97867	SWISSPROT	ADAM-11 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
9203	22131	36487	0.76	4.1E-02	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9897	22622	36000	0.96	4.1E-02	AA372398.1	EST_HUMAN	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13040	25890	31479	12.28	4.1E-02	AJ271909.1	NT	Bressia napus gln gene for plastid glutamine synthetase, exons 1-12
1689	14899	27659	1.32	4.0E-02	AB75392.1	EST_HUMAN	wb98r01.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2313745 3'
3290	16337	29240	4.8	4.0E-02	AB040804.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3864	16893	29777	1.39	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5273	18259	31111	0.7	4.0E-02	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
5379	18361	31201	1.06	4.0E-02	BF242746.1	EST_HUMAN	601877607F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106280 5'
5564	18642	31520	5.92	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6458	19503	32678	1.61	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:075296 075296 R29124.1;
8143	21052	34384	6.09	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
8217	21122		0.42	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
8235	21140	34472	0.88	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8235	21140	34473	0.88	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
8292	21196	34533	0.48	4.0E-02	AF288153.1	NT	Homo sapiens erythrocyte topomodulin (E-TMOD) gene, exon 7
9276	22204	35661	2.41	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
10170	23081		0.72	4.0E-02	BF079376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
10193	23084	36486	2.36	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
10490	23378		0.9	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds

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12188	25022		1.76	4.0E-02	AJ001018.1	NT	Kluyveromyces lactis gene for Ca++ ATPase
12403	25730	31668	14.22	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1147	14189	27128	2.67	3.9E-02	BF616149.1	EST_HUMAN	U1-H-BW1-ant-h-08-0-U1.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1373	14405	27358	1.89	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1975	14993	27976	2.67	3.9E-02	AJ403386.1	NT	Musculus DNA for desmin-binding fragment DesD7
2754	15745		1.98	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5884	18757	31680	0.76	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5884	18757	31681	0.76	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5933	19000	32120	1.15	3.9E-02	BE968841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
6071	19132	32266	0.63	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7411	20110	33344	1.21	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8409	21312	34644	0.44	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8422	21354	34692	1.67	3.9E-02	BF239513.1	EST_HUMAN	601906849F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8638	21569	34907	0.81	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8638	21569	34908	0.81	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11844	21312	34844	1.81	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12271	25854		13.04	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12870	25472		2.28	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TORBJ1S1, TORBJ1S2>
12988	25786		18.85	3.9E-02	ALD49866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
2133	15146		0.94	3.8E-02	AJ251973.1	NT	Homo sapiens partial steath-1 gene
6040	18037	30893	1.24	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
5628	18702	31601	1.01	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6324	19374	32542	1.1	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7702	20634	33931	1.42	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8034	20849		0.43	3.8E-02	AA392700.1	EST_HUMAN	EST96937 Testis 1 Homo sapiens cDNA 5' end
9222	22150		1.39	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
11097	24028	37472	2.4	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1019	14068	27011	2.9	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1415	14448	27400	1.1	3.7E-02	L14661.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2252	15262	28271	6.12	3.7E-02	A1984806.1	EST_HUMAN	wr85e08.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2615	15613	28608	0.96	3.7E-02	AB018281.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3097	16148	29045	0.73	3.7E-02	P78944	SWISSPROT	EOMESODERMIN
3099	16150	29046	6.51	3.7E-02	BF312963.1	EST_HUMAN	601899233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
6676	16908	33121	0.47	3.7E-02	AJ132405.1	NT	Homo sapiens GDF-9B gene
7434	25980		0.86	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 8/7
8146	21055	34387	0.57	3.7E-02	AE003975.1	NT	Xyella fastidiosa, section 121 of 229 of the complete genome
10518	23405		1.05	3.7E-02	AA782516.1	EST_HUMAN	al55c09.s1 Soares parathyroid tumor NbhPA Homo sapiens cDNA clone 1360912 3'
12310	25116	38578	9.66	3.7E-02	BF124974.1	EST_HUMAN	601782117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12628	25769	31574	2.33	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3722	16754	29642	0.88	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3730	16762	29649	0.88	3.6E-02	AL096808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5612	18688	31568	0.65	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5612	18688	31583	0.65	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5690	18763	31688	0.54	3.6E-02	AF161722.1	NT	Homo sapiens RUP2AS (RUP2) mRNA, complete cds
7004	20031	33262	5.25	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7004	20031	33263	5.25	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7294	18463	31333	0.46	3.6E-02	U67675.1	NT	Melanococcus jannaschii section 117 of 150 of the complete genome
7444	20385	33654	1.89	3.6E-02	AF025962.1	NT	Chromatium vinosum sulfur globule protein Cy2 precursor (sgp2) gene, complete cds
7689	20622	33922	2.87	3.6E-02	AA714521.1	EST_HUMAN	hw20e05.s1 NCJ_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2 TUBULIN BETA-1 CHAIN (HUMAN);
8081	20993	34311	0.77	3.6E-02	BE143078.1	EST_HUMAN	MRO-HT0168-030200-003-b08 HT0168 Homo sapiens cDNA
9928	22833	36220	2.52	3.6E-02	U20608.1	NT	Dicystostellium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9928	22833	36221	2.62	3.6E-02	U20608.1	NT	Dicystostellium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
10139	23030	36427	0.8	3.6E-02	BF347588.1	EST_HUMAN	60202045F1 NCJ_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156116 5'
11625	24532	38000	1.67	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11625	24532	38001	1.57	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
920	13972	26919	1.72	3.5E-02	U09506.1	NT	Drosophila melanogaster tiggtr mRNA, complete cds
1038	14083	27023	1.29	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1584	14815	27577	2.74	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1584	14815	27578	2.74	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4309	17323	30190	2.4	3.5E-02	AE001773.1	NT	Thermococcus maritima section 85 of 136 of the complete genome
4420	17431	30293	1.07	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6466	18511	32886	1.82	3.5E-02	J01238.1	NT	Maize ac1n 1 gene (MAc1), complete cds
8558	21487		0.8	3.5E-02	H29851.1	EST_HUMAN	yp44a05.r1 Soares retina N255HR Homo sapiens cDNA clone IMAGE:180256 5' similar to contains Alu repetitive element;
9183	22111	35470	3.08	3.5E-02	BE938970.1	EST_HUMAN	601044701R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3929737 3'
10521	23408	36820	1.88	3.5E-02	X76842.1	NT	L.lactis MG1363 grpE and dnaK genes
10567	23453	36874	0.51	3.5E-02	BE581042.1	EST_HUMAN	601344561F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11926	24771	38268	2.03	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-281289-002-H03 CT0328 Homo sapiens cDNA
11926	24771	38269	2.03	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-281289-002-H03 CT0328 Homo sapiens cDNA
12922	25785		6.42	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
600	13667	26569	1.13	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
600	13667	26570	1.13	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
601	13667	26569	2.94	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
601	13667	26570	2.94	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1077	14121	27058	2.46	3.4E-02	AW274020.1	EST_HUMAN	xv26d07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P33601 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1234	14270		6.05	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2415	15419	28420	2.11	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3492	16531	29431	1.83	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3996	17023	29913	4.82	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4708	17713	30576	2.88	3.4E-02	X59789.1	NT	M.musculus S-antigen gene promoter region
5195	18187		3	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5212	18202	31046	1.82	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6447	19493		0.62	3.4E-02	BF131628.1	EST_HUMAN	601820446F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4062434 6'
7173	18445	31314	5.04	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8837	21767		3.39	3.4E-02	AI869529.1	EST_HUMAN	w88d04.x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9307	22235	35596	1.05	3.4E-02	AA684886.1	EST_HUMAN	nu70f08.s1 NCI_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ;
9474	22402		5.03	3.4E-02	AA194306.1	EST_HUMAN	zq04f11.s1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
10287	23187		0.85	3.4E-02	A092719.1	EST_HUMAN	IPISGKPLPKVTL SRDGVPLKATMRFNTEITAEINLTKESVTADAGRYEITAAISSGTTKAFINIVLDRPG
393	13477		7.84	3.3E-02	AA398735.1	EST_HUMAN	PPT GPVMSDITEESVTLKWEPPKYDGSQVNTYLLKRETSTAVW TEVSATVARTMMKVMKL ...;
1194	14233	27172	10.27	3.3E-02	AB035987.1	NT	0289d08.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:728198 3'
1820	14551	27513	0.91	3.3E-02	L16870.1	NT	z175e08.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1665	14995	27655	1.13	3.3E-02	AF110763.1	NT	Oricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1767	14793		0.97	3.3E-02	AE000700.1	NT	Homo sapiens cytochrome P4502C18 (CYP2C18) gene, exons 2 and 3
2097	15111		2.44	3.3E-02	R09112.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2476	15478	28479	1.42	3.3E-02	6755862	NT	Aquifex edicus section 32 of 109 of the complete genome
3416	18458	29364	0.89	3.3E-02	H02389.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:121888 5'
4273	14895	27655	3.48	3.3E-02	AF110763.1	NT	Mus musculus tumor rejection antigen gp86 (Trat), mRNA
4578	17587	30449	2.71	3.3E-02	6755862	NT	y35f02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
6698	19734	32935	19.31	3.3E-02	BF245995.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
6998	19734	32936	19.31	3.3E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp86 (Trat), mRNA
7931	20953	34161	0.53	3.3E-02	AF124162.1	NT	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9862	22777	36164	0.84	3.3E-02	BF115621.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9862	22777	36165	0.84	3.3E-02	BF115621.1	EST_HUMAN	Nicotiana plumbaginifolia molybdopterin synthase sulphurylase (crs6) gene, partial cds
9958	22863	36250	0.63	3.3E-02	AA488202.1	EST_HUMAN	7m92404.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
9958	22863	36251	0.63	3.3E-02	AA488202.1	EST_HUMAN	7m92404.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
11067	23951		0.52	3.3E-02	H98109.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:977673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11561	24670	37636	3.27	3.3E-02	BF691107.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:977673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
12072	24913	38416	1.4	3.3E-02	AF077337.1	NT	y61f11.s1 Soares retina N2b-HFR Homo sapiens cDNA clone IMAGE:190889 3'
12484	25227		3.82	3.3E-02	T66545.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12600	25296		1.68	3.3E-02	AF289665.1	NT	Zea mays heat shock protein 101 (HSP101) gene, complete cds
12628	25311		2.2	3.3E-02	M81890.1	NT	y649f11.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:121101 5'
136	13238	26157	1.46	3.2E-02	AJ002005.1	NT	Mus musculus EIF4H gene, partial cds; LmK1 gene, complete cds; and ELN gene, partial cds
1153	14184	27132	8.71	3.2E-02	AF096275.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
							Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
							Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68a allele, complete cds

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1153	14194	27133	8.71	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 88 (hsp88) gene, hsp88d allele, complete cds
2131	15144		1.94	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2885	13238	26157	1.01	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3179	16229	29123	17.23	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3946727 5'
3777	16808	28696	1.42	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4315	17329		17.61	3.2E-02	X94768.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4880	17679	30744	3.77	3.2E-02	AF114182.1	NT	Saxifraga nidifica maburase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
4941	17940	30797	0.69	3.2E-02	AF087083.1	NT	Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Trp repressor binding protein gene, partial cds; and unknown genes.
5061	18058		0.92	3.2E-02	AF109908.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70L and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5725	18798	31890	1.69	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
5726	18798	31891	1.69	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
6802	19835	33046	2.31	3.2E-02	M32437.1	NT	Ra/polyomavirus left junction in cell line W98.14
6805	19838		27.99	3.2E-02	T89367.1	EST_HUMAN	yc33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6895	19925	33140	3.81	3.2E-02	AF173845.1	NT	Alu repetitive element; contains LTR1 repetitive element ;
8231	21136	34468	0.9	3.2E-02	11424049	NT	Sagittinus oedipus tissue kallikrein gene, complete cds
8401	21304	34639	0.46	3.2E-02	AA555015.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
8875	21805	35158	4.16	3.2E-02	6680569	NT	h07d11.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1029621 similar to gb:X05923 UBIQUITIN-LIKE PROTEIN FUBI (HUMAN);
9496	22424		0.95	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9768	22690	36076	1.32	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9768	22690	36076	1.32	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1892063 3'
10559	23445		4.52	3.2E-02	AA716795.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1892063 3'
10644	23730	37153	1.15	3.2E-02	U96762.1	NT	zq54b12.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
12211	25045		1.43	3.2E-02	AL163302.2	NT	gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1287	14320		2.17	3.1E-02	4603416	NT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1331	14365	27314	1.12	3.1E-02	P18945	SWISSPROT	Homo sapiens distal specificity phosphatase 4 (DUSP4) mRNA
1910	14931	27908	1.41	3.1E-02	6671564	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1990	15008		1.05	3.1E-02	Z50097.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5445	18526	31252	1.22	3.1E-02	U78104.1	NT	Drosophila melanogaster mRNA for headcase protein
							Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5545	18623		2.38	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5844	18915	32031	0.89	3.1E-02	BF687742.1	EST_HUMAN	802068783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085789 5'
5916	25835	32104	0.42	3.1E-02	AJ391284.1	NT	Nisseria meningitidis DNA for region 2 (flaB- and flaC-homologs, unknown genes) and flanking genes, strain FAM18
10534	23420	36836	2.6	3.1E-02	AF034778.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1646	14877		1.74	3.0E-02	AF187125.1	NT	Pityrialeas minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2623	15821	28814	1.41	3.0E-02	AA402242.1	EST_HUMAN	z65h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3625	16861	28861	1.22	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3721	16753	28841	3.17	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3808	16838		0.76	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150200-040-e08 ST0286 Homo sapiens cDNA
4027	17054		0.95	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5185	18177	31022	8.94	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5186	18177	31023	8.94	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5576	18654		3.18	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1673 protein, partial cds
6503	19547	32724	0.7	3.0E-02	N99815.1	EST_HUMAN	z639a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element;
6503	19547	32725	0.7	3.0E-02	N99815.1	EST_HUMAN	z639a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element;
7098	20304	33563	2.45	3.0E-02	AJ242006.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
7235	20144	33363	2.96	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7235	20144	33364	2.96	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7426	20125	33363	2.14	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7426	20125	33364	2.14	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7601	20536	33825	1.19	3.0E-02	M86524.1	NT	Human dystrophin gene
8019	20935		0.68	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
9180	22108	35466	0.55	3.0E-02	BE512570.1	EST_HUMAN	601171628F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3545047 5'
9200	22128	35484	0.83	3.0E-02	BF333889.1	EST_HUMAN	IL5-H10704-280600-108-c04 H10704 Homo sapiens cDNA
9351	22279		1.65	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10939	23824	37251	1.94	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 138 of the complete genome
11025	23909	37350	0.53	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11681	24586	38062	2.47	3.0E-02	M81367.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12114	24955	38458	8.71	3.0E-02	AA483216.1	EST_HUMAN	ne8704.s1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12581	25937	31373	2.56	3.0E-02	R32019.1	EST_HUMAN	yt6304.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12013	25496		7.82	3.0E-02	AW896565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12982	25931		4.22	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Galglucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
3033	16085	28935	1.12	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3033	16085	28987	1.12	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
4004	17031	29921	0.81	2.9E-02	HT2805.1	EST_HUMAN	yt07a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
4070	17086	28979	0.68	2.9E-02	O15440	SWISSPROT	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5 (ABC TRANSPORTER MOAT-O) (PABC11) (SMRP)
5144	18139	30981	0.91	2.9E-02	XG5137.1	NT	S. vulgaris pepC gene for PEP carboxylase
5144	18139	30982	0.91	2.9E-02	XG5137.1	NT	S. vulgaris pepC gene for PEP carboxylase
5250	18414		3.66	2.9E-02	RO9112.1	EST_HUMAN	yt25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
6298	16349	32517	1.31	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6545	19588	32775	0.16	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
7286	20239	33489	0.57	2.9E-02	AJ391284.1	NT	Nelisseria meningitidis DNA for region 2 (flaB- and flhA-homologs, unknown genes) and flanking genes, strain FAM18
7619	20554	33847	10.47	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7827	20765	34060	0.54	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8577	21508	34853	1.01	2.9E-02	AF129278.1	NT	Buchnera aphidicola natural host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8577	21508	34854	1.01	2.9E-02	AF129278.1	NT	Buchnera aphidicola natural host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
10183	23074	36474	2.06	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10183	23074	36475	2.06	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10366	23275		0.85	2.9E-02	AW976597.1	EST_HUMAN	EST388706 MAGE resequences, MAGN Homo sapiens cDNA
10832	23718	37143	1.17	2.9E-02	AP000084.1	NT	Aeropyrum pernix genomic DNA, section 777
11485	18426	31350	2.04	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12583	25853		1.73	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002862 5'
557	13655		0.78	2.8E-02	AW070153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3425	16466	29373	1.77	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3425	16466	29374	1.77	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
5676	18750	31672	10.93	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
7120	20324	33598	1.05	2.8E-02	IT78980.1	EST_HUMAN	yt21b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8903	21833	35188	1.61	2.8E-02	AJ005820.1	NT	Craterosigma plantaginum mRNA for homeodomain leucine zipper protein (hb-1)
9588	22495	35858	0.92	2.8E-02	AA280782.1	EST_HUMAN	zs96c06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9749	22673	36057	1.23	2.8E-02	AF187872.1	NT	Cavia porcellus inward-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9853	22768	36153	0.65	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12204	25039	38542	1.49	2.8E-02	L33697.1	NT	Chlamydomonas reinhardtii kinesin-homologous protein (FLA10) mRNA, complete cds
1507	14539	27500	1.38	2.7E-02	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
3493	18332	28432	1.72	2.7E-02	AL181494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4288	17312	30178	2.1	2.7E-02	N47258.1	EST_HUMAN	y88h12.r1 Scores_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4288	17312	30179	2.1	2.7E-02	N47258.1	EST_HUMAN	y88h12.r1 Scores_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'
5383	18365	31204	1.22	2.7E-02	T95073.1	EST_HUMAN	ye36f04.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120127 3' similar to contains Alu repetitive element;
5428	18510	31234	0.51	2.7E-02	BF245872.1	EST_HUMAN	60186481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5927	18703	31602	1.16	2.7E-02	R12245.1	EST_HUMAN	yf33d09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6120	19179	32314	0.68	2.7E-02	X61870.1	NT	T aestivum pTTH20 mRNA for wheat type V thionin
6204	19260	32407	0.52	2.7E-02	AB004799.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6886	19915		0.89	2.7E-02	X97580.1	NT	A.bisporus pgkA gene
7421	20120	33357	1.92	2.7E-02	AA93571.1	EST_HUMAN	o99f03.s1 Scores fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1824681 3'
8363	21267		0.6	2.7E-02	AK024456.1	NT	Homo sapiens mRNA for FLJ00048 protein, partial cds
8388	21901	34632	0.56	2.7E-02	9265542	NT	Mus musculus G21 protein (G21), mRNA
8927	21857		1.28	2.7E-02	A1377038.1	EST_HUMAN	tc28q09.x1 Scores total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
593	13660	26563	1.12	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2389	15394	28396	3.01	2.6E-02	AA490021.1	EST_HUMAN	ab02802.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2391	15398	28398	2.97	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2391	15398	28399	2.97	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2958	16010		1.3	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; B1, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
4019	17046		1.25	2.6E-02	AA071307.1	EST_HUMAN	zmf73f09.s1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:531305 3'
4392	17409		1.13	2.6E-02	Y07848.1	NT	Homo sapiens ELWS, gar22, rp22 and bam22 genes
5013	18011	30869	3.87	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5199	18191	31033	1.29	2.6E-02	AE002014.1	NT	Delinococcus radiodurans R1 section 151 of 228 of the complete chromosome 1
6227	18216	31062	2.49	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCI CGAP_Ser4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
6058	19120		0.47	2.6E-02	AL101563.2	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
6107	19167		0.51	2.6E-02	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6464	18509		7.05	2.6E-02	AL206030.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6693	19729	32829	2.29	2.6E-02	BE621748.1	EST_HUMAN	q927f11.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
7140	20248	33499	0.78	2.6E-02	Z99064.1	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
7140	20248	33500	0.78	2.6E-02	Z99064.1	NT	Vaccinia virus ORF1L, strain Wjeth
7238	20147	33387	5.57	2.6E-02	6981271	NT	Vaccinia virus ORF1L, strain Wjeth
7878	20612	33911	0.7	2.6E-02	P21894	SWISSPROT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
9072	22001	35355	0.87	2.6E-02	AA80946.1	EST_HUMAN	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
9898	22886	36270	1.45	2.6E-02	11432020	NT	ak2204.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408719 3'
10236	23127	36529	0.77	2.6E-02	AF114952.1	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
10236	23127	36530	0.77	2.6E-02	AF114952.1	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10888	23773	37199	4.93	2.6E-02	AL163303.2	NT	Saccharomyces cerevisiae NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
11925	24745		2.19	2.6E-02	AA279351.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G103
11955	24837	38336	1.87	2.6E-02	AW500547.1	EST_HUMAN	z884c02.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
555	13624	26532	1.51	2.6E-02	AI793130.1	EST_HUMAN	U1-HF-BNO-ekj-10-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077468 5'
555	13624	26533	1.51	2.6E-02	AI793130.1	EST_HUMAN	on26f08.y6 NCI CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1657827 5'
835	13890	26827	13.09	2.5E-02	BE974314.1	EST_HUMAN	on26f08.y6 NCI CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1657827 5'
894	13947	26894	4.47	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2813	15802		2.54	2.5E-02	U12571.1	NT	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2997	16049	28961	1.88	2.6E-02	X99697.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2997	16049	28962	1.88	2.6E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4129	18403	30027	1.28	2.5E-02	BE701165.1	EST_HUMAN	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4129	18403	30028	1.28	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4301	17315	30181	6.15	2.5E-02	AW592114.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
5361	18393		0.96	2.5E-02	BE277116.1	EST_HUMAN	h36f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5912	18981	32099	0.58	2.5E-02	AI732776.1	EST_HUMAN	601178025F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543822 5'
6434	19481		4.75	2.5E-02	BE970128.1	EST_HUMAN	z883c10.x5 Soares_ovary_tumor_NH0T Homo sapiens cDNA clone IMAGE:810354 3'
							7630c09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.L1 L1 repetitive element;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6453	19498		4.42	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928054 5'
6593	19634	32816	0.83	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
8116	21027	34353	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCJ_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213406 5'
8116	21027	34354	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCJ_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213406 5'
8360	21285	34600	0.48	2.5E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (P-HF2) gene, complete cds
8558	21489	34828	0.63	2.5E-02	BE252469.1	EST_HUMAN	601108291F1 NIH_MGC 18 Homo sapiens cDNA clone IMAGE:3344278 5'
8984	22312	35674	0.73	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
10568	23454		0.78	2.5E-02	XT1303.1	NT	D radicum 28S ribosomal RNA, D2 domain
11055	23939	37377	0.68	2.5E-02	AI147616.1	EST_HUMAN	qb22a08.x1 Soares_pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:1696982 3'
11249	24173	37620	2.37	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11249	24173	37621	2.37	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11299	24218	37668	4.26	2.5E-02	AJ237936.1	NT	Bos taurus partial stat5B gene, exons 17-19
11318	24237						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds;
12181	25017		3.87	2.5E-02	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-IP
12215	25049		1.74	2.5E-02	AB007646.1	NT	Homo sapiens gene for LECT2, complete cds
12477	25865		1.43	2.5E-02	X88999.1	NT	Pseudomonas sp. transposon Tn5041 DNA
12653	25749		2.05	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12740	25380		1.7	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
184	13283	26200	2.18	2.5E-02	U60169.1	NT	Dicotyledon discoidium putative protein kinase MicaA (mkaA) gene, complete cds
1621	14651	27614	1.01	2.4E-02	AI378582.1	EST_HUMAN	ic72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
2058	15915	28075	1.71	2.4E-02	H65884.1	EST_HUMAN	y75111.r1 Soares_fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
2058	15915	28076	1.71	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4475	17486	30345	2.53	2.4E-02	J05110.1	NT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4641	17647	30511	1.5	2.4E-02	P01901	SWISSPROT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4641	17647	30512	1.5	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5294	18279	31129	1.1	2.4E-02	8922702	NT	Homo sapiens hypothetical protein FLJ10844 (FLJ10844), mRNA
6459	19504	32679	1.05	2.4E-02	W66690.1	EST_HUMAN	zh63104.s1 Soares_fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
6620	19660	32844	0.51	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
6620	19660	32845	0.51	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7590	20526	33816	0.79	2.4E-02	Z20573.1	EST_HUMAN	HSAACCKVX.T. Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7607	20542	33832	0.83	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7607	20542	33833	0.83	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8397	21300	34630	0.56	2.4E-02	P98092	SWISSPROT	HEMOCYTIN PRECURSOR (HUMORAL LECTIN)
8397	21300	34631	0.56	2.4E-02	P98092	SWISSPROT	HEMOCYTIN PRECURSOR (HUMORAL LECTIN)
8470	21401		0.74	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-h06 ST0186 Homo sapiens cDNA
8522	21453		0.81	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
9009	21938		0.87	2.4E-02	H78376.1	EST_HUMAN	y412c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element ;
9095	22024	35380	2.18	2.4E-02	N69442.1	EST_HUMAN	z85g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gb K02809 RATSR7K Rat (rRNA); contains A3R b1 A3R repetitive element ;
9638	22465	35828	0.6	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
9561	22488	35849	0.99	2.4E-02	AA625660.1	EST_HUMAN	z181c06.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:746354 3' similar to gb J04422 SLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
10322	23211	36623	2.67	2.4E-02	AV692854.1	EST_HUMAN	XTR repetitive element ;
10487	23375	36790	3.35	2.4E-02	AA483894.1	EST_HUMAN	AV692854 GK Homo sapiens cDNA clone GKQDSC03 5'
							nh07b72.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element ;
12005	24847	38344	2.3	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12005	24847	38345	2.3	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
12296	25106		4.99	2.4E-02	8827909	NT	Bacteriophage bL67, complete genome
12428	25190	31879	2.48	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
12530	25253	31829	1.86	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12530	25253	31867	1.86	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
12693	25350		13.1	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1895	14916		3.58	2.3E-02	W05340.1	EST_HUMAN	z84g08.t1 Soares_fetal_jung_NbH-19W Homo sapiens cDNA clone IMAGE:289294 5'
1907	14928		6.73	2.3E-02	U64165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2373	15378	28380	2.77	2.3E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
3749	16781	29670	5.63	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
3778	16809		0.66	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3' end

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4248	17264	30130	0.91	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4248	17264	30131	0.91	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4527	17536	30398	1.12	2.3E-02	AW599107.1	EST_HUMAN	CM4-HN0080-290400-180-b04 NN0080 Homo sapiens cDNA
4559	17568	30427	1.12	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4559	17568	30428	1.12	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4560	18405	30429	1.15	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4560	18405	30430	1.15	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4705	17710	30573	3.03	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4705	17710	30574	3.03	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5141	18136	30978	0.92	2.3E-02	A1783177.1	EST_HUMAN	q235c03.x3 NCL CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2028868 3'
5141	18136	30979	0.92	2.3E-02	A1783177.1	EST_HUMAN	q235c03.x3 NCL CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2028868 3'
5164	18156	31003	1.02	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-280100-011-a07 CN0051 Homo sapiens cDNA
5560	18638	31517	3.68	2.3E-02	U66303.1	NT	Caubacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcdB) homolog gene, partial cds
6483	19528	32706	0.5	2.3E-02	BF106464.1	EST_HUMAN	801822821R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6908	19938	33157	4.37	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7320	18488	31260	1.11	2.3E-02	BE141475.1	EST_HUMAN	MRO-HT0080-011099-002-c09 HT0080 Homo sapiens cDNA
7867	20794	34096	0.43	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8456	21368	34727	6.56	2.3E-02	U63610.1	NT	Human plectin (PLECT) gene, exons 3-32, and complete cds
8041	21970	35329	0.97	2.3E-02	AJ288105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9041	21970	35330	0.97	2.3E-02	AJ288105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9254	22182	35636	0.8	2.3E-02	AI885380.1	EST_HUMAN	wa78r10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9254	22182	35637	0.8	2.3E-02	AI885380.1	EST_HUMAN	wa78r10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9881	22607	35980	0.85	2.3E-02	P41986	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10373	23262	36884	0.79	2.3E-02	P60532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10533	23419	36834	1.63	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10533	23419	36835	1.63	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11221	24147	37598	2.04	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12214	25048		1.41	2.3E-02	AF159132.1	NT	Metapneus ensis fushi tarazu-factor 1 mRNA, complete cds
12408	25736		5.09	2.3E-02	BE278331.1	EST_HUMAN	801179858F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12891	25481	31765	3.4	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12939	25963		3.37	2.3E-02	U11077.1	NT	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
761	13818	26747	2.85	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1773	14799		1.22	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2028	15045	28040	1.4	2.2E-02	Z82001.1	NT	S.pneumoniae popA gene and open reading frames
2774	15933	28759	1.24	2.2E-02	AF108633.1	NT	Mus musculus eis variant protein ER81 gene, exons 1 through 4
3498	16535		1.99	2.2E-02	AA577786.1	EST_HUMAN	nm24a04.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3715	16747		4.46	2.2E-02	AF083084.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3920	16948	29830	1.15	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-304-b03 BT0340 Homo sapiens cDNA
3995	17022	29912	0.65	2.2E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4726	17731		0.9	2.2E-02	P16759	SWISSPROT	HYPOTHETICAL PROTEIN UL21
6509	19553	32733	0.51	2.2E-02	BF109222.1	EST_HUMAN	760b11.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525836 3' similar to TR-Q12899 Q12899 ACID FINGER PROTEIN ;
7617	20552	33845	3.24	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8943	21873	35233	1.89	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8943	21873	35234	1.89	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9368	22296	35659	0.8	2.2E-02	X79468.1	NT	P.vulgaris alpha tub 2 mRNA
10210	23101	36501	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10210	23101	36502	2.26	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10701	23587		1.17	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssat1), mRNA
11664	24560	38031	1.69	2.2E-02	BE797601.1	EST_HUMAN	601584309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571 5'
12656	25329		2.8	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCL_CGAP_C88 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
442	13513		6.01	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
471	13542		6.53	2.1E-02	AF029726.1	NT	Dictpetalum discordeum histidine kinase C (dhkc) mRNA, complete cds
1290	14323	27269	5.86	2.1E-02	U72073.1	NT	Bacillus subtilis cotK(LM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1414	14444	27397	1.06	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1414	14444	27398	1.06	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1806	14832	27800	0.98	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1806	14832	27801	0.98	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1806	14832	27802	0.98	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1977	14995	27979	1.02	2.1E-02	AF190899.1	NT	Tegula aureolincta major acrosomal protein precursor (TMAP) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2048	15065	28066	0.95	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2048	15065	28067	0.95	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2624	15622	28615	1.28	2.1E-02	AA225095.1	EST_HUMAN	nc21g03.r1 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008820
2883	13881	28788	3.42	2.1E-02	N28286.1	EST_HUMAN	y43h07.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264541 5'
3182	15065	28066	0.95	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3182	15065	28067	0.95	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3645	16881	29578	1.28	2.1E-02	AA461271.1	EST_HUMAN	z63b09.r1 Soares fetal fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4227	17243	30111	0.72	2.1E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
4414	17425	30287	0.97	2.1E-02	BF343655.1	EST_HUMAN	6020163067-1 NC1_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4554	17563	30422	2.02	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4565	17573	30436	1.59	2.1E-02	AI768127.1	EST_HUMAN	wg81d111.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4823	17824	30683	6.16	2.1E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4933	17932	30761	0.69	2.1E-02	AI823432.1	EST_HUMAN	wh54a05.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5838	18907	32022	0.81	2.1E-02	AW379529.1	EST_HUMAN	QV4-HT0244-111199-Q40-H05 HT0244 Homo sapiens cDNA
7420	20119	33356	0.78	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8084	22013	35370	0.92	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
10034	22934	36322	0.61	2.1E-02	AA884288.1	EST_HUMAN	am83e07.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
10157	23048	36447	2.31	2.1E-02	AJ243213.1	NT	Alu repetitive element; contains element MER11 repetitive element ;
10157	23048	36448	2.31	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10489	23377	36792	1.41	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10563	23449	36871	0.71	2.1E-02	AA884288.1	EST_HUMAN	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and
12638	18429		13.76	2.1E-02	Y19213.1	NT	UmuC MucA homolog genes, complete cds, and unknown genes
13026	25567	31737	12.1	2.1E-02	AF183913.1	NT	am83e07.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
18	13134	26020	0.77	2.0E-02	BF002932.1	EST_HUMAN	Alu repetitive element; contains element MER11 repetitive element ;
19	13135	26021	7.06	2.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
278	13373	26287	3.1	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
315	13407	26325	2.79	2.0E-02	AA456538.1	EST_HUMAN	aar15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
825	13880	26817	1.99	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1114	14156	27095	135.42	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [p36.33] of Homo sapiens
1227	14264	27207	1.04	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1227	14264	27208	1.04	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1898	14917	27895	1.45	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1898	14917	27896	1.45	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2846	15835		2.15	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3128	13134	26020	1.75	2.0E-02	BF002932.1	EST_HUMAN	Tg51c08.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3309988 3' similar to contains MER1.13 MER1 repetitive element;
3187	16236		1.42	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3274	16322		1.54	2.0E-02	AF095598.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4092	17117	29895	1.44	2.0E-02	M18095.1	NT	P. vulgaris hydroxylase-rich glycoprotein (HRGP) mRNA, 3' end
5285	18271	31119	0.65	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
5349	18332	31180	0.98	2.0E-02	Z21088.1	EST_HUMAN	HSAAADMI TEST1, Human adult Testis tissue Homo sapiens cDNA clone CA
5370	18352		0.97	2.0E-02	BF085913.1	EST_HUMAN	GM0-GN0038-150900-548-f09 GN0038 Homo sapiens cDNA
5831	18902	32017	0.41	2.0E-02	U34778.1	NT	Caenorhabditis elegans sma-2 mRNA, complete cds
6115	19174	32308	0.6	2.0E-02	L36321.2	NT	Dictyostellum discoideum class VII unconventional myosin (myo) gene, complete cds
7982	20903	34218	0.98	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (417)
7982	20903	34219	0.98	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt position (417)
10369	23278		2.21	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10847	23733	37156	2.12	2.0E-02	AB40342.1	EST_HUMAN	wat1b02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
11087	24019	37460	5.61	2.0E-02	Z73968.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11810	24731	38222	2.1	2.0E-02	D98184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
12107	24948	38450	1.58	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12107	24948	38451	1.58	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12241	18271	31119	1.98	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12673	15835		1.84	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13085	25605		6.43	2.0E-02	T80037.1	EST_HUMAN	y404c09.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:24675 5'
717	13775	26695	1.72	1.8E-02	AA572764.1	EST_HUMAN	n16a07.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914186 similar to contains L1.14 L1 repetitive element;
1639	14670	27633	1.13	1.9E-02	P18488	SWISSPROT	ENPTY SPIRACLES HOMEOTIC PROTEIN
2053	15070	28070	3.41	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2053	15070	28071	3.41	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2531	15532	28533	1.27	1.9E-02	AL181550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2949	16001	28902	10.55	1.9E-02	AA713856.1	EST_HUMAN	nr04f05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2994	16046	28949	2.01	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3304	16351		0.75	1.9E-02	AB033611.1	NT	Utrichus talpoides mitochondrial gene for cytochrome b, complete cds
3675	16708		1.04	1.9E-02	N52250.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:284331 3'
3768	16900		5.45	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
4131	17153	30030	1.85	1.9E-02	AF141940.1	NT	Mycoplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds
4289	17303	30171	1.76	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4289	17303	30172	1.76	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4657	17662	30530	3.59	1.9E-02	AI452699.1	EST_HUMAN	U46404.x1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
4851	17853		0.9	1.9E-02	AF178754.3	NT	Homo sapiens lithium-sensitive myo-inositol monophosphatase A1 (IMPA1) gene, promoter region and partial cds
5137	15532	28533	2.44	1.9E-02	AL181550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5499	18578	31426	1.09	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5955	18729	31634	1.41	1.9E-02	L47572.1	NT	Meleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
5998	19063		0.69	1.9E-02	AB019507.1	NT	Drosophila kareid gene for glycerol-3-phosphate dehydrogenase, complete cds
7460	20400	33673	1.28	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7460	20400	33674	1.28	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
9134	22062		1.42	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
9971	22786	36178	1.26	1.9E-02	BF316128.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
10235	23126	36528	0.55	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10548	23434	36854	1.2	1.9E-02	BF65832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10947	23533	36965	0.57	1.9E-02	N39160.1	EST_HUMAN	yy46h08.s1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:276839 3'
10746	23632	37065	0.64	1.9E-02	D64001.1	NT	Synochocystis sp. PCC6803 complete genome, 20/27, 2539000-2844794
12438	25741	31971	3.54	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament glierin mRNA, complete cds
368	13453	26365	1	1.8E-02	AW771104.1	EST_HUMAN	hm52c06.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
709	13768	26684	1.12	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1187	14226	27165	1.12	1.8E-02	X17684.1	NT	H.francisci mRNA for myelin basic protein (MBP)
2727	15720	28717	1.86	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3257	16305		1.18	1.8E-02	AI803629.1	EST_HUMAN	te52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3956	16984	29868	1.13	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3956	16984	29869	1.13	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4174	17195		1.29	1.8E-02	AA861446.1	EST_HUMAN	alc24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1405835 3'
4537	17546	30407	1.47	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
6070	18067	30917	1.71	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
6048	19087	32878	0.63	1.8E-02	AE002518.1	NT	Nabseria meningitidis serogroup B strain MC58 section 160 of 206 of the complete genome
6648	19687	32879	0.63	1.8E-02	AE002518.1	NT	Nabseria meningitidis serogroup B strain MC58 section 160 of 206 of the complete genome
7121	20325	33589	0.81	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5REGION
7873	20800	34103	0.45	1.8E-02	BF125680.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028280 5'
7901	20800	34103	0.54	1.8E-02	BF125680.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028280 5'
8708	21637	34984	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
9037	21966	35325	0.87	1.8E-02	AW903327.1	EST_HUMAN	QV2-NN1073-220400-159-H09 NN1073 Homo sapiens cDNA
9078	22007	35363	1.33	1.8E-02	6578943	NT	Mus musculus microtubule-associated protein 2 (Mtap2), mRNA
10025	22925	36313	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
10025	22925	36314	0.67	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
10168	23059		2.33	1.8E-02	AA897543.1	EST_HUMAN	aj62f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC FINGER PROTEIN 91 (HUMAN);
10565	23451	36872	1.73	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866963 5'
10721	23607	37036	1.4	1.8E-02	X86933.1	NT	L. steinialis mRNA for myomodulin neuropeptide precursor
11037	23921	37363	0.59	1.8E-02	O75330	SWISSPROT	HYALURONAN MEDIATED MOTILITY RECEPTOR (INTRACELLULAR HYALURONIC ACID BINDING PROTEIN) (RECEPTOR FOR HYALURONAN-MEDIATED MOTILITY)
11037	23921	37364	0.59	1.8E-02	O75330	SWISSPROT	HYALURONAN MEDIATED MOTILITY RECEPTOR (INTRACELLULAR HYALURONIC ACID BINDING PROTEIN) (RECEPTOR FOR HYALURONAN-MEDIATED MOTILITY)
11869	23969	37405	1.96	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11869	23969	37406	1.96	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
12040	24882	38388	2.8	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1465000 nt. position (6/7)
12052	24893	38396	3.11	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
13030	25720		1.93	1.8E-02	AF202180.1	NT	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
931	13983	26928	1.36	1.7E-02	BE394889.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1813	14838	27810	2.31	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element ;
1813	14838	27811	2.31	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element ;
1894	14915		2.75	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2125	15138		10.65	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for miteugumin29, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2312	15320	28321	1.05	1.7E-02	S74188.1	NT	(microsatellite INRA41) [Ovis aries-sheep, Genomic, 361 nt, segment 1 of 2]
2888	15882		44.07	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3041	16093	28996	0.74	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3571	16608		5.93	1.7E-02	AW827368.1	EST_HUMAN	hm46a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains
3691	16724		0.72	1.7E-02	P04829	SWISSPROT	MER19.b1 MER19 repetitive element;
							HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4265	17281		1.14	1.7E-02	AA669618.1	EST_HUMAN	ac1904.s1 Strategene ovary (#837217) Homo sapiens cDNA clone IMAGE:855927 3' similar to contains Alu
4298	17310		2.21	1.7E-02	R02503.1	EST_HUMAN	repetitive element; contains element MER24 repetitive element;
							ye88f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 6'
4564	17572	30435	1.04	1.7E-02	AI305279.1	EST_HUMAN	qno8g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC
							FINGER PROTEIN 30 (HUMAN);
4645	17651	30516	1.58	1.7E-02	AW573183.1	EST_HUMAN	h134a03.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains
4827	17828	30686	1.57	1.7E-02	V00841.1	NT	L1.11 L1 repetitive element;
4927	17926		8.83	1.7E-02	AI015076.1	EST_HUMAN	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
5200	18192	31034	0.85	1.7E-02	6981289	NT	ov16d02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
							Rattus norvegicus N-arginine dibasic convertase 1 (Nrd1), mRNA
6365	19414	32579	1.74	1.7E-02	AI769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_f8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to
6747	19781		0.49	1.7E-02	Z28383.1	NT	contains Alu repetitive element;
6861	19893	33106	1.8	1.7E-02	AI038280.1	EST_HUMAN	T.rivulim (ATCC34921) simA gene for cyclosporine synthetase
7403	20102	33337	1.13	1.7E-02	AF190930.1	NT	cy65h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7570	20506	33794	1.89	1.7E-02	8400716	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7748	20678	33977	0.98	1.7E-02	L07899.1	NT	Homo sapiens nebulin (NEB), mRNA
7748	20679	33978	0.98	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
8207	21113		2.17	1.7E-02	AI010770.1	NT	Human apolipoprotein (a) gene, exon 1
8970	21328	34861	1.1	1.7E-02	U21854.1	NT	Homo sapiens hypoxanthine gene, exons 1-50
10221	23112	36314	1.31	1.7E-02	AL040554.1	EST_HUMAN	Caenorhabditis elegans cCAF1 protein gene, complete cds
12199	25034	38534	1.86	1.7E-02	5902007	NT	DKFZp434i0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434i0314 5'
12953	25891	31480	2.08	1.7E-02	AW603482.1	EST_HUMAN	Homo sapiens serum constituent protein (MSE55), mRNA
							CMA-NN1030-040400-130-f06 NN1030 Homo sapiens cDNA
13073	25597	31729	1.63	1.7E-02	AA846926.1	EST_HUMAN	ce08d04.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1
534	13603		2.07	1.6E-02	AL021928.1	NT	repetitive element;
							Mycobacterium tuberculosis H37Rv complete genome; segment 131/162
1683	14713	27675	3.49	1.6E-02	Y18889.1	NT	Treponema maltophilum flaB2, flaB3 and flID genes for flagellin subunit proteins and C4P protein homologue

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2264	15274	28279	1.1	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2264	15274	28280	1.1	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2800	15598	28563	1.31	1.6E-02	AJ006345.1	NT	Human sapiens KVLQ11 gene
2691	15685	28684	1.32	1.6E-02	AA494872.1	EST_HUMAN	ne81d08.s1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910867
2744	15737		1.42	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3587	16624	29527	6.8	1.6E-02	AW850552.1	EST_HUMAN	IL3-CT0219-180200-063-C07 CT0219 Homo sapiens cDNA
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fes-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Secm21 gene, partial>
4271	17287		2.09	1.6E-02	AF110520.1	NT	
4402	17414	30281	1.14	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-f07 PT0012 Homo sapiens cDNA
5135	18131	30972	0.94	1.6E-02	AA853047.1	EST_HUMAN	ns71f12.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1189103 similar to gb:M24902
5135	18131	30973	0.94	1.6E-02	AA853047.1	EST_HUMAN	PROSTATIC ACID PHOSPHATASE PRECURSOR (HUMAN);
5203	18194	31036	1.06	1.6E-02	AI769132.1	EST_HUMAN	ns71f12.s1 NCL CGAP_P2 Homo sapiens cDNA clone IMAGE:1189103 similar to gb:M24902
5434	18516	31241	0.52	1.6E-02	AI281385.1	EST_HUMAN	PROSTATIC ACID PHOSPHATASE PRECURSOR (HUMAN);
5818	18980	32003	1.29	1.6E-02	6871715	NT	qu42b09.x1 NCL CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967417 3'
6834	19963	33184	2.06	1.6E-02	AB015281.1	NT	Mus musculus CD5 antigen (Cd5), mRNA
7261	20170	33410	0.65	1.6E-02	AB027571.1	NT	Candida albicans CagGCR3 gene, complete cds
7261	20170	33411	0.65	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
8170	21077	34407	0.86	1.6E-02	AL161508.2	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8698	21629	34974	0.76	1.6E-02	AJ277682.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8757	21687		2.09	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10543	23429		2.79	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10902	23787	37214	1.7	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10902	23787	37215	1.7	1.6E-02	AA572818.1	EST_HUMAN	P29294 TELOKIN. [1];
11347	25098	37706	2.4	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LE0260 (T1611E11))
11661	24567	38040	2.39	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11661	24567	38041	2.39	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11643	24787	38283	2.23	1.6E-02	AI373558.1	EST_HUMAN	q296r10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
12417	15274	28279	2.57	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12417	15274	28280	2.57	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
775	13832		35.52	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2157	15169	28171	3.69	1.5E-02	N39521.1	EST_HUMAN	y27b07.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:243925 3'
2188	15199	28204	1.21	1.5E-02	AL161594.2	NT	Aethiops thaliana DNA chromosome 4, contig fragment No. 90
3108	18159	29054	1.11	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3108	18159	29055	1.11	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3788	16819	29707	0.88	1.5E-02	BF032942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
4239	17255	30121	0.83	1.5E-02	AA180687.1	EST_HUMAN	zq40g10.r1 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632226 5'
6348	18329	31178	1.06	1.5E-02	4503634	NT	Homo sapiens eukaryotic translation initiation factor 4E (EIF4E) mRNA
6547	18590	32777	1.92	1.5E-02	Q08711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7703	20835		1.73	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7800	20729	34031	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8315	21220	34556	0.47	1.5E-02	AE004347.1	NT	Vibrio cholerae chromosome II, section 4 of 93 of the complete chromosome
8454	21386	34728	1.7	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8461	21392	34734	4.2	1.5E-02	11417739	NT	Homo sapiens valyl-RNA synthetase 2 (VARS2), mRNA
9389	22317	35678	0.88	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4164504 5'
10001	22818		0.55	1.5E-02	AF086774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
10099	22948	36337	1.39	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10327	23216	36629	1.48	1.5E-02	R32867.1	EST_HUMAN	yf54b10.r1 Soares placenta N52-IP Homo sapiens cDNA clone IMAGE:133531 5'
10327	23216	36630	1.48	1.5E-02	R32867.1	EST_HUMAN	yf54b10.r1 Soares placenta N52-IP Homo sapiens cDNA clone IMAGE:133531 5'
11044	23928	37368	0.53	1.5E-02	BE965719.2	EST_HUMAN	601659778R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896226 3'
11610	24518	37988	2.52	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11650	24658	38025	1.73	1.5E-02	AL111238.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
12618	25778		2.73	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
440	13511		1.51	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 68 of 94 of the complete genome
1145	14187	27125	3.18	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC57225), mRNA
1284	14317		1.27	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1324	14358		2.43	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1538	14568		1.2	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3259	16307	29211	2.05	1.4E-02	AF160969.2	NT	Blifdacterium longum Na ⁺ /H ⁺ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosaminylase repressor protein (nagCxyR) gene, partial cds
3458	16499	29402	0.79	1.4E-02	AW074212.1	EST_HUMAN	x609d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2675793 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3543	16581	29484	6.95	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3543	16581	29485	6.95	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3580	16617	29620	0.95	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3724	16756	29844	6.32	1.4E-02	6989918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4602	17610	30468	10.61	1.4E-02	AW962688.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4602	17610	30469	10.61	1.4E-02	AW962688.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4773	17778	30846	0.97	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4773	17778	30847	0.97	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4983	17982	30839	8.31	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842280 5'
4983	17982	30840	8.31	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842280 5'
6001	25974		0.53	1.4E-02	X91338.1	NT	H. sapiens La/SS-B pseudogene 3
6982	19718	32918	4.54	1.4E-02	AA659030.1	EST_HUMAN	nl1c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1028980 3' similar to contains Alu repetitive element
6982	19718	32919	4.54	1.4E-02	AA659030.1	EST_HUMAN	nl1c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1028980 3' similar to contains Alu repetitive element
8717	21648		1.59	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
9455	22383	35745	1.01	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9998	22623	36001	1.12	1.4E-02	AJ27265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9936	22841	36230	2.26	1.4E-02	BE544581.1	EST_HUMAN	601078239F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3464241 5'
11034	23318		0.77	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11078	23360	37396	0.54	1.4E-02	X61308.1	NT	Z. mays Knotted-1 (Kn1) gene
12337	25132	38166	4.93	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12669	25337		2.38	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12928	25500		1.89	1.4E-02	11426868	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1969	14987	27969	2.17	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2465	15468	28467	1.07	1.3E-02	AE002445.1	NT	Neisseria meningitidis serogroup B strain MC58 section 87 of 208 of the complete genome
3260	16308	29212	2.24	1.3E-02	BF697081.1	EST_HUMAN	602129476F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4286203 5'
3260	16308	29213	2.24	1.3E-02	BF697081.1	EST_HUMAN	602129476F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4286203 5'
4052	17079		1.23	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
							Human germ-line T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBD1S1, TCRBJ1S2, Rfex gene for thiredoxin h, complete cds
5039	18036	30892	0.99	1.3E-02	U66061.1	NT	
5314	18298		0.71	1.3E-02	D26547.1	NT	

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5428	18508	31284	1.31	1.3E-02	AL049886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mrxq28orf
5428	18508	31285	1.31	1.3E-02	AL049886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mrxq28orf
6405	19453	32825	1.35	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
6439	19486	32862	0.83	1.3E-02	M62982.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7298	18467	31287	1.64	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7298	18467	31288	1.64	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
8012	20929	34247	4.84	1.3E-02	AI031593.1	EST_HUMAN	ow0805.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8418	21321	34654	0.48	1.3E-02	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
9051	21980	35337	1.91	1.3E-02	AF156061.1	NT	Homo sapiens human endogenous retrovirus W gag(C3.37 G gag (gag) gene, complete cds
10703	23589	37016	2.22	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10771	23657	37088	0.84	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
11430	24346	37790	3.79	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11430	24346	37791	3.79	1.3E-02	AW268563.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12318	25914		2.51	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
12768	25397		1.86	1.3E-02	9683069	NT	Human herpesvirus 6B, complete genome
12931	25712		74.42	1.3E-02	AF162238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
227	13325		16.45	1.2E-02	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
375	13461	26376	2.66	1.2E-02	AA059299.1	EST_HUMAN	zfb5g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
475	13548	28468	1.51	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR53 REGION
762	13819	28748	10.78	1.2E-02	AI183522.1	EST_HUMAN	qd68e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1, L1 L1 repetitive element;
2190	15201	28206	1.98	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2467	15470	28470	1.63	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2508	15507	28509	1.5	1.2E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2520	15521	28524	1.29	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3454608 5'
2520	15521	28525	1.29	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3454608 5'
2682	15470	28470	1.85	1.2E-02	AW172350.1	EST_HUMAN	x37e09.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3148	16198		8.7	1.2E-02	AA075418.1	EST_HUMAN	zn88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3331	16377	29277	2.38	1.2E-02	R62805.1	EST_HUMAN	yf11608.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4990	17989	30846	1.05	1.2E-02	6754367	NT	Mus musculus interferon regulatory factor 5 (Irf5), mRNA
5025	18022	30880	2.33	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5172	18164		1.62	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbig1 mRNA, partial cds
5219	18209	31055	2.09	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5883	18952		0.47	1.2E-02	AA756018.1	EST_HUMAN	ai29f10.s1 Soares testis_NHT Homo sapiens cDNA clone 1344235 3'
5959	19028	32146	2.02	1.2E-02	D78569.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6355	19404	32571	0.85	1.2E-02	AF045555.1	NT	Homo sapiens wbcscr1 (WBCSCR1) and wbcscr5 (WBCSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7351	20347	33615	5.06	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7672	20606	33905	1.09	1.2E-02	H02197.1	EST_HUMAN	y54n12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7696	20628	33927	11.85	1.2E-02	AV732083.1	EST_HUMAN	AV732083 HTF Homo sapiens cDNA clone HTFBJC98 5'
7988	20807	34223	0.57	1.2E-02	BF216650.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8576	21507	34852	2.56	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NA06S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL4.2) (SIAT4-B)
8705	21636	34982	0.58	1.2E-02	R68831.1	EST_HUMAN	y43706.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8705	21636	34983	0.58	1.2E-02	R68831.1	EST_HUMAN	y43706.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8770	21700	35045	1.36	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8770	21700	35046	1.36	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9447	22375		0.9	1.2E-02	T76987.1	EST_HUMAN	yd72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
10165	23058	36455	2.49	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
10186	23087	36488	1.4	1.2E-02	AI246003.1	NT	Homo sapiens Speet gene for apesin protein
12938	25508		5.97	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-557G06 5'
1296	14329	27275	1.49	1.1E-02	AA070364.1	EST_HUMAN	zm69e11.s1 Stratigene neurospithellum (#637231) Homo sapiens cDNA clone IMAGE:530924 3'
1735	14762	27732	1.22	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1735	14762	27733	1.22	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2052	15069	28069	4.99	1.1E-02	BF345263.1	EST_HUMAN	802018037F1 NCL_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4163808 5'
2920	15973		4.58	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5'
3584	16621	29525	2.58	1.1E-02	AI653508.1	EST_HUMAN	tg95b10.x1 NCL_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPf_HUMAN Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
4200	17219		0.71	1.1E-02	AW813796.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4944	17943	30801	2.43	1.1E-02	AL048383.2	EST_HUMAN	DKFZp586E0924_s1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp586E0924
6389	19438	32806	0.84	1.1E-02	U68480.1	NT	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynab), YnaC (ynac), YnaD (ynad), YnaE (ynae), YnaF (ynaf), YnaG (ynag), YnaH (ynah), YnaJ (ynaj), YnaK (ynak), YnaL (ynal), YnaM (ynam), YnaN (ynan), YnaO (ynao), YnaP (ynap), YnaQ (ynaq), YnaR (ynar), YnaS (ynas), YnaT (ynat), YnaU (ynau), YnaV (ynav), YnaW (ynaw), YnaX (ynax), YnaY (ynay), YnaZ (ynaz), YnaAa (ynaAa), YnaAb (ynaAb), YnaAc (ynaAc), YnaAd (ynaAd), YnaAe (ynaAe), YnaAf (ynaAf), YnaAg (ynaAg), YnaAh (ynaAh), YnaAi (ynaAi), YnaAj (ynaAj), YnaAk (ynaAk), YnaAl (ynaAl), YnaAm (ynaAm), YnaAn (ynaAn), YnaAo (ynaAo), YnaAp (ynaAp), YnaAq (ynaAq), YnaAr (ynaAr), YnaAs (ynaAs), YnaAt (ynaAt), YnaAu (ynaAu), YnaAv (ynaAv), YnaAw (ynaAw), YnaAx (ynaAx), YnaAy (ynaAy), YnaAz (ynaAz), YnaAa (ynaAa), YnaAb (ynaAb), YnaAc (ynaAc), YnaAd (ynaAd), YnaAe (ynaAe), YnaAf (ynaAf), YnaAg (ynaAg), YnaAh (ynaAh), YnaAi (ynaAi), YnaAj (ynaAj), YnaAk (ynaAk), YnaAl (ynaAl), YnaAm (ynaAm), YnaAn (ynaAn), YnaAo (ynaAo), YnaAp (ynaAp), YnaAq (ynaAq), YnaAr (ynaAr), YnaAs (ynaAs), YnaAt (ynaAt), YnaAu (ynaAu), YnaAv (ynaAv), YnaAw (ynaAw), YnaAx (ynaAx), YnaAy (ynaAy), YnaAz (ynaAz)
8040	20954	34269	2.63	1.1E-02	BE149811.1	EST_HUMAN	RC1-H10256-100300-016-h07 HT0256 Homo sapiens cDNA
8316	21221	34557	0.88	1.1E-02	8631284	NT	Meianoplus sanguinipes entomopoxvirus, complete genome
8832	21762	35108	0.53	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8832	21762	35109	0.53	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
9189	22127	35483	0.7	1.1E-02	AW996160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
9381	22309	35670	0.79	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4040
9459	22387	35750	7.8	1.1E-02	Q61082	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10439	23328	38748	2.31	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10596	23482	36911	5.32	1.1E-02	AA314695.1	EST_HUMAN	EST186484 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
11417	24333	37782	2.52	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
12281	25095					EST_HUMAN	ab77f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains Alu repetitive element
7	13122	26010	3.66	1.1E-02	AA688236.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
1545	14576	27536	7.5	1.0E-02	AW848120.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
2607	15505		1.31	1.0E-02	AW368128.1	EST_HUMAN	cc22h08.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1350495 3'
3139	16189	29082	1.97	1.0E-02	AA806389.1	EST_HUMAN	RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3307	16354	29266	3.21	1.0E-02	BE835556.1	EST_HUMAN	801849987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3567	16504		0.99	1.0E-02	BE968996.1	EST_HUMAN	MRQ-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
3550	16978	29862	0.75	1.0E-02	AW845921.1	EST_HUMAN	HAQ921 Human fetal liver cDNA library Homo sapiens cDNA
4607	17616	30476	0.66	1.0E-02	A065088.1	EST_HUMAN	NEUROGENIC LOCUS NOTCH 3 PROTEIN
4805	17808	30872	0.67	1.0E-02	Q61082	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
4889	17888	30753	0.91	1.0E-02	AV696814.1	EST_HUMAN	AV696814 GKC Homo sapiens cDNA clone GKCDG05 5'
4957	17965	30813	6.61	1.0E-02	AV696814.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
5142	18137	30980	5.9	1.0E-02	R68667.1	NT	y454h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
5601	18677	31555	0.69	1.0E-02	L05632.1	NT	Human glycoprotein hormone alpha-subunit (GCA) gene, 5' flank
5953	19020	32140	0.84	1.0E-02	H92681.1	EST_HUMAN	y038h11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:236941 6'
6354	19403	32570	0.67	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-A1c4 (Nfatc4) gene, exons 1 and 2
6422	19469	32642	1.17	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (SY2) gene, complete cds
6422	19469	32643	2.64	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0358-070100-201-h01 BT0358 Homo sapiens cDNA
6422	19469	32643	2.64	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0358-070100-201-h01 BT0358 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7087	20273	33529	1.52	1.0E-02	Z29842.1	NT	Z.mays U3snRNA pseudogene
9920	22834	36222	8.21	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9920	22834	36223	8.21	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11710	24612		2.1	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11739	24641						ig55h07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X16183_cds1
11808	24727	38219	1.41	1.0E-02	AI417961.1	EST_HUMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5 repetitive element;
12356	25971		1.89	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12409	25756	31572	1.97	1.0E-02	Q82203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12422	25805		3.12	1.0E-02	AW935921.1	EST_HUMAN	RC2-DT0007-120200-016-102 DT0007 Homo sapiens cDNA
12917	25856		4.23	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
			2.94	1.0E-02	XG2654.1	NT	H sapiens gene for Me491/CD63 antigen
918	13970	25917	1.44	9.0E-03	AI796126.1	EST_HUMAN	wh42f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2393433 3' similar to contains element
1291	14324		1.51	9.0E-03	BE781899.1	EST_HUMAN	MER22 MER22 repetitive element;
2418	15422	28423	2.29	9.0E-03	AL161559.2	NT	601470242F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3873346 5'
2427	15431	28432	1.25	9.0E-03	AF096934.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2950	16002	28903	1.06	9.0E-03	AI251744.1	EST_HUMAN	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2950	16002	28904	1.06	9.0E-03	AI251744.1	EST_HUMAN	qh80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3693	16002	28903	0.74	9.0E-03	AI251744.1	EST_HUMAN	qh80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3693	16002	28904	0.74	9.0E-03	AI251744.1	EST_HUMAN	qh80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3736	16768	29654	0.83	9.0E-03	J05184.1	NT	qh80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5380	18362	31202	0.91	9.0E-03	AJ278120.1	NT	S.acidocaldarius thermopsin gene, complete cds
6021	19083		1.01	9.0E-03	AI809792.1	EST_HUMAN	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
6920	19950		4.43	9.0E-03	BE745988.1	EST_HUMAN	wt77f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
7872	20799	34102	0.59	9.0E-03	AI242219.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7891	20817	34123	0.9	9.0E-03	8922570	NT	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
8455	21387		0.64	9.0E-03	AL039991.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8924	21754						DKFZp434L0412 r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L0412 5'
10376	23265	36887	1.71	9.0E-03	P20908	SWISSPROT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exon 7-49, and partial cds, alternatively spliced
11424	24340		2.36	9.0E-03	V18000.1	NT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
11451	24367	37817	1.8	9.0E-03	BE395380.1	EST_HUMAN	Homo sapiens NF2 gene
							601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3832181 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit -BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12079	24920	38421	1.47	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12079	24920	38422	1.47	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12545	25972		1.93	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
12745	25985		23.57	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
13014	25561		33.64	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
524	13594		2.38	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pitheel_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
1016	14066	27009	23.83	8.0E-03	AF106856.1	NT	Alu repetitive element;
2172	15184	28189	1.85	8.0E-03	AL163283.2	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
2584	15583	28575	1.03	8.0E-03	P10266	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3412	16454	29360	1.04	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3743	16775	29662	1.75	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3743	16775	29663	1.75	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4355	17369	30233	1.16	8.0E-03	BE840049.1	EST_HUMAN	QV6-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4480	17501	30364	5.73	8.0E-03	BF363327.1	EST_HUMAN	GM4-NN0119-300600-223-565 NN0119 Homo sapiens cDNA
4830	17831	30700	0.71	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4830	17831	30701	0.71	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
6343	18326	31176	1.07	8.0E-03	U02970.1	NT	Plasmodium wickerhamii 263-11 complete mitochondrial DNA
5713	18786	31717	4.02	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
6440	25648	32663	1.26	8.0E-03	AP000002.1	NT	RPS18 genes, complete cds; Sacm21 gene, partial>
7054	20080	33313	4.22	8.0E-03	P55577	SWISSPROT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (217)
7248	20157		1.2	8.0E-03	V01109.1	NT	PROBABLE PEPTIDASE Y4NA
7574	20510	33768	1.71	8.0E-03	M17197.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7972	20894		1.76	8.0E-03	AB038267.1	NT	A. californica (marine gastropod mollusc) neurotrophin gene (bag cell), exon 1, 5' end
9440	22368	35730	0.76	8.0E-03	P98160	SWISSPROT	Turquoise truncatus mRNA for p40-phox, complete cds
9467	22395	35767	3.04	8.0E-03	AW808602.1	EST_HUMAN	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9531	22458	35821	0.84	8.0E-03	9788956	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
10455	23343		6.49	8.0E-03	BE086509.1	EST_HUMAN	MR1-ST0111-111199-011-H06 ST0111 Homo sapiens cDNA
11205	24131	37579	1.76	8.0E-03	BE788441.1	EST_HUMAN	MR1-ST0111-111199-011-H06 ST0111 Homo sapiens cDNA
11423	24939		2.75	8.0E-03	Z49652.1	NT	Mus musculus fusion 2 (human) (Fue2), mRNA
							QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
							801475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
							S. cerevisiae chromosome X reading frame ORF YJR162w

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12137	24977	38478	4.04	8.0E-03	AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12291	25102		2.46	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
12334	25130		5.42	8.0E-03	AB038101.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
718	13776	26896	9.8	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
718	13776	26897	9.8	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1003	14052	28998	3.55	7.0E-03	AF243378.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1143	14185	27123	2.85	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1391	14422		1.34	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1422	14453	27407	5.81	7.0E-03	AA668298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HNF-2)
1522	14553	27514	3.36	7.0E-03	AW303599.1	EST_HUMAN	ab78b08.s1 Stralagens fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2274	16920	28292	1.99	7.0E-03	P04629	SWISSPROT	xx21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3631	16961	29744	0.97	7.0E-03	AW444463.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3880	16909	29760	0.89	7.0E-03	AF196344.1	NT	UI-H-B13-akb-o-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4105	16861	29744	0.7	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4708	17714		1.02	7.0E-03	AW630888.1	EST_HUMAN	UI-H-B13-akb-o-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
5110	18107		1.98	7.0E-03	AL163278.2	NT	hh89a05.v1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868936 5'
5334	18318	31166	0.96	7.0E-03	AI970415.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6031	18063		0.6	7.0E-03	H71106.1	EST_HUMAN	wr10b02.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2481099 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
6350	25946		5.23	7.0E-03	AW861059.1	EST_HUMAN	yr82g01.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:K14723 CLUSTERIN PRECURSOR (HUMAN);
6569	19810	32795	1.56	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050-400-018-c08 CT0286 Homo sapiens cDNA
6816	19849	33059	2.87	7.0E-03	AA327129.1	EST_HUMAN	zd33f10.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:342475 5'
6846	19878	33092	0.93	7.0E-03	BE857385.1	EST_HUMAN	EST30874 Colon 1 Homo sapiens cDNA 5' end
7438	20180	33423	1.98	7.0E-03	BE928133.1	EST_HUMAN	7g34b10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.12 TAR1 repetitive element;
7943	20865	34170	5.7	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7943	20865	34177	5.7	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8430	21362	34701	0.57	7.0E-03	AJ229043.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8430	21362	34702	0.57	7.0E-03	AJ229043.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8689	21620	34962	3.04	7.0E-03	BE175697.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8933	22838		0.76	7.0E-03	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10122	23013	36410	0.67	7.0E-03	N52378.1	EST_HUMAN	y49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains Alu repetitive element
10242	23133	36536	2.9	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10242	23133	36537	2.9	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10795	23881		1.12	7.0E-03	AF687378.1	EST_HUMAN	AF687379 GKC Homo sapiens cDNA clone GKCAFC07 5'
10965	23849		0.97	7.0E-03	AF799734.1	EST_HUMAN	wc37e09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
11266	24189	37638	2.46	7.0E-03	AB008852.1	NT	Bos taurus mRNA for NDP52, complete cds
11340	24259	37698	1.65	7.0E-03	AJ004892.1	NT	Homo sapiens partial MUC5B gene, exon 1-28
11340	24259	37699	1.65	7.0E-03	AJ004892.1	NT	Homo sapiens partial MUC5B gene, exon 1-28
12795	25422		1.53	7.0E-03	BE263253.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160478 5'
12881	25478		1.96	7.0E-03	Y17455.1	NT	Homo sapiens LSPR2 gene, penultimate exon
13003	25955		2.11	7.0E-03	AL183300.2	NT	Homo sapiens chromosome 21 segment HS21C100
1268	14303	27250	8.83	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR ;
1268	14303	27251	8.83	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR ;
2933	15986	28884	4.43	6.0E-03	AA759135.1	EST_HUMAN	ah78a11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
2933	15986	28885	4.43	6.0E-03	AA759135.1	EST_HUMAN	ah78a11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
3291	16338		2.66	6.0E-03	H75690.1	EST_HUMAN	y77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3350	16396		1.02	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3440	16481	29388	0.97	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplatin reductase and vasotocin genes, complete cds
3440	16481	29389	0.97	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplatin reductase and vasotocin genes, complete cds
3605	16942		1.36	6.0E-03	W37985.1	EST_HUMAN	zat3a11.r1 Soares parathyroid tumor_NhrIPA Homo sapiens cDNA clone IMAGE:322172 5'
3728	16760	29647	2.47	6.0E-03	BF510986.1	EST_HUMAN	UH-HB14-epm-c-06-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3844	16873	29756	1.05	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3997	17024	29914	0.65	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240899-021-b10 CT0204 Homo sapiens cDNA
4040	17067		1.34	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859513 5'
4322	17336	30200	1.36	6.0E-03	AF026272.1	NT	Babesia bigemina RAP-1c (rap-1c) gene, complete cds, and YJR070c-like protein (YJR070c-like) gene, partial cds
4433	17444		0.92	6.0E-03	N58946.1	EST_HUMAN	yy62h10.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:278179 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4471	17482		2.1	6.0E-03	A1016833.1	EST_HUMAN	ov33c11.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4808	17809	30675	8.44	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5265	18251		1.08	6.0E-03	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
5274	18260	31112	1.05	6.0E-03	A1652527.1	EST_HUMAN	wb61b12.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2310143 3'
5340	18323	31172	0.86	6.0E-03	AA888972.1	EST_HUMAN	a95g09.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3'
6393	25847	32609	0.84	6.0E-03	9627521	NT	Varola virus, complete genome
7128	20332	33596	0.79	6.0E-03	O14894	SWISSPROT	SYNAPS III
7175	18447	31316	0.68	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7620	20555	33848	0.42	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7620	20555	33849	0.42	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
8095	21007	34332	0.7	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
8308	21212	34549	0.61	6.0E-03	P17964	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
8350	21264	34508	0.49	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
8440	21372	34713	14.27	6.0E-03	A1033980.1	EST_HUMAN	aw13a04.x1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646970 3' similar to contains MER10.b1 MER10 repetitive element;
8552	21483	34824	2.83	6.0E-03	AW769337.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8624	21555		1.74	6.0E-03	BF038198.1	EST_HUMAN	601454916F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:38868628 5'
10083	22876	36264	9.14	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
10546	23432		2.46	6.0E-03	A1432681.1	EST_HUMAN	tt22c02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW.R13A_HUMAN
10658	23944	36976	1.14	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A;
10785	23671		0.88	6.0E-03	AF084555.1	NT	Bacillus subtilis fnd gene
10889	23774	37200	0.82	6.0E-03	X68386.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
11185	24111	37559	1.71	6.0E-03	AW982164.1	EST_HUMAN	M.thermautotrophicum complete plasmid pFV1 DNA
11250	24174		2.31	6.0E-03	11548814	NT	EST1374237 MAGG resequences, MAGG Homo sapiens cDNA
11420	24336		5.66	6.0E-03	U14556.1	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
11421	24337	37785	4.02	6.0E-03	BE737895.1	EST_HUMAN	Mus musculus zinc-finger protein mRNA, complete cds
12394	25168		2.77	6.0E-03	AF010496.1	NT	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12504	25742		7.19	6.0E-03	AE000833.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12571	25796		2.38	6.0E-03	U30790.1	NT	Methanobacterium thermoautotrophicum from bases 429182 to 450296 (section 39 of 148) of the complete genome
12627	25310		1.75	6.0E-03	Q82209	SWISSPROT	Pneumocystis carinii f. sp. rattii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
							SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)

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12898	25487		2.9	6.0E-03	BE788019.1	EST_HUMAN	601482821F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3885388 5'
12914	25497		1.89	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
228	13326	26243	4.89	5.0E-03	X87944.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
692	13753	26669	1.93	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; emiocytyl-rRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
692	13753	26670	1.93	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-rRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
693	13753	26669	2.31	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-rRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
693	13753	26670	2.31	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-rRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1139	14181	27119	1.03	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1590	14921		1.11	6.0E-03	AH38977.1	EST_HUMAN	q079d05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1735669 3'
2730	15723	28719	2.35	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2978	16030	28932	0.79	5.0E-03	BE266057.1	EST_HUMAN	601194796F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3538799 5'
3181	16231	29126	5.03	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3198	16246		2.2	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3208	16256	29154	1.43	5.0E-03	RY1794.1	EST_HUMAN	y86g02.s1 Soares breast 2N6HBst Homo sapiens cDNA clone IMAGE:155666 3'
3322	16368		0.97	5.0E-03	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3764	16796	29665	6.51	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3822	16852	29736	0.71	5.0E-03	U38814.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4026	17053	29943	1.09	5.0E-03	X68363.1	NT	M. thermophilum complete plasmid pFV1 DNA
4055	17082		1.95	5.0E-03	AA299675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4408	17420	30284	0.84	5.0E-03	H78355.1	EST_HUMAN	yJ79g10.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:240066 5'
4410	16952	29736	0.99	5.0E-03	U38814.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4718	17723	30585	0.92	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4932	17833	30703	1.53	5.0E-03	AJ752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn15c02 random
5045	18042	30898	1.1	5.0E-03	P15265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
6006	19070	32198	5.58	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6279	19330	32496	2.44	5.0E-03	000507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6316	19366		0.95	5.0E-03	AE002234.2	NT	Chlamydomonas reinhardtii AF39, section 62 of 94 of the complete genome
6879	19309		7.95	5.0E-03	BE300091.1	EST_HUMAN	600944564 T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2680871 3'
7164	18436	31337	6.52	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7391	20090		0.97	5.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7447	20388	33658	2.03	5.0E-03	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaht11), mRNA
7905	20830	34133	0.88	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stragene (cat#336208) Homo sapiens cDNA clone HFB0893 similar to EST containing Alu repeat
8041	20855		1.2	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-007 CT0255 Homo sapiens cDNA
8236	21141	34474	8.9	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8305	21209	34544	0.57	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8305	21209	34545	0.57	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8815	21745	35093	1.9	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9172	22100		5.91	5.0E-03	M81132.1	NT	Mouse complement receptor (CR2) mRNA, 3' and
9365	22293	35658	1.46	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
10354	23243	36663	1.21	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
10477	23365	36778	0.61	5.0E-03	AW821888.1	EST_HUMAN	RCO-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10822	23708	37135	0.64	5.0E-03	7682657	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10957	23841		0.68	5.0E-03	AA653281.1	EST_HUMAN	ag48c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126280 3'
11163	24091		5.13	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
11378	24294	37739	2.46	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element;
11378	24294	37740	2.46	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element;
11478	24391	37841	2.08	5.0E-03	T49153.1	EST_HUMAN	y00604.r1 Stragene placenta (637225) Homo sapiens cDNA clone IMAGE:70686 5'
11523	24433	37891	1.76	5.0E-03	10948753	NT	Mus musculus hypothetical protein, MNCb-4760 (LOC58212), mRNA
11775	24874		4.05	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291622 5'
12519	25917		7.51	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12649	25324		19.86	5.0E-03	AF087253.1	NT	Brugia malayi Y chromosome marker

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12742	25382		2.31	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12772	25401		2.16	5.0E-03	AA456597.1	EST_HUMAN	zz75a03.s1 Soares ovary tumor NhHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to
12796	25750		4.71	5.0E-03	BF572332.1	EST_HUMAN	SW-DX42_MOUSE P14885 PROBABLE DIPHEENOL OXIDASE A2 COMPONENT ;
12964	25522	31743	2.44	5.0E-03	AW449109.1	EST_HUMAN	80207774.F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
251	13349	26282	2.07	4.0E-03	AW500196.1	EST_HUMAN	UH+B13-akt-4-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
341	13431	26345	1.75	4.0E-03	R46482.1	EST_HUMAN	UJ-HF-BN0-alk-h-04-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
466	13537	26459	0.69	4.0E-03	P54675	SWISSPROT	y65te04.s1 Soares infant brain T1N1B Homo sapiens cDNA clone IMAGE:35988 3'
624	13689	26592	2.29	4.0E-03	AA939339.1	EST_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (P13K)
902	13954	26903	1.77	4.0E-03	R46482.1	EST_HUMAN	on75g12.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
936	13988		3.87	4.0E-03	AW749101.1	EST_HUMAN	y65te04.s1 Soares infant brain T1N1B Homo sapiens cDNA clone IMAGE:35988 3'
1178	14218	27167	20.65	4.0E-03	AA099777.1	EST_HUMAN	RC3-BT0333-110100-012-01 BT0333 Homo sapiens cDNA
1197	14236	27176	1.67	4.0E-03	AW794740.1	EST_HUMAN	z181a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:610998 5'
1329	14363	27311	1.09	4.0E-03	AA284374.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1609	14839		1.26	4.0E-03	AV708305.1	EST_HUMAN	zs59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1771	14787	27767	1.98	4.0E-03	U33472.1	NT	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
2031	15048	28045	10.26	4.0E-03	AA099777.1	EST_HUMAN	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-49 mRNA, complete cds
2262	15272		1.67	4.0E-03	BE410659.1	EST_HUMAN	z181a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2297	15305	28311	1.48	4.0E-03	AW794740.1	EST_HUMAN	6013047161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2609	15607	28601	2.01	4.0E-03	U52111.2	NT	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2609	15607	28602	2.01	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
2741	15734	28728	2.8	4.0E-03	AJ277395.1	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
2741	15734	28729	2.8	4.0E-03	AJ277395.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2747	15739	28732	1.28	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3272	16320	29224	1.4	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens polyglutamine-containing C14ORF4 gene
3272	16320	29225	1.4	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
3592	16629	29532	0.93	4.0E-03	AW188426.1	EST_HUMAN	PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
3592	16629	29533	0.93	4.0E-03	AW188426.1	EST_HUMAN	PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
3689	16722	29615	0.68	4.0E-03	Q13606	SWISSPROT	X98104.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:2665279 3'
							X98104.x1 NCI_CGAP_C018 Homo sapiens cDNA clone IMAGE:2665279 3'
							OLFATORY RECEPTOR 511 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3701	16733	29824	0.8	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLC4D02 3'
3983	16722	29615	0.7	4.0E-03	Q13606	SWISSPROT	OLFATORY RECEPTOR 511 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
4005	17032	29922	0.8	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4081	17106		2.28	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4723	17728	30592	0.98	4.0E-03	A1732754.1	EST_HUMAN	ab18a08.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
5325	18309	31159	1.59	4.0E-03	AA699995.1	EST_HUMAN	z66b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436009 3'
5398	18398		1.02	4.0E-03	AW816104.1	EST_HUMAN	MR3-ST0220-110100-026-405 ST0220 Homo sapiens cDNA
5458	18539	31381	1.67	4.0E-03	AF005859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5584	18681	31536	20.71	4.0E-03	AF168826.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
6004	19068	32195	2.46	4.0E-03	P04196	SWISSPROT	(HPRG)
6008	19072	32197	1.6	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZOITE ANTIGEN PRECURSOR
6098	19152	32292	0.85	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014_11 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 5'
6321	19371		3.62	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6481	19528	32704	0.98	4.0E-03	AW550572.1	EST_HUMAN	hg46c07.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2948652 3'
6594	19605	32790	1.66	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6966	19694	33222	1.34	4.0E-03	AA813222.1	EST_HUMAN	aj3211.s1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'
7082	20288	33547	1.49	4.0E-03	U76408.1	NT	Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds
7425	20124	33361	1.01	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7425	20124	33362	1.01	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7562	20499	33797	4.55	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7835	20763	34068	1.04	4.0E-03	A1681483.1	EST_HUMAN	b37g12.x1 NCL CGAP_L024 Homo sapiens cDNA clone IMAGE:2271814 3'
7837	20765	34068	0.59	4.0E-03	BE670170.1	EST_HUMAN	7es1b02.x1 NCL CGAP_L124 Homo sapiens cDNA clone IMAGE:3284043 3'
7948	20870		0.79	4.0E-03	X92108.1	NT	H. sapiens hcgIX gene
8521	21452	34795	0.58	4.0E-03	Q9TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADAM-TS 11)
8626	21657	34896	4.61	4.0E-03	AF111944.1	NT	Dichostellum discoidium AX4 development protein DG122 (DG122) gene, partial cds
9273	22201	35558	7.93	4.0E-03	A1553983.1	EST_HUMAN	te4db11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
9446	22374		3.38	4.0E-03	AL162209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9456	22394	35746	3.88	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10437	23326	36743	0.52	4.0E-03	H30894.1	EST_HUMAN	yp42g12.r1 Soares retina N2b5fR Homo sapiens cDNA clone IMAGE:190150 5'
10864	23750	37175	0.84	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11041	23925		0.58	4.0E-03	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11569	24478	37944	5.77	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
11949	24793	38291	1.57	4.0E-03	AI208703.1	EST_HUMAN	qg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839176 3'
11949	24793	38292	1.57	4.0E-03	AI208703.1	EST_HUMAN	qg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839176 3'
12185	25021	38523	1.4	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12490	25933		4.6	4.0E-03	BE915173.1	EST_HUMAN	PM4-EN0138-180600-002-008 EN0138 Homo sapiens cDNA
12510	25244		1.64	4.0E-03	BE298290.1	EST_HUMAN	601118194F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12585	25284		3.2	4.0E-03	AW604273.1	EST_HUMAN	UIHF-EN0-alp-g-04-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12807	25430		3.15	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element ;
12841	25848		2.93	4.0E-03	AW614596.1	EST_HUMAN	ht02c07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953832 3' similar to contains element LTR5 repetitive element ;
12855	25465		1.99	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-03 ST0281 Homo sapiens cDNA
392	13476	26396	1.8	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
804	13856	26804	5.12	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1698	14718	27679	4.85	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.st NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2275	15284		1.07	3.0E-03	AF055066.1	NT	Homo sapiens MHC class 1 region
2313	15321		5.91	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2314	15322	28322	1.6	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2314	15322	28323	1.6	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2426	15430	28431	0.99	3.0E-03	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
3034	16086		0.7	3.0E-03	Y09008.1	NT	Arabidopsis thaliana rpm1 gene
3132	16182	28076	2.53	3.0E-03	BE379296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609633 5'
3194	16242	29137	3.05	3.0E-03	AW802687.1	EST_HUMAN	IL2-JM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3478	16518	29417	2.31	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3487	16526		7.9	3.0E-03	Y12500.1	NT	C.elegans smdc gene
4082	17088	29973	8.3	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4082	17088	29974	8.3	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4120	17143	30016	2.15	3.0E-03	AI792278.1	EST_HUMAN	an0400.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4502	17512	30376	10.13	3.0E-03	AJ011492.1	NT	Rattus norvegicus gdnf gene
4638	17644	30508	6.24	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4948	17947	30805	1.72	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4963	17961	30819	3.2	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855483 5'
5291	18276	31124	1.08	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5291	18276	31125	1.08	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5447	18528	31254	3.58	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5747	18820	31917	1.86	3.0E-03	AJ249581.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5821	18893	32006	1.02	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6834	18866	33080	10.99	3.0E-03	AA456701.1	EST_HUMAN	aa13f10.1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7374	20368	33637	0.65	3.0E-03	D37977.1	NT	Fugu tubripes mRNA for sodium channel alpha subunit, partial cds
7671	20507	33795	1.27	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pop3 gene for purine-cytosine permease
7948	20668	34180	3.67	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
8376	21280	34611	0.47	3.0E-03	P26859	SWISSPROT	DNA REPAIR HELICASE RADT15 (RHP3)
8517	21448	34760	0.97	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8517	21448	34791	0.97	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8734	21664	35009	1.74	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8890	21820		0.65	3.0E-03	M63498.1	NT	S. cerevisiae UGA35 gene, complete cds
9029	21958	35318	1.18	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
9052	21981	35338	1.61	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
9148	22076		1.4	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
9543	22470		11.53	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NOI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.1f L1 repetitive element;
9598	22524	35888	4.26	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9920	22546	35917	7.95	3.0E-03	AJ016731.1	EST_HUMAN	ov03d12.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_maf1 HISTONE H2B.2 (HUMAN);
9943	22848		0.85	3.0E-03	D90801.1	NT	Synedocystis sp. PCC6803 complete genome, 3/27, 271600-402289
10162	23053		0.77	3.0E-03	P03355	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
10229	23120		7.22	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
10407	23296	36716	1.65	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
10501	23389	36800	1.44	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10639	23525	36960	4.3	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11283	24204		1.87	3.0E-03	5903028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11627	20868	34180	1.63	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11819	24740	38231	1.96	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11870	23970	37407	1.46	3.0E-03	P22831	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11880	23980	37418	2.66	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11912	24759	38255	2.98	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11912	24759	38256	2.98	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11987	24830	38327	1.76	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12285	25762		2.16	3.0E-03	AB250568.1	EST_HUMAN	prerna-5.E07.7 b.tumor Homo sapiens cDNA 5'
12370	25877		1.68	3.0E-03	AB005668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12633	25256	31831	1.61	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
538	13607	26516	0.77	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
538	13607	26517	0.77	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
812	15885		11.14	2.0E-03	T70874.1	EST_HUMAN	yd15h03.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108341 5'
1390	14421	27376	1.75	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1393	14424	27378	1.14	2.0E-03	AA661605.1	EST_HUMAN	nu8691.s1 NCI CGAP AMT Homo sapiens cDNA clone IMAGE:1217593
1402	14433	27388	13.79	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1608	14539	27501	1.7	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1637	14567	27526	1.8	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1637	14567	27527	1.8	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1614	14644		6.77	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1796	14822	27760	1.28	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Scores_tetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:789114 5'
2011	15029	28022	1.35	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2265	15275	28281	0.92	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2817	15815		5.66	2.0E-03	AW137782.1	EST_HUMAN	ULH-B11-edl-g-10-Q-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3477	16517	29416	4.74	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Scores_tetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:789114 5'
3484	16523	29422	0.84	2.0E-03	BF568955.1	EST_HUMAN	602183660T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3734	16766	29652	7.03	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LIMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
4031	17058	29947	0.65	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4207	17224	30091	3.03	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4270	17286	30154	1.01	2.0E-03	AA178693.1	EST_HUMAN	zp13h01.r1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608381 5'
4317	17331		11.71	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4519	17528		1.9	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4534	17643		1.19	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BWUO-air-g-03-Q-UJ.s1 NC1 CGAP Sub66 Homo sapiens cDNA clone IMAGE:2730413 3'
4539	17548	30409	1	2.0E-03	A1064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4662	17667	30535	1.95	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (s1s) mRNA, complete cds
4662	17667	30536	1.95	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (s1s) mRNA, complete cds
4819	17820		1.25	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4824	17825		1.47	2.0E-03	R87773.1	EST_HUMAN	yo45602.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
5147	18142	30987	0.93	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5178	18168	31013	0.71	2.0E-03	P45969	SWISSPROT	HYPOTHETICAL 37.4 KD PROTEIN T09A5.9 IN CHROMOSOME III
5271	18257	31108	0.94	2.0E-03	AF187974.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
5279	18265		0.71	2.0E-03	AJ245167.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
5363	18345		1.09	2.0E-03	BE019692.1	EST_HUMAN	bb28h05.x1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:2964249 3'
5675	18749	31660	1.19	2.0E-03	BF241410.1	EST_HUMAN	601878385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5822	19533	32007	2.21	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5909	19878	32065	0.49	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
5909	19878	32086	0.49	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
5910	19879	32097	1.89	2.0E-03	U63711.1	NT	Xenopus laevis xellin mRNA, complete cds
6348	19398	32564	4.92	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6348	19398	32565	4.92	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6603	19844	32828	2.23	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP)
6603	19844	32827	2.23	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP)
6605	19846	32829	7.88	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6645	19684	32875	2.64	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6646	19685	32876	0.65	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6681	19717	32917	1.22	2.0E-03	X94451.1	NT	Lescaultum mRNA for lysyl-tRNA synthetase (LysRS)
6888	19918		1.28	2.0E-03	A1991089.1	EST_HUMAN	wu38h09.x1 Soares Dieckgreffe_colon_NHOD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;
6929	19958	33179	0.68	2.0E-03	AA677831.1	EST_HUMAN	z13a11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:430852 3'
7295	18464	31334	1.21	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galactin LEC-11, complete cds
7441	20183	33427	9.26	2.0E-03	BE067088.1	EST_HUMAN	CMA-B.T03665-061299.054-011 R.T0366 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7504	20443	33726	0.7	2.0E-03	AI288883.1	EST_HUMAN	q189d11.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898885 3'
7673	20807	33806	0.74	2.0E-03	T88569.1	EST_HUMAN	yt77g10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:114308 5'
8063	20976	34291	1.55	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8629	21560	34898	2.84	2.0E-03	AW592004.1	EST_HUMAN	h137b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY.;
8798	21728	35074	6.05	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NthM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
8798	21728	35075	6.05	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NthM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
8840	21770	35116	0.54	2.0E-03	Q82350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN CG9.05 IN CHROMOSOME I
8863	21793	35145	1.29	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8916	21845	35169	0.83	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8915	21845	35200	0.83	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8938	21868	35226	1.03	2.0E-03	AU136678.1	EST_HUMAN	AU136678 PLACE1 Homo sapiens cDNA clone IMAGE:1004639 5'
8980	21919		0.96	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9737	18978	32095	0.76	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9737	18978	32096	0.76	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9782	22706	36090	0.9	2.0E-03	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10056	22872	36361	0.98	2.0E-03	AF08732.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:184296 3'
10056	22872	36362	0.98	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:184296 3'
10087	22880	36268	3.48	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEH) (JI) (MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150- 225) (TENASCIN-C) (TN-C)
10192	23083	36494	1.19	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10192	23083	36485	1.19	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10244	23135	36539	0.65	2.0E-03	AF08732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10244	23135	36540	0.65	2.0E-03	AF08732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10428	23315	36732	1.09	2.0E-03	AW884269.1	EST_HUMAN	QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA
10545	23431		6.4	2.0E-03	AA251376.1	EST_HUMAN	zs10a06.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
11454	24370		2.49	2.0E-03	M86524.1	NT	Human dyatrophin gene
11920	20876	34291	2.33	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11975	24818		2.4	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-116-g04 BT0333 Homo sapiens cDNA

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11982	24825	38321	11.38	2.0E-03	Z11740.1	NT	Hi.septiens variable number tandem repeat (VNTR) locus DNA
12267	25084		3.38	2.0E-03	A1625745.1	EST_HUMAN	U65H03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
12283	25097	38573	4.23	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G; Homo sapiens SEL1L (SEL1L) gene, partial cds
12306	25113	38577	9.27	2.0E-03	A1084325.1	EST_HUMAN	oyk3g06.s1 Soares_papillary_thyroid_tumor_NbH-PA Homo sapiens cDNA clone IMAGE:1658634 3' similar to
12328	18265		8.88	2.0E-03	AJ245167.1	NT	TR:P97535 P97535 PS-PLA1 PRECURSOR. ; Carnellus dromedarius cnp19 gene for immunoglobulin heavy chain variable region
12514	25613		2.28	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKC Homo sapiens cDNA clone GKCXGD05 5'
12869	25471		1.82	2.0E-03	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b,
13025	25743		4.22	2.0E-03	AV697968.1	EST_HUMAN	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
462	13534	28464	1.21	1.0E-03	H98471.1	EST_HUMAN	AV697968 GKC Homo sapiens cDNA clone GKCXGD05 5'
854	13908	26852	1.63	1.0E-03	A1720263.1	EST_HUMAN	Y88c08.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
854	13908	26853	1.63	1.0E-03	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1122	14164	27101	1.99	1.0E-03	A1865788.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYOYL-COA HYDRATASE. ;
1142	14184	27122	1.78	1.0E-03	A1954572.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYOYL-COA HYDRATASE. ; wk86a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1193	14232	27171	1.87	1.0E-03	A1692616.1	EST_HUMAN	wk83e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
2041	15058	28059	2.6	1.0E-03	P47808	SWISSPROT	wd88a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu
2168	15180	28186	5.61	1.0E-03	AJ131016.1	NT	repetitive element.
3021	16073	28976	1.46	1.0E-03	AB033117.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
3234	16282	29182	1.05	1.0E-03	P18915	SWISSPROT	Homo sapiens SCL gene locus Homo sapiens mRNA for KIAA1291 protein, partial cds
3234	16282	29183	1.05	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3345	16391	29281	0.88	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3733	16765		1.72	1.0E-03	AB044400.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4010	17037	29827	0.74	1.0E-03	Z46849.1	NT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
4541	17550	30410	1.46	1.0E-03	BE939162.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4589	17597	30455	5.87	1.0E-03	RF246536.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15 S. cerevisiae chromosome X reading frame ORF YJR149w
							TCBAP1-D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo

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4775	17780	30650	0.73	1.0E-03	U28449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4837	17936	30793	2.63	1.0E-03	A073486.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4937	17936	30794	2.63	1.0E-03	A073486.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4938	17937		4.81	1.0E-03	BE194097.1	EST_HUMAN	PW0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5211	18201	31045	21.62	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5491	18571	31417	1.8	1.0E-03	AA280951.1	EST_HUMAN	zs44f01.1 NCJ CGAP GC81 Homo sapiens cDNA clone IMAGE:700345 5'
5587	18684	31540	3.24	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQ1 gene
5641	18716	31617	2.09	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5641	18716	31618	2.09	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5764	18837	31840	0.9	1.0E-03	BE786491.1	EST_HUMAN	601589841F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3943954 5'
5770	18843	31945	1.63	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5829	18900	32014	0.66	1.0E-03	N41974.1	EST_HUMAN	y07h06.1r1 Soares melanocyte 2NHIM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
5829	18900	32015	0.66	1.0E-03	N41974.1	EST_HUMAN	y07h06.1r1 Soares melanocyte 2NHIM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
6110	19170	32302	0.51	1.0E-03	AA773352.1	EST_HUMAN	ab65g12.s1 Stralagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:845734 3'
6133	19192		0.45	1.0E-03	BF541639.1	EST_HUMAN	602068042F1 NIH_MGC.58 Homo sapiens cDNA clone IMAGE:4066907 5'
6253	19308		3.24	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6294	19345	32613	1.06	1.0E-03	BE863939.2	EST_HUMAN	601657519R1 NIH_MGC.68 Homo sapiens cDNA clone IMAGE:3875693 3'
6433	19480		8.63	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6591	19632	32814	1.11	1.0E-03	T87761.1	EST_HUMAN	yd93a11.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:115772 5'
6674	19711		1.56	1.0E-03	AW802585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
7060	20085	33318	1.5	1.0E-03	L7570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7513	20452	33737	2.47	1.0E-03	D16928.1	NT	Human gene for fourth somatostatin receptor subtype
7807	20832		2.62	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8088	21000	34322	1.82	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cez2/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
8167	21074	34404	3.28	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
8224	21129	34460	0.86	1.0E-03	BE860044.1	EST_HUMAN	601491081F1 NIH_MGC.88 Homo sapiens cDNA clone IMAGE:3883276 5'
8469	21400	34740	0.77	1.0E-03	AF274591.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8528	21459	34802	5.56	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8722	21652	34969	0.87	1.0E-03	AA122270.1	EST_HUMAN	z687c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.11 L1 repetitive element;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8999	21928	35283	0.88	1.0E-03	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9156	22084	35442	0.81	1.0E-03	AA001613.1	EST_HUMAN	zh82a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
9156	22084	35443	0.81	1.0E-03	AA001613.1	EST_HUMAN	zh82a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
9498	22426		1.82	1.0E-03	Y11204.1	NT	V. cerat gene encoding volvoxopsin
9522	22448	35812	0.84	1.0E-03	AW840353.1	EST_HUMAN	CN3-L1T0079-170200-092-e07 L1T0079 Homo sapiens cDNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (ORTR), CDM protein (CDM), adrenoleukodystrophy protein >
9828	22552		0.88	1.0E-03	U52111.2	NT	
9863	22589	35961	3.11	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH6) c1 subunit mRNA, complete cds
9863	22589	35962	3.11	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH6) c1 subunit mRNA, complete cds
10134	23025	36420	1.98	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,5-galactosidase (aglA) gene, complete cds
10134	23025	36421	1.98	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,5-galactosidase (aglA) gene, complete cds
							BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10335	23224	36639	0.88	1.0E-03	Q01129	SWISSPROT	
10659	23545	36979	0.84	1.0E-03	AF003329.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10665	23551		0.79	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10805	23691	37119	1	1.0E-03	A024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1
11109	24040	37484	1.86	1.0E-03	AW362393.1	EST_HUMAN	MER39 MER39 repetitive element;
11109	24040	37485	1.86	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
11191	24117	37504	3.01	1.0E-03	BE170559.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
							QV3-HT0543-220300-130-a03 HT0549 Homo sapiens cDNA
11262	24185		2.91	1.0E-03	A1583847.1	EST_HUMAN	tt36a12.x1 NCL_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:22464446 3' similar to TR:Q26193 Q26195 PVA1 GENE;
11330	24249	37687	1.44	1.0E-03	AW237482.1	EST_HUMAN	xm72a12.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2689751 3'
11597	24508		3.18	1.0E-03	AV789949.1	EST_HUMAN	AV789949 MDS Homo sapiens cDNA clone MDSDDF11 5'
12262	25080	38571	3.88	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12707	25695		5.42	1.0E-03	A1347355.1	EST_HUMAN	tc05h11.x1 NCL_CGAP_Cof18 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12805	25915	31369	4.03	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872035 5'
6342	18325	31174	2.04	9.0E-04	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
6389	18371	31210	1.33	9.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5879	18948		1.82	9.0E-04	P08727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6508	19552		0.7	9.0E-04	AJ006345.1	NT	Homo sapiens KVLQ11 gene
6761	19795	33009	1.11	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10169	23060		1.57	9.0E-04	AB037203.1	NT	Glycerol kinase GkbAS1 mRNA for beta-amylin synthase, complete cds
1506	14537		1.07	8.0E-04	X98469.1	NT	X laevis mRNA for C4SR protein
3993	17020	29910	0.65	8.0E-04	R07008.1	EST_HUMAN	Y12h10.r1 Soares fetal liver spleen 1NFILS Homo sapiens cDNA clone IMAGE:126691 6'
4276	17290		5.2	8.0E-04	P08947	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4878	17877	30743	3.2	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11586	24496		2.53	8.0E-04	AA777084.1	EST_HUMAN	z22c10.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11742	24844		2.4	8.0E-04	AI571099.1	EST_HUMAN	tn85a08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2176310 3'
1851	14873	27855	1.24	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2421	15426	28428	0.93	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2763	15756	28750	1.18	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3324	16370	29271	1.05	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6333	19363	32551	0.73	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.b3 L1 L1 repetitive element ;
6549	19591	32778	0.47	7.0E-04	AI333675.1	EST_HUMAN	qq08h05.x1 Soares NIH-MP1u.S1 Homo sapiens cDNA clone IMAGE:1931961 3' similar to gb:X57025_ina1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN); contains Alu repetitive element; contains element MIR repetitive element ;
6781	19824		2.27	7.0E-04	AI768831.1	EST_HUMAN	wg35f09.x1 Soares NSF_F8.gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367208 3'
7597	20633		0.8	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
10320	23209	36620	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10320	23209	36621	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11998	24840		2.33	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
12023	24885	38366	2.84	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12746	25385		14.51	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
12963	25521		4.19	7.0E-04	R17338.1	EST_HUMAN	y913c06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'
12990	25546		4.86	7.0E-04	6005855	NT	Homo sapiens Retina-derived POJ-domain factor-1 (RPF-1), mRNA
2746	15738		0.96	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149297 5'
4044	17071	29957	1.77	6.0E-04	AI825235.1	EST_HUMAN	W15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4281	17285	30161	4.06	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4552	17561	30420	1.54	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA
4552	17561	30421	1.54	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-f09 HT0560 Homo sapiens cDNA
5391	18373	31213	1.08	6.0E-04	P12259	SWISSPROT	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)
5391	18373	31214	1.08	6.0E-04	P12259	SWISSPROT	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)
8447	21379		3.72	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8594	21525		0.87	6.0E-04	H92947.1	EST_HUMAN	y84c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element;
10486	23374		4.07	6.0E-04	AL048507.2	EST_HUMAN	DKFZp568M2024_r1 568 (synonym: hule1) Homo sapiens cDNA clone DKFZp568M2024
10582	23468	36894	2.41	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10827	23713		0.65	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoelar extracellular matrix protein precursor (ECM3) mRNA, complete cds
11916	24763	38260	2.68	6.0E-04	AJ28042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11989	24841	38337	4.62	6.0E-04	AW013847.1	EST_HUMAN	U1-HB0-aab-e-09-0-JL1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
12064	24905		2.18	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
12429	25810		3.04	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-281199-012-d08 HT0269 Homo sapiens cDNA
674	13736	26648	5.41	5.0E-04	O10341	SWISSPROT	HYPOPHOSPHATE 283 KD PROTEIN (ORF82)
1521	14562		1.8	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0226-021089-030-a07 CT0226 Homo sapiens cDNA
3474	16314	29413	1.67	5.0E-04	AA548531.1	EST_HUMAN	nk27e11.s1 NCL_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:1014704 3' similar to contains Alu repetitive element
3779	16810	29697	0.92	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5660	18734	31641	2.62	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6919	19949	33170	5.9	5.0E-04	AA195030.1	EST_HUMAN	zo33b09.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:5886693 5'
7769	20899	33999	13.69	5.0E-04	M23804.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
8534	21465	34806	5.87	5.0E-04	A1188382.1	EST_HUMAN	qd13f06.x1 Soares_placenta_8c0weeks_2NblHP8cdw Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN)/contains Alu repetitive element
8878	21808	35161	0.83	5.0E-04	AA814519.1	EST_HUMAN	ob86a02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
9817	22723	36106	2.14	5.0E-04	AA846545.1	EST_HUMAN	q156h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9910	22898	36285	0.69	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
10136	23027	36424	4.44	5.0E-04	AW270938.1	EST_HUMAN	xs06a02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10770	23656		0.63	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
11413	24329		2.25	5.0E-04	AL048507.2	EST_HUMAN	DKFZp568M2024_r1 568 (synonym: hule1) Homo sapiens cDNA clone DKFZp568M2024
12135	18734	31641	14.44	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12375	25751		2.07	5.0E-04	AA588513.1	EST_HUMAN	nf15h02.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
413	13486		1.71	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
696	13756	26673	1.2	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
872	13925	26872	1.23	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
872	13925	26873	1.23	4.0E-04	A1720263.1	EST_HUMAN	Q13925 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE. ;
1484	14515	27476	3.44	4.0E-04	AW753356.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2086	15110	28114	1.23	4.0E-04	AL163278.2	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENYOYL-COA HYDRATASE. ;
2147	15160		1.23	4.0E-04	AL046704.1	EST_HUMAN	RC3-CT0254-130100-023-R01 CT0254 Homo sapiens cDNA
2873	15869	28688	2.08	4.0E-04	O98615	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
3414	16456	28362	0.82	4.0E-04	AV696624.1	EST_HUMAN	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
3936	16964		1.13	4.0E-04	AL163287.2	NT	SERPIN2 (SILK GUM PROTEIN 2)
4429	17440	30289	4.02	4.0E-04	AA576331.1	EST_HUMAN	AV696624 GKG Homo sapiens cDNA clone GKCFH07 5'
4429	17440	30300	4.02	4.0E-04	AA576331.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C067
4653	17659	30528	1.11	4.0E-04	AA086324.1	EST_HUMAN	nh10a10.s1 NCL_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
5222	18211	31057	3.87	4.0E-04	BE560680.1	EST_HUMAN	nh10a10.s1 NCL_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
5309	18283		0.66	4.0E-04	BE176880.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
7644	20579	33874	1.25	4.0E-04	P48442	SWISSPROT	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
7644	20579	33874	1.25	4.0E-04	P48442	SWISSPROT	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
7862	20884		4.7	4.0E-04	AL161566.2	NT	PM4-HT0608-030400-001-H11 HT0608 Homo sapiens cDNA
8179	21086	34420	0.71	4.0E-04	AL122079.1	EST_HUMAN	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
9100	22029	35394	1.02	4.0E-04	BF240712.1	EST_HUMAN	Aradopsis thaliana DNA chromosome 4, contig fragment No. 66
9108	22038	35390	2.15	4.0E-04	N25607.1	EST_HUMAN	AL122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
10214	23105	36505	3.89	4.0E-04	A1025699.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
10355	23244		0.71	4.0E-04	AF022885.1	NT	yc39a12.r1 Soares melanocyte 2NchM Homo sapiens cDNA clone IMAGE:264142 5'
12716	25729		2.21	4.0E-04	AF254822.1	NT	ov67h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
166	13267	26184	3.52	3.0E-04	AL119426.1	EST_HUMAN	Mus musculus neuroligin-2(a17) mRNA, alternatively spliced, complete cds
208	13307	26224	6.78	3.0E-04	P49289	SWISSPROT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
805	13957	26905	1.67	3.0E-04	U93951.1	NT	DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
1863	14885	27865	1.36	3.0E-04	A126100.1	EST_HUMAN	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
1878	14889		0.91	3.0E-04	A126100.1	EST_HUMAN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
3354	16399	28299	5.56	3.0E-04	P25147	SWISSPROT	qz28d03.y1 NCL_CGAP_Jk111 Homo sapiens cDNA clone IMAGE:2028197 5'
							ih23a02.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
							INTERNAL B PRECURSOR

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4047	17074	28980	3.18	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4141	17152		1.67	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4182	17202		1.41	3.0E-04	BE140606.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
4930	17928		6.87	3.0E-04	BE153778.1	EST_HUMAN	PV0-HT0339-180200-007-g12 HT0339 Homo sapiens cDNA
4992	17991	30848	0.77	3.0E-04	AW937723.1	EST_HUMAN	QV9-DT0045-221299-046-d09 DT0045 Homo sapiens cDNA
6383	19432		5.49	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
7132	20240	33480	3.75	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7331	18489	31275	0.62	3.0E-04	AW983981.1	EST_HUMAN	RC4-NN0027-060400-011-b08 NN0027 Homo sapiens cDNA
8031	20947	34284	0.85	3.0E-04	P23488	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8835	21765	35112	4.88	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10431	23320	36737	1.19	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10674	23560	36992	0.76	3.0E-04	AI092139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); w75a11.x1 Soares thymus NHFTh Homo sapiens cDNA clone IMAGE:2513276 3'
10938	23923	37250	3.8	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares testis NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); nc38e04.r1 NCL OGAP_P72 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element;
12332	25934	31372	4.37	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
12674	25791	31578	2.8	3.0E-04	AB018292.1	NT	DKFZp547L185_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547L185 5'
13041	25577		2.71	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
186	13285	26201	1.65	2.0E-04	AF217796.1	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
501	13571	26489	2.25	2.0E-04	AU146707.1	EST_HUMAN	Human dystrophin gene
932	13984	26929	8.04	2.0E-04	M86524.1	NT	Human dystrophin gene
932	13984	26930	8.04	2.0E-04	M86524.1	NT	Human dystrophin gene
1207	14246		3.43	2.0E-04	AI286021.1	EST_HUMAN	qh8a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1655052 3' similar to contains MER3.b2 MER3 repetitive element;
1214	14252		1.51	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1856	14578		1.22	2.0E-04	AF224288.1	NT	Mus musculus 5' flanking region of Pib3 gene
2169	15210		0.98	2.0E-04	AA475980.1	EST_HUMAN	zu38b05.s1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2611	15609	28804	6.18	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3029	16081	28982	0.98	2.0E-04	AI124528.1	EST_HUMAN	am98c09.XT Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3382	16425	28328	1.02	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3497	16636	29434	3.47	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3524	16592	29486	1.65	2.0E-04	U94374.1	NT	Human tyrosine kinase TXK (tk) gene, exons 9 and 10
3886	17013	29802	0.75	2.0E-04	AW978441.1	EST_HUMAN	EST390560 MAGe resequences, MAGP Homo sapiens cDNA
4241	17257		7.68	2.0E-04	U01029.1	NT	Phaeosolus vulgaris nitrate reductase (PvNIR2) gene, complete cds
4780	17785	30655	1.65	2.0E-04	H86285.1	EST_HUMAN	yu01e11.1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4780	17785	30656	1.65	2.0E-04	H86285.1	EST_HUMAN	yu01e11.1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4911	17910		1.82	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5194	18186	31028	1.77	2.0E-04	AB037997.1	NT	Danio rerio hagarono gene, exons 1 to 6, partial cds
5247	18234	31084	1.03	2.0E-04	AF057019.1	NT	Dicystostellum discoidaleum Interaplin (abpD) gene, complete cds
5302	18286	31138	1	2.0E-04	7262289	NT	Homo sapiens ARP3 (actin-related protein 3, yeast) homolog (ACTR3), mRNA
5302	18286	31139	1	2.0E-04	7262289	NT	Homo sapiens ARP3 (actin-related protein 3, yeast) homolog (ACTR3), mRNA
5735	18808	31902	2.43	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLC00H10 3'
5748	18821	31918	1.76	2.0E-04	AF60882.1	EST_HUMAN	ttq3b11.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
5956	18023	32143	0.86	2.0E-04	AA298652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6172	19229	32375	0.78	2.0E-04	4768179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6486	19531	32709	1.63	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7599	20535		2.37	2.0E-04	AU121712	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7709	20641		0.74	2.0E-04	AW809903.1	EST_HUMAN	QV0-CT0387-180300-187-e10 CT0387 Homo sapiens cDNA
8088	20981		13.86	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8078	20990	34308	1.11	2.0E-04	P54298	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8533	21464	34804	0.96	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8533	21464	34805	0.96	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8861	21791	35142	1.31	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8861	21791	35143	1.31	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9128	22056	35416	2.26	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHLT) gene, exon 5
9302	22230	35590	0.52	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9653	22858	36246	0.58	2.0E-04	P18716	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF26.1
10481	23368	36781	0.97	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-505 HT0254 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10520	23407	39819	2.08	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
11286	24207	37657	3.82	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
11618	24626		2.47	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 6
11750	24651	38132	3.46	2.0E-04	AJ440282.1	EST_HUMAN	ij01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
11858	24748	38240	2.82	2.0E-04	AW136740.1	EST_HUMAN	UI-H-B11-adm-c-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
13088	25948		130.57	2.0E-04	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
793	13848	26782	2.47	1.0E-04	H99646.1	EST_HUMAN	yc26c09.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element
1102	14145	27083	2.17	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1141	14183	27120	3.59	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1141	14183	27121	3.59	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1360	14391		2.89	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1651	14682	27644	2.56	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1651	14682	27645	2.56	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1886	14907	27892	1.23	1.0E-04	AB048342.1	NT	(LAMP) genes, complete cds
2656	15680	28680	1.05	1.0E-04	AF199953.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2666	15680	28681	1.05	1.0E-04	AF199953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2738	15731	28726	0.91	1.0E-04	BE218833.1	EST_HUMAN	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2738	15731	28727	0.91	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3328	16374	28275	1.42	1.0E-04	Q62203	SWISSPROT	hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3798	18829	29716	0.9	1.0E-04	AI440282.1	EST_HUMAN	SPLICING FACTOR 3A SUBUNIT 2 (SF3A68)
4145	17166	30040	1.69	1.0E-04	MT4042.1	NT	ij01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element
4170	17191	30063	1.62	1.0E-04	AV647727.1	EST_HUMAN	Mouse alpha 1 type-IV collagen mRNA
4576	17584	30449	1.03	1.0E-04	P08547	SWISSPROT	AV647727 GLC Homo sapiens cDNA clone GLOCBD04 3'
5231	18219	31066	1.14	1.0E-04		NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5231	18219	31067	1.14	1.0E-04	7682015	NT	Homo sapiens KIAA0237 gene product (KIAA0237). mRNA
6074	19135	32269	1.74	1.0E-04	P08547	SWISSPROT	Homo sapiens KIAA0237 gene product (KIAA0237). mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6148	19207	32345	0.46	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6148	19207	32346	0.46	1.0E-04	T19615.1	EST_HUMAN	753F Heart Homo sapiens cDNA clone 753
6707	19743	32946	0.88	1.0E-04	AA171711.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:252
7151	20259	33513	0.6	1.0E-04	AA564561.1	EST_HUMAN	n25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993466 3' similar to db:M97252
7550	20488	33777	14.75	1.0E-04	AI251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
8004	20488	33777	15.42	1.0E-04	AI251980.1	EST_HUMAN	q57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
8574	21505	34848	1.13	1.0E-04	AA630453.1	EST_HUMAN	q57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
9876	22791	36181	2.74	1.0E-04	AI806220.1	EST_HUMAN	q57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
9886	22801	36188	1.38	1.0E-04	O88969	SWISSPROT	ab94g08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854654 3'
9959	22864		0.82	1.0E-04	T77153.1	EST_HUMAN	wf26a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2366742 3'
10172	23063	36460	1.61	1.0E-04	10883876	NT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN B)
10675	23561		5.84	1.0E-04	P08547	SWISSPROT	yd72a08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 5'
10711	23597	37024	1.04	1.0E-04	P08548	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
11781	24680		2.01	1.0E-04	M28587.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12077	24918	38418	1.85	1.0E-04	AB032958.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12116	24957	38460	2	1.0E-04	AW265061.1	EST_HUMAN	Mouse alpha leukocyte interferon gene, complete cds
12146	24986	38486	1.98	1.0E-04	Q03696	SWISSPROT	Homo sapiens mRNA for KIAA1142 protein, partial cds
12146	24986	38487	1.98	1.0E-04	Q03696	SWISSPROT	xv49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12216	25050		1.48	1.0E-04	AJ251885.1	NT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
722	13780	26702	2.01	9.0E-05	AA718933.1	EST_HUMAN	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
5382	18364	31203	1.17	9.0E-05	AF156186.1	NT	Homo sapiens partial SL C22A2 gene for organic cation transporter (OCT2), exon 1
6190	19247	32393	1.5	9.0E-05	Q60716	SWISSPROT	alt45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
8011	20928	34245	0.79	9.0E-05	AW204958.1	EST_HUMAN	Homo sapiens putative tumor suppressor mRNA
8011	20928	34246	0.79	9.0E-05	AW204958.1	EST_HUMAN	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
10009	22826		2.87	9.0E-05	D85606.1	NT	UI-H-B11-ear-d-05-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
10011	22828	36215	3.12	9.0E-05	AF120982.1	NT	UI-H-B11-ear-d-05-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
11576	24485	37953	3.04	9.0E-05	AW073078.1	EST_HUMAN	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
11688	24580	38067	2.15	9.0E-05	AI287678.1	EST_HUMAN	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
12042	19247	32393	3.86	9.0E-05	Q60716	SWISSPROT	xa34g05.x1 NCI_CGAP_B18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element
							q23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
							MIR repetitive element
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12521	25818		4.65	9.0E-05	AF120756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
846	13901	26841	1.38	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
889	13942		4.34	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
4595	17603	30459	0.69	8.0E-05	AW044605.1	EST_HUMAN	wy8a04.x1 Soares NSF FB 9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
9308	22236	35587	0.53	8.0E-05	Y11686.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11591	24500	37899	2.95	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13070	25804		1.45	8.0E-05	AA276933.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704893 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
367	13434	26366	4.31	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
367	13434	26367	4.31	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
589	13657	26560	6.85	7.0E-05	L49075.1	EST_HUMAN	HJMG72014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
589	13657	26561	6.85	7.0E-05	L49075.1	EST_HUMAN	HJMG72014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1082	14126	27064	1.13	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2767	15759	28763	4.27	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3201	16249	29145	3.16	7.0E-05	AB009080.1	NT	Dicystrellum discoidium gene for TRFA, complete cds
4142	17163		0.81	7.0E-05	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4479	17490	30350	2.12	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4556	17565	30423	0.66	7.0E-05	U60980.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
5037	18034	30891	0.88	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
8803	21733	35082	1.17	7.0E-05	AA505582.1	EST_HUMAN	nh93g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966066 3'
10082	22875	36263	4.71	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Strabagene (cat#936206) Homo sapiens cDNA clone HFBED60
11600	24509		6.96	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2040	15057	28067	1.14	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2040	15057	28068	1.14	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2628	16626	28620	1.38	6.0E-05	A1665241.1	EST_HUMAN	wb54h06.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb.J03250 DNA TOPOISOMERASE I (HUMAN);
2733	15726	28722	1.11	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA28B10
2733	15726	28723	1.11	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA28B10
2661	13762	26678	2.66	6.0E-05	AF036630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6134	19193	32329	3.87	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6134	19193	32330	3.87	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6668	19706	32901	1.46	6.0E-05	N72826.1	EST_HUMAN	y50g11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246212 5'
7263	20172	33413	0.73	6.0E-05	AA897680.1	EST_HUMAN	qj80a03.s1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1604688 3'
8663	21694	34933	1.06	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-H08 BT0311 Homo sapiens cDNA
8663	21594	34934	1.06	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-H08 BT0311 Homo sapiens cDNA
8011	21640	35296	0.58	6.0E-05	AA150482.1	EST_HUMAN	z108c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
9016	21945	35301	3.62	6.0E-05	AW896629.1	EST_HUMAN	PW4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
9143	22071	35433	0.63	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
8764	22758	36143	1.71	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
8794	22758	36144	1.71	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
10051	22867	36358	0.69	6.0E-05	T94149.1	EST_HUMAN	y28c12.1 Strabagena lung (#337210) Homo sapiens cDNA clone IMAGE:119062 5'
11189	24115	37663	2.41	6.0E-05	R75639.1	EST_HUMAN	yf69d08.s1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR repetitive element;
11950	24784	38293	3.33	6.0E-05	AA044015.1	EST_HUMAN	zk5802.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12723	25802	31562	9.63	6.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-230400-001-f09 NT0038 Homo sapiens cDNA
13069	25595	31728	2.44	6.0E-05	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
1429	14460	27412	9.5	5.0E-05	AW392086.1	EST_HUMAN	QV4-S10234-241199-040-h11 S10234 Homo sapiens cDNA
1888	14809		3.15	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2680	15578	28573	1.04	5.0E-05	P23249	SWISSPROT	PROTEIN MOV-10
2803	15957	28857	0.97	5.0E-05	AJ251058.1	NT	Homo sapiens MEP1A gene, promoter region and exon 1
4064	17080	29975	3.75	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (ELMT), exon 1
5301	18285	31136	0.65	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
5301	18285	31137	0.65	5.0E-05	Q28422	SWISSPROT	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)
6715	18788	31719	10.89	5.0E-05	X58855.1	NT	Human MLG1emb gene for embryonic myosin alkaline light chain, 3'UTR
6224	19279	32433	3.28	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3'
6409	19457	32631	0.79	5.0E-05	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7716	20648		1.24	5.0E-05	AB037664.1	NT	Mus musculus gene for catenin, exon 1
12518	25400		7.16	5.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12771	25400		5.69	5.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2854	13343		3.02	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4596	17604	30460	1.24	4.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4596	17604	30461	1.24	4.0E-05	P49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4982	17981		1.2	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5148	18141	30988	0.74	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7271	20179	33422	0.69	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (hP) gene, 5' region
10053	22960		7.1	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
10508	23393	36805	0.61	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE)
10891	23776	37202	0.63	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
11207	24133	37581	4.6	4.0E-05	AW627946.1	EST_HUMAN	h38c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element;
12412	25181	31877	1.89	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
704	13763	26680	0.71	3.0E-05	A1248061.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1086	14130	27088	1.71	3.0E-05	AW273851.1	EST_HUMAN	x24q03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1158	14189	27135	1.29	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1188	14199	27136	1.29	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1543	14573	27532	0.89	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
1543	14573	27533	0.99	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3335	16381		0.71	3.0E-05	A1288919.1	EST_HUMAN	q19g11.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:008632
4489	17600	30362	8.18	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN;
4489	17500	30363	8.18	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4578	17566	30447	0.86	3.0E-05	AA368679.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4878	17586	30448	0.86	3.0E-05	AA368679.1	EST_HUMAN	EST79998 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein
4732	17737	30599	0.71	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4849	17851	30719	0.95	3.0E-05	P97468	SWISSPROT	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
4951	13763	26680	0.68	3.0E-05	A1248061.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
5749	18822	31919	1.71	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
7062	20086	33319	1.08	3.0E-05	A1225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7062	20086	33320	1.08	3.0E-05	A1225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8478	21409	34747	2.38	3.0E-05	BE733167.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842202 5'
9450	22382	35741	1.85	3.0E-05	AW770982.1	EST_HUMAN	h84e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009639 3'
9454	22382	35744	1.77	3.0E-05	6912431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9458	22386	35748	0.73	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN-8 (IMAGE-8 ANTIGEN)
9675	22801		0.6	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9860	22775	36161	1.73	3.0E-05	AA372562.1	EST_HUMAN	EST844475 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end
10187	23078		3.49	3.0E-06	A1769331.1	EST_HUMAN	wg36709.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
11014	23898	37333		3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
11014	23898	37334	0.9	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12420	25185		1.72	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
12595	25291		1.5	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2346	15354	26357	1.36	2.0E-05	A1286021.1	EST_HUMAN	qh8e11.x1 Soares_NFL_T_QEC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2620	15618	28611	0.69	2.0E-05	M13792.1	NT	MER3.b2 MER3 repetitive element;
2762	16754		5.86	2.0E-05	AA160562.1	EST_HUMAN	Human adenosine deaminase (ADA) gene, complete cds
3182	16232	29127	1.93	2.0E-05	BE068036.1	EST_HUMAN	z446a12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3397	16439	29343	0.92	2.0E-05	AF184614.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3427	16468	29377	0.85	2.0E-05	X99211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3553	16591		0.77	2.0E-05	X95485.1	NT	H. sapiens DNA for endogenous retroviral like element
3875	16904		0.67	2.0E-05	AL039107.1	EST_HUMAN	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4803	17804		1.23	2.0E-05	BE378471.1	EST_HUMAN	DKFZp5681064.L1 568 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5681064 5'
5866	18033	32154	2.01	2.0E-05	AJ011712.1	NT	607236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608663 5'
6139	19198		0.76	2.0E-05	AF028308.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6199	19255	32401	2.23	2.0E-05	Q13183	SWISSPROT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
6199	19255	32402	2.23	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6398	19446	32817	0.68	2.0E-05	A1149272.1	EST_HUMAN	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6475	19520	32896	0.52	2.0E-05	P36085	SWISSPROT	qc72a02.x1 Soares_placenta_86c9weeks_2NkHP86c9W Homo sapiens cDNA clone IMAGE:1715114 3' similar to contains L1.13 L1 repetitive element;
6913	19943	33162	2.19	2.0E-05	AA714330.1	EST_HUMAN	CALCIUM-BINDING PROTEIN
7230	20139	33378	2	2.0E-05	Y08926.1	NT	rw06d12.st NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
7242	20151	33390	1.15	2.0E-05	A1492960.1	EST_HUMAN	P. falciparum mRNA for AARP1 protein, partial
7252	20161		7.05	2.0E-05	A1991025.1	EST_HUMAN	qz47b06.x1 NCL_CGAP_KM11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:002711
							O02711 PRO-POL-DUTPASE POLYPYRROLINE;
							wu35f07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7514	20453	33738	2.27	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7514	20453	33739	2.27	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7759	20889		0.98	2.0E-05	AF128847.1	NT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
8465	21398	34737	2.28	2.0E-05	AI381040.1	EST_HUMAN	ig20h05.x1 NCJ_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9666	22592	35985	0.56	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9668	22592	35986	0.56	2.0E-05	BE244840.1	EST_HUMAN	TCBAP2E1590 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1590
9807	22713	36095	0.52	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9807	22713	36098	0.52	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10434	23323	36741	0.6	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10634	23520	36954	0.92	2.0E-05	BF059339.1	EST_HUMAN	7759g09.y1 NCJ_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
11062	23946	37383	2.74	2.0E-05	N41751.1	EST_HUMAN	yw01e06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
11062	23946	37384	2.74	2.0E-05	N41751.1	EST_HUMAN	yw01e06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
11089	20161		2.43	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2522077 3'
11888	23986	37424	2.34	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
12529	25738		5.85	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR-Q12832
12629	25886		10.39	2.0E-05	AW074604.1	EST_HUMAN	Q12832 GLYCOPHORIN HEP2;
12677	25727		2.42	2.0E-05	AF275948.1	NT	repetitive element;
12817	25438	31795	1.45	2.0E-05	AU131513.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
13104	25919		2.09	2.0E-05	AI200970.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2286	15294	28302	1.24	1.0E-05	P27448	SWISSPROT	qf68g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1756236 3'
2745	15932	28731	2.24	1.0E-05	AL163282.2	NT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78
3718	16750	29638	2.1	1.0E-05	AF088273.1	NT	Homo sapiens chromosome 21 segment HS21C082
3881	16910		1.51	1.0E-05	AF223391.1	NT	Drosophila melanogaster strain Larito 120 Suppressor of Hairless (Su(H)) gene, partial cds
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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4050	17077	28952	15.85	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4268	17284	30151	1.2	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4375	17369	30252	2.22	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_tetis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4951	17959	30817	2.78	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCL_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5081	18078	30927	0.7	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7056	20082	33314	1.68	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7169	18441	31344	0.48	1.0E-05	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7440	20182	33426	3.21	1.0E-05	AA641846.1	EST_HUMAN	ns19g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.11 L1
7442	20383	33552	12.61	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
8109	21021	34347	0.63	1.0E-05	BF222846.1	EST_HUMAN	7b57d01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3648945 3' similar to contains MER10.b3
8251	21156		2.43	1.0E-05	P19474	SWISSPROT	MER10 repetitive element;
9472	22400		2.89	1.0E-05	AL163227.2	NT	B2 KD RO PROTEIN (SJOJOREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9612	22538	35908	2.81	1.0E-05	AA462578.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9827	22733	36115	13.49	1.0E-05	AA236110.1	EST_HUMAN	z33h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to
9905	22893	36279	0.77	1.0E-05	AV732190.1	EST_HUMAN	gb.L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
10353	23242	36661	0.89	1.0E-05	AW510902.1	EST_HUMAN	z305e11.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu
10353	23242	36662	0.89	1.0E-05	AW510902.1	EST_HUMAN	repetitive element; contains element TAR1 repetitive element;
10427	23316	36733	2.56	1.0E-05	AW291521.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'
10427	23316	36734	2.56	1.0E-05	AW291521.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
10881	23567		1.76	1.0E-05	AW463895.1	EST_HUMAN	OFFR.11 OFFR repetitive element;
10881	23567		1.76	1.0E-05	AW463895.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains
10881	23567		1.76	1.0E-05	AW463895.1	EST_HUMAN	OFFR.11 OFFR repetitive element;
10881	23567		1.76	1.0E-05	AW463895.1	EST_HUMAN	UI-H-BI2-agk-a-08-0-UJ.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10881	23567		1.76	1.0E-05	AW463895.1	EST_HUMAN	UI-H-BI2-agk-a-08-0-UJ.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10881	23567		1.76	1.0E-05	AW463895.1	EST_HUMAN	ha07c10.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1
10881	23567		1.76	1.0E-05	AW463895.1	EST_HUMAN	repetitive element;
11356	24274	37716	2.1	1.0E-05	U01928.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11356	24274	37717	2.1	1.0E-05	U01928.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12981	25980	31477	2.31	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Table 4
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2721	15714	28713	7.88	9.0E-06	AI583811.1	EST_HUMAN	tt73a06.x1 NC1_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3143	16193	28086	4.94	9.0E-06	AI218083.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8tcdweeks_2NkHP8t9W Homo sapiens cDNA clone IMAGE:1759191 3'
3874	16707		2.83	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6123	19182	32317	2.63	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7188	20188	33431	1.03	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-e07 BT0313 Homo sapiens cDNA
7844	20771	34074	0.89	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8246	21151	34486	12.99	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
9033	21982	35322	1.7	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9534	22481	35823	3.66	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9534	22481	35824	3.66	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9763	22887	36073	3.9	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11377	24293	37738	3.53	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2557	15828	28555	1.62	8.0E-06	AW362839.1	EST_HUMAN	RC3-CT0283-201199-011-f11 CT0283 Homo sapiens cDNA
11012	23996	37330	0.78	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
11012	23996	37331	0.78	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1006	14055		1.62	7.0E-06	AA069729.1	EST_HUMAN	ab90f10.s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element;
1458	14490	27451	3.05	7.0E-06	7852177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2916	15969		15.08	7.0E-06	AB68252.1	EST_HUMAN	qw16g09.x1 NC1_CGAP_U3 Homo sapiens cDNA clone IMAGE:1091296 3' similar to contains Alu repetitive element;
3822	16958		0.87	7.0E-06	AA365542.1	EST_HUMAN	EST198205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5894	18963		5.3	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-f01 OT0062 Homo sapiens cDNA
6015	19078	32203	0.94	7.0E-06	N98645.1	EST_HUMAN	yf65c07.t1 Soares_multiple_sclerosis_2NHMSP Homo sapiens cDNA clone IMAGE:278412 5'
9347	22275	35637	1.11	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF88S1E), mRNA
10412	23301		0.56	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12288	26906	31366	1.86	7.0E-06	BF216972.1	EST_HUMAN	601881522F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4093972 5'
2960	16012	28910	1.56	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3758	18780	29680	1.11	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4866	16036	28938	2.37	6.0E-06	Q01466	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4874	17873	30737	2.75	6.0E-06	A040089.1	EST_HUMAN	ox08e02.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER.8.12 MER8 repetitive element;
5533	18612	31461	1.37	6.0E-06	AF187441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5594	18670	31549	1.18	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
10370	23259		2.19	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
13061	25587	31740	1.95	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
6288	18347	32515	4.53	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6594	19835	32817	2.11	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7401	20100	33335	0.62	5.0E-06	BE145171.1	EST_HUMAN	CM2-HT0193-191089-022-R06 HT0193 Homo sapiens cDNA
7603	20338	33827	0.97	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
9028	21957	35316	0.69	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
9028	21957	35317	0.69	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10603	23489	36918	9.02	5.0E-06	AA313820.1	EST_HUMAN	EST186486 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10992	23876	37305	0.66	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12970	25534	31749	4.21	5.0E-06	A065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
670	13732	26643	4.55	4.0E-06	R16287.1	EST_HUMAN	ye48c03.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:63254 5' similar to contains Alu repetitive element; contains L1 repetitive element;
871	13824	26871	9.61	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCL CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2889574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element;
1362	14393	27347	5.1	4.0E-06	AI334928.1	EST_HUMAN	ib33e09.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1362	14393	27348	5.1	4.0E-06	AI334928.1	EST_HUMAN	ib33e09.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1492	14523	27485	3.4	4.0E-06	BF356612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2282	15281	28299	1.85	4.0E-06	AW015401.1	EST_HUMAN	UI-H-BIO-aat-F05-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3111	16162	29058	0.78	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3964	16992	29876	1.26	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4922	17921	30784	1.94	4.0E-06	AB86939.1	EST_HUMAN	w64c10.x1 NCL CGAP_Brr28 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
9068	21995	35348	0.79	4.0E-06	Q15393	SWISSPROT	TRANSMEMBRANE PROTEINASE, SERINE 2
9358	22286	35649	4.48	4.0E-06	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
10230	23121	36523	1.1	4.0E-06	AA127285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11883	23983	37421	4.56	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488
2176	15188	28193	1.58	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.L1 L1 repetitive element;

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2176	15188	28184	1.58	3.0E-06	AA700662.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2284	15292		1.63	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2364	16016	28913	1.26	3.0E-06	AA888218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 LTR1 repetitive element;
3310	16357		2.18	3.0E-06	AB57779.1	EST_HUMAN	w22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425816 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ;contains L1.12 L1 repetitive element ;
3849	16878	29792	1.4	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3849	16878	29763	1.4	3.0E-06	BE047094.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4588	17596	30454	0.71	3.0E-06	T50266.1	EST_HUMAN	y678b10.r1 Stralagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4677	17682	30550	4.38	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
6401	19449	32620	0.79	3.0E-06	AU159412.1	EST_HUMAN	AU159412 THYROT1 Homo sapiens cDNA clone THYRO1001602 3'
7598	20534		2.11	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8601	21592	34931	0.98	3.0E-06	BE562964.1	EST_HUMAN	601336213F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3690314 5'
9242	22170	35522	0.77	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12883	25342		10.26	3.0E-06	AW385262.1	EST_HUMAN	RCO-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
216	13314		3.41	2.0E-06	P54966	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1688	14819		4.75	2.0E-06	P21414	SWISSPROT	POL. POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2401	15406	28409	1.54	2.0E-06	AB72138.1	EST_HUMAN	wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1 MER30 repetitive element;
2490	15492	28492	2.28	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2601	15589	28594	2.38	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3679	16616	29519	1.39	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLOFDB05 3'
3828	16858	29739	2.19	2.0E-06	AA173518.1	EST_HUMAN	zp02a05.r1 Stralagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3836	16865	29748	0.88	2.0E-06	AW450215.1	EST_HUMAN	UI-H19-aky-g-05-0-U1.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738178 3'
3843	16872	29755	2.32	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6326	19376		0.79	2.0E-06	AA974932.1	EST_HUMAN	or34f01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6358	19407	32572	0.77	2.0E-06	AF539448.1	EST_HUMAN	ts51f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537 Q13537 MER37 TRANSDUCIBLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
6709	19745	32948	5.73	2.0E-06	AB1819424.1	EST_HUMAN	wf80b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410083 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7894	20810	34118	0.58	2.0E-06	AA688423.1	EST_HUMAN	rw69c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1.13 L1 repetitive element;
8498	21427		1.17	2.0E-06	AW869223.1	EST_HUMAN	MR3-SN0067-120400-002-702 SN0067 Homo sapiens cDNA
8698	21599	34939	0.78	2.0E-06	T12238.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9394	22322		0.98	2.0E-06	AA772497.1	EST_HUMAN	zh27c11.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70487 P70487 REVERSE TRANSCRIPTASE;
9407	22335	35699	1.62	2.0E-06	H62051.1	EST_HUMAN	y437c04.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9757	22681	36066	1.09	2.0E-06	AF003528.1	NT	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
9757	22681	36057	1.09	2.0E-06	AF003529.1	NT	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
9777	22701		0.6	2.0E-06	AI473460.1	EST_HUMAN	ff16g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
10223	23114	36515	0.82	2.0E-06	N30576.1	EST_HUMAN	yw66e03.s1 Soares_placenta_8tc0weeks_2NbtHP8b9W Homo sapiens cDNA clone IMAGE:257212 3'
10430	23319		0.66	2.0E-06	AV748969.1	EST_HUMAN	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
12592	25909	31367	1.78	2.0E-06	P23249	SWISSPROT	PROTEIN MOV-10
12735	25376		3.99	2.0E-06	BE328232.1	EST_HUMAN	hs9202.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144689 3' similar to contains L1.12 L1 repetitive element;
35	13151	26040	1.77	1.0E-06	O760B2	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 6) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
680	13742	26657	1.51	1.0E-06	AF084384.1	NT	Mus musculus DMM5E protein (DMM5e) mRNA, complete cds
1470	14501	27462	2	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1646	14577	27537	1.22	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1592	14623	27583	1.2	1.0E-06	AA034141.1	EST_HUMAN	z08a12.s1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element
1592	14623	27584	1.2	1.0E-06	AA034141.1	EST_HUMAN	z08a12.s1 Soares_fetal_liver_spleen_1NfLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element
1606	14637		1.18	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2010	15028	28020	6.69	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2010	15028	28021	6.69	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4476	17487	30346	15.6	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5246	18233	31082	1.05	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5246	18233	31083	1.05	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5473	18554	31396	4.81	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5498	18577	31424	1.15	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-404 FN0004 Homo sapiens cDNA
5498	18577	31425	1.15	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-404 FN0004 Homo sapiens cDNA
5683	18737	31645	1.06	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6005	19069		0.59	1.0E-06	BE069527.1	EST_HUMAN	CM0-BT0281-031199-087-H04 BT0281 Homo sapiens cDNA
7198	20198	33444	5.2	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1(A) CHAIN PRECURSOR
8208	25987		0.52	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8580	21511		0.95	1.0E-06	AA912623.1	EST_HUMAN	q129c08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8849	21779	35126	1.04	1.0E-06	A1347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928842 3'
9057	21888	35340	1.5	1.0E-06	A1287878.1	EST_HUMAN	q123f06.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
9844	22962	36341	1.11	1.0E-06	N74635.1	EST_HUMAN	MIR repetitive element;
9918	22905	36295	0.67	1.0E-06	Q36575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
10207	23098	36497	3.3	1.0E-06	U82668.1	NT	Homo sapiens chox gene, alternatively spliced products, complete cds
10207	23098	36498	3.3	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
10248	23139	36545	5.28	1.0E-06	AA132611.1	EST_HUMAN	z017e08.11 Striatagene colon (#837204) Homo sapiens cDNA clone IMAGE:587174 5'
10307	23197		2.79	1.0E-06	AA449257.1	EST_HUMAN	z04d11.s1 Soares_t04a_fetus Nb24F8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to
10966	23950		2.3	1.0E-06	AL163203.2	NT	g01D26129 RIBONUCLEASE PANGREATIC PRECURSOR (HUMAN);
12076	24917		3.35	1.0E-06	AW690941.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12826	25309	31816	7.93	1.0E-06	L78610.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
381	13466	26383	1.26	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
381	13466	26384	1.26	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8978	21808		0.59	9.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11693	24595	38072	3.1	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
4883	17882	30747	5.27	8.0E-07	A1288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4883	17882	30748	5.27	8.0E-07	A1288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6103	19164		7.68	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8581	21512		12.29	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
12047	24988		7.22	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Striatagene (cat#836206) Homo sapiens cDNA clone HFBEN89
12270	25087		5.99	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5709	18782	31712	0.69	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5709	18782	31713	0.69	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1929	14950	27928	3.2	6.0E-07	AW655568.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2515	15516	28520	2.42	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
4066	17083		1.98	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4.P33 INTERGENIC REGION
9684	22610	35984	1.57	6.0E-07	BF001867.1	EST_HUMAN	7c94t07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR.O75920 O75920 4F3L
12207	25042	38545	3.58	6.0E-07	A1762850.1	EST_HUMAN	cm8705.y5 NCI_CGAP_K183 Homo sapiens cDNA clone IMAGE:1564177 5'
12498	25881		2.14	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-250300-121-112 NN1029 Homo sapiens cDNA
346	13435		1.93	5.0E-07	A1831883.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2385547 3'
1084	14128		2.59	5.0E-07	AA380630.1	EST_HUMAN	EST93615 Supt cells Homo sapiens cDNA 6' end
3078	16128		0.78	5.0E-07	A1831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2385547 3'
6359	19408	32573	1.36	5.0E-07	U65087.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
6449	19485	32670	0.44	5.0E-07	AA278183.1	EST_HUMAN	z08e09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712552 5' similar to gb.X53741_rnet
7418	20117	33353	1.54	5.0E-07	A1393981.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7418	20117	33354	1.54	5.0E-07	A1393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_GCL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
7735	20667	33964	15.89	5.0E-07	AW070885.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_GCL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element;
8851	21781	35128	1.11	5.0E-07	Q9WUQ1	SWISSPROT	xa31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb.X15341
9059	21988		1.04	5.0E-07	P09593	SWISSPROT	CYTOKROME C OXIDASE POLYPEPTIDE VIA LIVER (HUMAN);
10854	23740	37163	7.25	5.0E-07	A1908587.1	EST_HUMAN	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
11108	24037	37482	1.66	5.0E-07	P08647	SWISSPROT	MOTIFS 1 (ADAMTS-1) (ADAM-TS1)
11947	24781	38289	3.91	5.0E-07	P11087	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
12012	24854		2.6	5.0E-07	AJ271735.1	NT	CM-BT178-220499-014 BT178 Homo sapiens cDNA
12890	25774		3.27	5.0E-07	AW862537.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4085	17110	29989	1.66	4.0E-07	AW009602.1	EST_HUMAN	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
7542	20481		0.99	4.0E-07	AJ272265.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
7643	20578	33872	0.58	4.0E-07	Q922V6	SWISSPROT	QY0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
7643	20578	33873	0.58	4.0E-07	Q922V6	SWISSPROT	ws84h05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
8501	21432	34773	0.85	4.0E-07	AL163207.2	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9604	22530	35897	4.84	4.0E-07	AW418134.1	EST_HUMAN	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDAT1)
							HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDAT1)
							Homo sapiens chromosome 21 segment HS21C007
							xy49g11.x1 NCI_CGAP_L184.1 Homo sapiens cDNA clone IMAGE:2856548 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10814	23700	37128	0.65	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11376	24292	37736	3.3	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCL_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2399703 3'
11376	24292	37737	3.3	4.0E-07	A1765528.1	EST_HUMAN	w181b08.x1 NCL_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2399703 3'
11670	24574		1.78	4.0E-07	BE001828.1	EST_HUMAN	PM1-BND083-030300-003-e12 BND083 Homo sapiens cDNA
464	13536	26456	4.44	3.0E-07	U19719.1	NT	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
604	13670	26573	1.48	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1401	14432	27387	2.03	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
1649	14680		2.08	3.0E-07	M84857.1	NT	Human IgK subgroup 1 germline gene, exons 1 and 2, V-region 018 allele
2060	15076		1.07	3.0E-07	AA526763.1	EST_HUMAN	nt56b09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1 t3 L1 repetitive element;
2307	15315	28318	1.77	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
2492	15494	28404	4.09	3.0E-07	BE005077.1	EST_HUMAN	MRO-BND0115-020300-001-f11 BND0115 Homo sapiens cDNA
2492	15494	28495	4.09	3.0E-07	BE005077.1	EST_HUMAN	MRO-BND0115-020300-001-f11 BND0115 Homo sapiens cDNA
3081	16132	29028	0.84	3.0E-07	T84704.1	EST_HUMAN	y450t2.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:111695 5'
3202	16250	29146	2.3	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4840	17841	30710	8.54	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4876	17875	30740	0.87	3.0E-07	A1797236.1	EST_HUMAN	we8b12.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2347987 3'
5198	18190	31031	1.7	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5198	18190	31032	1.7	3.0E-07	T57850.1	EST_HUMAN	gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5983	18934	32063	11.51	3.0E-07	O98807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6202	19258	32405	0.81	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
7000	20027		4.82	3.0E-07	AA815176.1	EST_HUMAN	cc04c10.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7932	20854	34162	4.02	3.0E-07	AW767768.1	EST_HUMAN	QV1-UM0036-200300-119-g02 UM0036 Homo sapiens cDNA
8114	21025		0.75	3.0E-07	AI691065.1	EST_HUMAN	tw28f11.x1 NCL_CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element;
11931	24776		1.48	3.0E-07	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
12084	24925		2.07	3.0E-07	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
13092	25609		6.32	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
30	13146	28034	2.82	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
164	13265	26182	6.85	2.0E-07	L77669.1	NT	Homo sapiens D1George syndrome critical region, telomeric end
164	13265	26183	6.85	2.0E-07	L77669.1	NT	Homo sapiens D1George syndrome critical region, telomeric end
183	13291	26206	33.69	2.0E-07	U98849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
772	13829	26760	3.24	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
772	13829	26761	3.24	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
785	13841		0.88	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ; ENDONUCLEASE]
971	14022	26966	2.78	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gbL131860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
972	14023	26967	7.01	2.0E-07	T63042.1	EST_HUMAN	yc15p04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1190	14223	27168	0.95	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1623	14653	27617	2.21	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3684	16717		0.68	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3754	16786	29676	26	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5280	18268		0.78	2.0E-07	AW902219.1	EST_HUMAN	QV3-NN1023-260400-168-111 NN1023 Homo sapiens cDNA
5628	18607	31455	1.79	2.0E-07	AW898068.1	EST_HUMAN	RC3-NN0068-280400-021-g11 NN0068 Homo sapiens cDNA
6831	25695	33077	0.69	2.0E-07	AW448988.1	EST_HUMAN	UI-H-B13-ake-b-01-Q-UI.s1 NCL_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734008 3'
6957	19986	33210	1.78	2.0E-07	AI208715.1	EST_HUMAN	cg56405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
6971	19998	33228	0.57	2.0E-07	AA572953.1	EST_HUMAN	nm33a06.s1 NCL_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:1061938 similar to contains Alu repetitive element;
9039	21968		4.66	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
9253	22181	35535	1.24	2.0E-07	AA035198.1	EST_HUMAN	zk27g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
10281	23171		1.73	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10760	23646	37079	7.43	2.0E-07	AW892607.1	EST_HUMAN	GM4-NN0003-280300-124-906 NN0003 Homo sapiens cDNA
10967	23851	37275	1.08	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/05 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
10967	23851	37276	1.08	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/05 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12231	25525		1.88	2.0E-07	BE15317.1	EST_HUMAN	FM0-1T0339-260100-008-H07 HT0339 Homo sapiens cDNA
12309	25775		2.33	2.0E-07	A1732482.1	EST_HUMAN	zn85h11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:665029 3' similar to contains THR.b2 THR repetitive element;
1128	14171		0.97	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1996	15004	27991	1.33	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1996	15004	27992	1.33	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2406	15411	28414	0.94	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2875	14575	27535	2.43	1.0E-07	P08296	SWISSPROT	GLYCOPROTEIN GPV
3807	14171		1.11	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4395	17408	30274	3.97	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4395	17408	30276	3.97	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6780	19813	33025	1.27	1.0E-07	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CAL T), NAD(P)H dehydrogenase-like protein (NSDHL), and Lp-
7192	20192	33435	5.49	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7192	20192	33436	5.49	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7914	20838	34141	8.93	1.0E-07	N56081.1	EST_HUMAN	w43d07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
8097	21009	34334	0.68	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-505 TN0024 Homo sapiens cDNA
8097	21009	34335	0.68	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-505 TN0024 Homo sapiens cDNA
8130	21040	34369	1.32	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8354	21259	34593	0.46	1.0E-07	P97435	SWISSPROT	Homo sapiens chromosome 21 segment HS21C003
8794	21724	35071	2.11	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8794	21724	35072	2.11	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9509	22436	35800	3.72	1.0E-07	AA083576.1	EST_HUMAN	z51e10.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
9810	22716	36068	1.14	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
10143	23034	36432	0.58	1.0E-07	BE327843.1	EST_HUMAN	h228h06.x1 NCI_CGAP_Meh15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10445	23334	36752	3.54	1.0E-07	BF674524.1	EST_HUMAN	MER18 repetitive element;
10453	23342	36759	1.25	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428 5'
10943	23828		1.54	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12559	25754	31671	2.88	1.0E-07	BE048770.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
7660	20594	33892	0.75	9.0E-08	AI593932.1	EST_HUMAN	h753c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR-O95722 O95722
10399	23288	36710	2.31	9.0E-08	AV734819.1	EST_HUMAN	DJ1163J1.1;
11626	24533	38002	2.18	9.0E-08	AI891052.1	EST_HUMAN	h51506.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
12093	24634	39441	2.86	9.0E-08	AL163301.2	NT	AV734819 cda Homo sapiens cDNA clone cdABFB08 5'
							w130a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2448932 3' similar to contains OFR.12
							OFR repetitive element;
							Homo sapiens chromosome 21 segment HS21C101

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12509	25243		2.37	9.0E-08	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
630	16879		3.17	8.0E-08	AI011352.1	EST_HUMAN	wdt6805.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
1078	14120		0.81	8.0E-08	BE785463.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
3603	16840		1.22	8.0E-08	BE785469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
9298	22226	35586	3.14	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9298	22226	35587	3.14	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
10153	23044	35443	3.47	8.0E-08	AW970693.1	EST_HUMAN	EST382776 MAGE resequences, MAGK Homo sapiens cDNA
11692	24594		2.08	8.0E-08	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
83	13196	26109	2.1	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1388	14419	27374	6.53	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3637	16673	29570	1.33	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3637	16673	29571	1.33	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11253	24177		2.02	7.0E-08	AI555743.1	EST_HUMAN	cong3.P11.A5 contom Homo sapiens cDNA 3'
12098	24939	35443	5.9	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12942	16673	29570	3.2	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12942	16673	29571	3.2	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
842	13897	26834	3.05	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
842	13897	26835	3.05	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2366	15391	26395	1.7	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0166-191199-004-q09 HT0166 Homo sapiens cDNA
3109	16160	26056	0.99	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4346	17360	30225	1.12	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8529	21460		0.7	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9868	22783		0.66	6.0E-08	AA827076.1	EST_HUMAN	ob56c05.s1 NCI_CGAP_Q081 Homo sapiens cDNA clone IMAGE:1335388 3' similar to contains MER12.b3 MER12 repetitive element ;
11848	24698	38189	2.34	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
11984	24807		1.64	6.0E-08	AL163209.2	NT	ENDONUCLEASE
87	13200	25113	2.33	6.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C009
2251	15261	28270	2.16	5.0E-08	AA493851.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
12272	25088		6.77	5.0E-08	P06881	SWISSPROT	rh03b09.s1 NCI_CGAP_Thyl Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
12448	25201	31849	1.58	5.0E-08	AW851878.1	EST_HUMAN	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
							QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1785	14811	27779	1.19	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1785	14811	27780	1.19	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2927	15980		0.66	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_r1_434 (synonym: HES3) Homo sapiens cDNA clone DKFZp434J0426 5'
3112	16163		1.35	4.0E-08	AI078417.1	EST_HUMAN	α25e02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element
3987	17014	29903	0.72	4.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6870	19707	32902	1.08	4.0E-08	P52824	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9366	22284	35646	0.79	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9692	22608	35981	0.84	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
10171	23082		0.95	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10819	23705		1.48	4.0E-08	AI016342.1	EST_HUMAN	α78d12.s1 Soares_tumor_Willms_tumor_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622803 3'
10874	23760	37187	4.41	4.0E-08	AI060027.1	EST_HUMAN	repetitive element; contains element MER22 repetitive element ;
11512	24422	37878	1.69	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11512	24422	37879	1.69	4.0E-08	AA393627.1	EST_HUMAN	z176b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11533	24443	37803	3.91	4.0E-08	BF692493.1	EST_HUMAN	G02248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11533	24443	37804	3.91	4.0E-08	BF692493.1	EST_HUMAN	G02248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12277	25888		1.88	4.0E-08	W76159.1	EST_HUMAN	z185g03.r1 Soares_fetal_heart_Nb2HF8_19w Homo sapiens cDNA clone IMAGE:348556 5' similar to contains L1.11 L1 repetitive element ;
12878	25476		2.28	4.0E-08	AB343353.1	EST_HUMAN	tb95a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
5805	18877	31984	2.76	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
7316	18484	31308	4.02	3.0E-08	AF792737.1	EST_HUMAN	SYNTAXIN 17. ;
7969	20891	34203	1.5	3.0E-08	AL163246.2	NT	qs76f11.y5 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:1944045 5'
							Homo sapiens chromosome 21 segment HS27C046
8216	21121		3.33	3.0E-08	AF466352.1	EST_HUMAN	tb93h09.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
10470	23289		0.67	3.0E-08	AF055093.1	NT	Homo sapiens MHC class 1 region
12006	24849	38346	1.53	3.0E-08	R65279.1	EST_HUMAN	yp12b10.s1 Soares_breast_3NBH18st Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34079 TAT BINDING PROTEIN-1 (HUMAN);

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12006	24848	38347	1.53	3.0E-08	R86279.1	EST_HUMAN	yp12b10.s1 Soares breast 3NBHb1st Homo sapiens cDNA clone IMAGE:187195 3' similar to gb:M34078 TAT-BINDING PROTEIN-1 (HUMAN);
12247	25070		28.09	3.0E-08	R18420.1	EST_HUMAN	y92004.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
219	13318		6.29	2.0E-08	AW302996.1	EST_HUMAN	zw4807.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2767139 3'
246	13344		6.67	2.0E-08	AA425598.1	EST_HUMAN	Alu repetitive element; contains element MER15 repetitive element;
519	13589	28502	2.35	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
683	13745	28659	8.21	2.0E-08	AW888438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
683	13745	28660	8.21	2.0E-08	AW888438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1017	14067		19.93	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1371	14403	27357	1.66	2.0E-08	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1769	14795		2.44	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1879	14900		3.29	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2574	15573		1.96	2.0E-08	K00216.1	NT	Sheep Hls-rRNA-GUG
3253	16301	29206	6.87	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3253	16301	29207	6.87	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3926	16864		2.68	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-181099-012-b03 ST0197 Homo sapiens cDNA
4164	17185	30058	0.73	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4511	17521		2.15	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
5072	18069		4.82	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
5832	18903	32018	0.9	2.0E-08	AA813204.1	EST_HUMAN	af80h11.s1 Soares testis_NHT Homo sapiens cDNA clone 1377189 3'
6046	19108	32238	0.87	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.b3
8583	21514	34858	0.95	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element;
8888	21619	34961	1.57	2.0E-08	AA490121.1	EST_HUMAN	POL POLYPOLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9831	22567		1.1	2.0E-08	AU139978.1	EST_HUMAN	ab02g08.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
10999	23883	37314	0.91	2.0E-08	N78097.1	EST_HUMAN	AU139978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10999	23883	37315	0.91	2.0E-08	N78097.1	EST_HUMAN	y7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
13008	25929		1.77	2.0E-08	11431676	NT	y7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
							Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1529	15903	27519	1.33	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1800	14826	27704	1.79	1.0E-08	AF126348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2065	16090		2.62	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150999-001-112-HT0130 Homo sapiens cDNA
3235	16283	29184	1.16	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3235	16283	29185	1.16	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5793	18865	31973	3.89	1.0E-08	AJ010770.1	NT	Homo sapiens hypoxanthine gene, exons 1-50
8238	21143	34476	1.14	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9111	22039	35395	2.15	1.0E-08	AJ015304.1	EST_HUMAN	cd35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736.3
9746	22670	36053	0.75	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-402 BT0546 Homo sapiens cDNA
10472	23360	36774	0.95	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CITP)
11032	23916	37356	0.95	1.0E-08	P99063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11780	24661	38146	4.28	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12622	25307		1.89	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
4341	17355	30219	5.3	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4341	17355	30220	5.3	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10584	23450		0.59	9.0E-09	T97950.1	EST_HUMAN	ye88a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918.3
6756	19790		0.57	8.0E-09	AI270615.1	EST_HUMAN	qu86e11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978964.3 similar to contains L1.13 L1 repetitive element ;
7639	20574	33868	7.89	8.0E-09	AI183500.1	EST_HUMAN	q442e07.x1 Soares_fetal heart_NthH19W Homo sapiens cDNA clone IMAGE:1732164.3 similar to contains MSR1.t1 MSR1 repetitive element ;
8578	21510	34856	2.58	8.0E-09	AW900159.1	EST_HUMAN	OM0-NN1004-100300-273-e06 NN1004 Homo sapiens cDNA
9540	22467		3.07	8.0E-09	AA938892.1	EST_HUMAN	op74408.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575.3
3670	16703		2.5	7.0E-09	D88842.1	NT	Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4093	17118		2.83	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (S.TM2) gene, complete cds
8625	21556		0.94	7.0E-09	AA256200.1	EST_HUMAN	zr80c05.r1 Soares_NHMP1U_S1 Homo sapiens cDNA clone IMAGE:881992.5 similar to contains L1.12 L1 repetitive element ;
9802	22708	35091	2.99	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10880	23566	36996	1.86	7.0E-09	BE254850.1	EST_HUMAN	60111173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351834.5
10833	23719		1.72	7.0E-09	AA058628.1	EST_HUMAN	zf58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156.3 similar to contains L1.12 L1 repetitive element ;

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11117	24047		3.29	7.0E-09	T97950.1	EST_HUMAN	yes8a12.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:121918 3'
5102	18059	30947	9.39	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-105 HT0527 Homo sapiens cDNA
5392	18374	31215	1.19	6.0E-09	AA557940.1	EST_HUMAN	nt17a11.s1 NCL CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element ;
5585	18643	31521	8.92	6.0E-09	AW195784.1	EST_HUMAN	zn85f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
9139	22067	35428	1.4	6.0E-09	BE161653.1	EST_HUMAN	MR3-HT0446-260300-201-112 HT0446 Homo sapiens cDNA
9718	22843	36024	2.66	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10769	23655		4.23	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
11173	24100	37549	1.41	6.0E-09	BF108755.1	EST_HUMAN	745610.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
12122	24953	38466	1.8	6.0E-09	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12122	24953	38467	1.8	6.0E-09	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12197	25032	38533	1.49	6.0E-09	C01803.1	EST_HUMAN	HUMG0003762 Human adult (K. Okubo) Homo sapiens cDNA
1436	14463	27425	4.58	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-110 HT0252 Homo sapiens cDNA
1877	14898	27882	1.16	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6675	19712	32906	3.42	5.0E-09	AA359454.1	EST_HUMAN	EST68746 Fetal lung II Homo sapiens cDNA 5' end
7166	18498	31340	0.63	5.0E-09	U66039.1	NT	Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV5S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
10597	23483	36912	3.23	5.0E-09	AW799687.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
544	13613		1.75	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
991	14041		1.82	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1488	14519	27480	1.57	4.0E-09	9559718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2036	15053	28051	1.23	4.0E-09	AF176325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF-4A1) gene, partial cds
2036	15053	28052	1.23	4.0E-09	AF176325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF-4A1) gene, partial cds
2454	15458	28456	4.22	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
8429	21361	34700	0.74	4.0E-09	AA495747.1	EST_HUMAN	zn04c06.r1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:788298 5'
11514	24424	37882	1.58	4.0E-09	AB86401.1	EST_HUMAN	wn04f10.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
11557	24466		1.62	4.0E-09	AA195142.1	EST_HUMAN	zn34a12.r1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:668278 5' similar to gb.L07807 DYNAMIN-1 (HUMAN);
2374	15378	28381	4.49	3.0E-09	BE222239.1	EST_HUMAN	hu09a09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2587	15585	28579	1.65	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2699	15693	28687	1.11	3.0E-08	P23249	SWISSPROT	MER18 repetitive element; PROTEIN MOV-10
3376	16420	29322	1.03	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3434	16475		0.75	3.0E-09	AA442272.1	EST_HUMAN	MER18 repetitive element;
4187	17207		0.64	3.0E-09	X16874.1	EST_HUMAN	z154e04.f1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4533	17542	30404	4	3.0E-09	AF175325.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
4633	17639	30502	2.44	3.0E-09	Q9Y3R5	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds 258.1 KDA PROTEIN C21ORF5 (KIAA0933)
5327	18311		0.9	3.0E-08	D86842.1	NT	Homo sapiens DNA for 3-ketoadyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
8480	21411	34748	1.19	3.0E-09	BE465780.1	EST_HUMAN	hx80a02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR-O56091
10741	23927	37057	2.07	3.0E-09	AL163247.2	NT	O56091 IMPACT PROTEIN.;
11480	24375	37823	4.02	3.0E-09	BF109943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11480	24375	37824	4.02	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1285	14318	27266	5.55	2.0E-09	AL163284.2	NT	7172c08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1685	14715		6.07	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2348	15356	28356	1.41	2.0E-09	Q9Y3R5	SWISSPROT	DKFZp761B1710.1 761 (synonym: hanny2) Homo sapiens cDNA clone DKFZp761B1710 5'
4013	17040	28929	4.32	2.0E-09	O60241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
5368	18350	31192	0.99	2.0E-09	P25823	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5921	18988	32107	0.61	2.0E-09	AI004062.1	EST_HUMAN	MATERNAL TUDOR PROTEIN
6390	19439		0.62	2.0E-09	AL163248.2	NT	alpha7b09.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
7087	20293		0.68	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7855	20782	34085	8.73	2.0E-09	AA461430.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7947	20809	34181	0.64	2.0E-09	W28834.1	EST_HUMAN	z603r09.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:798187 5' similar to contains Alu repetitive element;
8269	21174	34509	0.46	2.0E-09	AJ243732.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8347	21282	34596	0.63	2.0E-09	AW862126.1	EST_HUMAN	ql88g10.x1 Soares_NFL_I_G8C_S1 Homo sapiens cDNA clone IMAGE:1854114 3'
9271	22199	35557	1.27	2.0E-09	AJ271795.1	NT	MR1-CT0352-240200-105-908 CT0352 Homo sapiens cDNA
11712	24614	38090	1.87	2.0E-09	AL163248.2	NT	Homo sapiens Xq pseudautosomal region, segment 112
12761	18422		15.23	2.0E-09	X16674.1	NT	Homo sapiens chromosome 21 segment HS21C048
12820	25957		1.74	2.0E-09	AA228070.1	EST_HUMAN	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase nc11a02.f1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;

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1022	14071		1.98	1.0E-09	W78182.1	EST_HUMAN	z079d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to gb:U02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1136	14178	27115	1.51	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1136	14178	27116	1.51	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1658	14888		0.91	1.0E-09	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2625	15526		1.28	1.0E-09	AJ356086.1	EST_HUMAN	q64e11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER1212
2831	15984	28883	1.74	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2968	16020	28917	2.04	1.0E-09	M28688.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2968	16020	28918	2.04	1.0E-09	M28688.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3083	16136	29032	0.86	1.0E-09	BE533440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4914	17913		8.66	1.0E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
5693	18766	31690	1.1	1.0E-09	AL163283.2	NT	Alu repetitive element; contains element MER22 repetitive element ;
6043	19105	32235	1.39	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS21C083
6384	19433	32600	3.04	1.0E-09	P26694	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
8329	21234	34598	0.59	1.0E-09	AV728645.1	EST_HUMAN	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8961	21891	35250	0.68	1.0E-09	AJ688474.1	EST_HUMAN	AV728648 HTC Homo sapiens cDNA clone HTCBIG07 5'
10803	23689		2.91	1.0E-09	AL163283.2	NT	w439b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
12198	25033		1.88	1.0E-09	AL163283.2	NT	MER25.11 MER25 repetitive element ;
12670	25897	31481	1.52	1.0E-09	11418127	NT	Homo sapiens chromosome 21 segment HS21C083
12778	25407		1.52	1.0E-09	157368.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
13054	25821		2.18	1.0E-09	AF260225.1	NT	y451g12.s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:74758 3'
1335	14369	27319	1.6	9.0E-10	AW867740.1	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2881	15936	28841	5.32	9.0E-10	AJ870071.1	EST_HUMAN	MFR-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
7147	20256	33607	4.61	9.0E-10	AJ452982.1	EST_HUMAN	w478h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
157	13257	28175	8.63	8.0E-10	U83630.2	NT	SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 :contains element PTR9 repetitive element ;
3391	16434	29337	0.93	8.0E-10	BE080748.1	EST_HUMAN	y46b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
4297	17311	30177	4.63	8.0E-10	AA376832.1	EST_HUMAN	TR:O00372 O00372 PUTATIVE P150 ;
						NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
						EST_HUMAN	QV1-BT0631-150200-071-f01 BT0631 Homo sapiens cDNA
						EST_HUMAN	EST89564 Small intestine 1 Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10471	23359		3.22	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
726	13763	26707	17.58	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
726	13763	26708	17.58	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1645	14676	27640	2.31	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2594	15592		20.7	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3137	16187	28079	2.65	7.0E-10	X00856.1	NT	H. sapiens DHFR gene, exon 3
6426	19473	32647	4.28	7.0E-10	A345220.1	EST_HUMAN	EST161247 Gall bladder II Homo sapiens cDNA 5' end
7817	20746	34051	1.36	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
8105	21017		1.61	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8554	21485	34826	1.44	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8554	21485	34826	1.44	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
12085	24026	38430	1.82	7.0E-10	AW778769.1	EST_HUMAN	h012g02.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains Alu repetitive element; contains MER7.b1 MER7 repetitive element;
938	13990	26932	2.8	6.0E-10	AJ400877.1	NT	Homo sapiens ASC13 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2726	15719	28716	1.66	6.0E-10	A424405.1	EST_HUMAN	h02d07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2096021 3'
4806	17614	30475	0.66	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4852	17654		3.3	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0284-031089-012-g12 CT0264 Homo sapiens cDNA
9342	22270	35632	1.03	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9342	22270	35633	1.03	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
10160	23051	36452	0.7	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
766	13842		6.7	6.0E-10	AL046804.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
7706	20638		1.88	6.0E-10	BF105159.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
10065	22981	36371	2.15	6.0E-10	P34678	SWISSPROT	DKFZp434N219.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5'
10065	22981	36372	2.15	6.0E-10	P34678	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
115	13223		1.09	4.0E-10	A1221083.1	EST_HUMAN	HYPOPHYSICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
2012	15030	28028	1.34	4.0E-10	AW594709.1	EST_HUMAN	HYPOPHYSICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
2610	19608	28603	7.51	4.0E-10	AL163303.2	NT	qg06f08.x1 Soares_placenta_3to6weeks_2Nbh-IP8to9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element;
7540	20479	33767	18.76	4.0E-10	AF224669.1	NT	hg56g03.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
						NT	Homo sapiens chromosome 21 segment HS21C103
						NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds

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10926	23811	37239	0.95	4.0E-10	AI267342.1	EST_HUMAN	eq93h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
940	13991	26934	1.42	3.0E-10	N36113.1	EST_HUMAN	yy3206.s1 Soares melanocyte 2NbhHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1 L1 repetitive element;
1390	14412		5.11	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
4652	17658	30524	1.06	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4652	17658	30525	1.06	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5640	18715	31616	0.82	3.0E-10	N50109.1	EST_HUMAN	yz11g08.s1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:282782 3'
6444	19490	32667	1.99	3.0E-10	P20350	SWISSPROT	RHOMBLOID PROTEIN (VEINLET PROTEIN)
6609	19650	32834	2.88	3.0E-10	BE302970.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
8228	21133	34463	1.77	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8228	21133	34464	1.77	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
9289	22217	35575	1.21	3.0E-10	H87208.1	EST_HUMAN	ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
9602	22528	35894	1.72	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9602	22528	35895	1.72	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9879	22794		0.66	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10941	23826		1.4	3.0E-10	T65891.1	EST_HUMAN	yc11e12.r1 Stratagene lung (#937270) Homo sapiens cDNA clone IMAGE:80398 5'
11065	23949		1.37	3.0E-10	AA769294.1	EST_HUMAN	nz36g03.s1 NCJ CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1286908 3'
12911	25494	31768	2.23	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
37	13153	26042	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
37	13153	26043	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1915	14936		2.21	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
3028	16080		0.65	2.0E-10	BF675047.1	EST_HUMAN	602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5382	18344	31188	1.52	2.0E-10	P11227	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
6014	19077		2.91	2.0E-10	Q28640	SWISSPROT	(HPRG)
6499	19543	32719	1.52	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7772	20702	34001	8.3	2.0E-10	BE791082.1	EST_HUMAN	601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8592	21523	34867	0.7	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8592	21523	34868	0.7	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

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9942	22747		1.18	2.0E-10	BF434565.1	EST_HUMAN	7c78d08.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
1828	14559		1.5	1.0E-10	AW887707.1	EST_HUMAN	MRO-SN0038-290300-001-f01 SN0038 Homo sapiens cDNA
1829	14559	27822	3.22	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2819	15817		1.64	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191799-088-a08 CT0225 Homo sapiens cDNA
3558	16595	29499	0.85	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161169-013-g10 TT0003 Homo sapiens cDNA
3600	16637		0.74	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3913	16637		0.99	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
4101	17126		8.43	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4225	17241	30108	7.39	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4225	17241	30109	7.39	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4233	17249	30118	2.13	1.0E-10	AB031089.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4266	17282		2.53	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5316	18300		1.02	1.0E-10	A1797745.1	EST_HUMAN	w82f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element;
7014	20041	33275	0.43	1.0E-10	AA631233.1	EST_HUMAN	nc81a05.s1 NCI_CGAP_Cc9 Homo sapiens cDNA clone IMAGE:1158704 3'
7130	20334	33588	0.45	1.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7895	20821		0.73	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8136	21045	34375	0.55	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003761 5'
8816	21746	35094	1.48	1.0E-10	AW408990.1	EST_HUMAN	IB_6A4 Fetal brain library Homo sapiens cDNA
9213	22141		1.27	1.0E-10	AI268940.1	EST_HUMAN	qm04610.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;
10698	23584		8.22	1.0E-10	AA081898.1	EST_HUMAN	zn29g08.r1 Strategene neuroepithelium NT2RAM1 697234 Homo sapiens cDNA clone IMAGE:648314 5'
11352	24270	37712	2.96	1.0E-10	AI038280.1	EST_HUMAN	ov65f03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
281	13376	26260	0.82	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2116	15129	28134	6.04	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
2116	15129	28135	6.04	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3442	16483	28391	3.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.11 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
3442	16483	28392	3.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.11 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D225 5'
4621	17628	30492	0.99	9.0E-11	AA776985.1	EST_HUMAN	aa7801.e1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5768	18839		4.2	9.0E-11	BE079780.1	EST_HUMAN	RC8-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA
10651	23537	36970	1.49	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10651	23537	36971	1.49	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12599	25295	31844	3.3	9.0E-11	C16835.1	EST_HUMAN	C16835 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506B08 5'
3161	16211		15.85	8.0E-11	H19971.1	EST_HUMAN	Y6311.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4046	17073	28959	0.69	8.0E-11	A1478617.1	EST_HUMAN	Im54-c9.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
4127	17150	30025	7.52	8.0E-11	N23712.1	EST_HUMAN	Yw46606.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5311	18295	31148	5.12	8.0E-11	A056038.1	EST_HUMAN	alpha404.s1 Soares total_fetus_Nb2HF8_0w Homo sapiens cDNA clone IMAGE:1659343 3' similar to gb1.D2832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
6003	19067	32184	0.72	8.0E-11	AW874316.1	EST_HUMAN	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982 3'
6968	19996		0.56	8.0E-11	AW166158.1	EST_HUMAN	Y45h11.x1 NCI_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2621061 3' similar to contains MER10.11
1467	14498	27459	1.62	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
9065	21994	35347	2.34	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10724	23610		1.45	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
12733	25374		1.71	7.0E-11	AV701653.1	EST_HUMAN	ENDONUCLEASE]
435	13506	28431	4.25	6.0E-11	M55270.1	NT	AV701656 ADB Homo sapiens cDNA clone ADBABC08 5'
435	13506	28432	4.25	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
7023	20049	33282	1.04	6.0E-11	L44140.1	NT	Human matrix Gla protein (MGP) gene, complete cds
8147	21056	34388	3.32	6.0E-11	P08547	SWISSPROT	Homo sapiens chromosome X region from filarlin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
8896	21866	35224	11.62	6.0E-11	AV727859.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9854	22769	36154	0.61	6.0E-11	BE063509.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5'
12	13127	26013	0.84	5.0E-11	AL163283.2	NT	CMQ-BT0281-031199-087-e03 BT0281 Homo sapiens cDNA
3421	13127	26013	1.23	6.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4328	17342	30208	2	5.0E-11	P48034	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
6794	19827	33037	1.58	5.0E-11	AL163213.2	NT	ALDEHYDE OXIDASE
7955	20877	34188	11.23	5.0E-11	11416799	NT	Homo sapiens chromosome 21 segment HS21C013
1428	14457		1.32	4.0E-11	AA436042.1	EST_HUMAN	Homo sapiens protocadherin beta 3 (PCDH3B3), mRNA
							zu01b12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2838	15827	28823	11.8	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH MGC_71 Homo sapiens cDNA clone IMAGE:3909296 5'
3010	16062	28909	1.57	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4731	17736	30598	0.89	4.0E-11	D44696.1	EST_HUMAN	HUMSUPY089 Human brain cDNA Homo sapiens cDNA clone 069
6750	19784	32897	2.67	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
7345	20341	33607	1.19	4.0E-11	AA442630.1	EST_HUMAN	z69f10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757963 5' similar to TR:G1055250
7767	20697		4.05	4.0E-11	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9831	22836		1.91	4.0E-11	BE149426.1	EST_HUMAN	RC1-HT0256-210100-013-08 HT0256 Homo sapiens cDNA
10186	23077	38479	1.07	4.0E-11	A1609753.1	EST_HUMAN	tf82g12.x1 NC1_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2106830 3' similar to WP:ZK353.1
12782	25419	31791	4.36	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1510	14541	27503	3.15	3.0E-11	6679077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
2943	15995		0.92	3.0E-11	AB16933.1	EST_HUMAN	wj35406.x1 NC1_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2404811 3'
4374	17398		1.42	3.0E-11	AA309246.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
986	14037	26980	1.31	2.0E-11	A1150502.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1213	14251	27193	4.27	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element;
1213	14251	27194	4.27	2.0E-11	R24807.1	EST_HUMAN	y943e12.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1636	14666	27628	3	2.0E-11	L17432.1	NT	y943e12.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1636	14666	27629	3	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
2815	15804	28802	1.26	2.0E-11	AF087913.1	NT	COR3 beta (COR3 beta) genes, complete cds
3240	16288	29192	8.7	2.0E-11	P10263	SWISSPROT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
3371	16415	28316	0.9	2.0E-11	A1478617.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
4553	17562		0.92	2.0E-11	BE065537.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
4716	17721		0.73	2.0E-11	AL163227.2	NT	hm54c09.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161636 3'
5048	18045		1.42	2.0E-11	BE082558.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
5125	18121	30963	1.02	2.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C027
5162	18155	31002	2.96	2.0E-11	AA307931.1	EST_HUMAN	QV2-BT0288-261-089-014-e01 BT0258 Homo sapiens cDNA
6375	18424	32590	1.28	2.0E-11	AW877808.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
							EST178228 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and similar to alpha-2-macroglobulin
							QV2-PT0073-280300-108-h08 PT0073 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6565	19606	32791	1.81	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.11 NCL CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST
7559	20496	33786	0.85	2.0E-11	BF592945.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16. ;
8462	21363		0.72	2.0E-11	P37072	SWISSPROT	7197c03.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442565 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9794	22686		1.89	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10776	23662	37060	5.29	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10995	23879	37309	0.88	2.0E-11	AW85874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10996	23879	37310	0.96	2.0E-11	AW85874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11553	24482	37928	1.75	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11553	24482	37927	1.75	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11553	24492	37960	1.84	2.0E-11	AA261956.1	EST_HUMAN	zs18h04.11 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685519 5'
12371	25887		2.11	2.0E-11	AA704195.1	EST_HUMAN	zj77a03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12398	26171		2.44	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12421	25187	31878	2.51	2.0E-11	BF377858.1	EST_HUMAN	OM2-TND140-070800-372-g01 TND140 Homo sapiens cDNA
12806	25429		3.91	2.0E-11	P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13079	25601		3.36	2.0E-11	11417868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
899	13758	26675	2.54	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
810	13863	26801	1.05	1.0E-11	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C009
1245	14261	27223	1.89	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1516	14547		1.83	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2051	15068	28068	0.86	1.0E-11	P16288	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2140	16153	28164	4.14	1.0E-11	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
3557	16594	28498	1.22	1.0E-11	BE004316.1	EST_HUMAN	CN0-BN0105-170300-282-d12 BN0105 Homo sapiens cDNA
5515	18594	31442	14.58	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6044	19106	32236	0.75	1.0E-11	BF222846.1	EST_HUMAN	7b57d01.x1 NCL CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3649946 3' similar to contains MER10.b3
8328	21233		0.46	1.0E-11	AB042297.1	NT	MER10 repetitive element ;
8780	21710	35066	2.97	1.0E-11	4885546	NT	Homo sapiens PTS gene for 6-pyruvoyl-tetrahydropterin synthase, complete cds
9144	22072	35434	6.62	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9601	22527	35892	1.26	1.0E-11	BF365119.1	EST_HUMAN	y73d08.11 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:28166 5'
9601	22527	35893	1.26	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
11732	24634	38116	8.73	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
12877	25708		2	1.0E-11	Z20377.1	EST_HUMAN	602164807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977 5'
							HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2993	16045	26948	0.79	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10314	23203	36613	1.33	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10314	23203	36614	1.33	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9877	22792		1.22	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
12469	25215		5.13	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4772	17777	30645	1.68	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11788	24710	38201	8.81	7.0E-12	AA704735.1	EST_HUMAN	z23g01.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone HTFAWF06 5'
3606	16643		0.81	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4457	17468	30325	11.13	6.0E-12	AA732516.1	EST_HUMAN	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;
6852	19691	32884	0.49	6.0E-12	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphatase hydrolase (FHTT) gene, exon 5
9547	22474	35831	1.29	6.0E-12	AF003249.1	NT	Marone sarafalis myosin heavy chain FM3A (FM3A) mRNA, complete cds
10007	22824		1.32	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER28.12
1069	14113	27053	1.73	5.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element ;
3449	16480	28397	1.37	5.0E-12	BE047779.1	EST_HUMAN	EST04462 Fetal brain, Striatagene (cat#336206) Homo sapiens cDNA clone HFB0V33
3791	16822	29709	9.07	5.0E-12	AJ271736.1	NT	tz42b05.y1 NCI_CGAP_Bm62 Homo sapiens cDNA clone IMAGE:2291217 5'
6264	19307	32469	5.66	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6254	19307	32470	5.65	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6767	19601	33012	10.4	5.0E-12	AW974760.1	EST_HUMAN	EST336850 MAGE resequences, MAGN Homo sapiens cDNA
7382	20092	33326	0.94	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7393	20092	33326	1.15	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8807	21737	35087	1.26	5.0E-12	AA033745.1	EST_HUMAN	z101g12.s1 Scores_fetal_heart_NbHH-19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains
9225	22153		0.6	5.0E-12	AW887037.1	EST_HUMAN	L1.13 L1 repetitive element ;
9546	22473		0.61	5.0E-12	AL079591.1	EST_HUMAN	RC1-OT0086-220300-011-b07 OT0086 Homo sapiens cDNA
9853	22579	35951	2.51	5.0E-12	AJ271735.1	NT	DKFZp434J0426_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9957	22862	36249	1.23	5.0E-12	P34982	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 1/2
10768	23654		5.1	5.0E-12	AL163303.2	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10850	23739	37159	0.76	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
263	13359	26274	3.89	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
264	13359	26274	4.24	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'

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4733	17738	30600	0.75	4.0E-12	AF089884.1	EST_HUMAN	tx28105.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
8067	20980		0.63	4.0E-12	BF445140.1	EST_HUMAN	MARINER TRANSPOSASE.; nad21b03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2
8819	21749		3.74	4.0E-12	AF109907.1	NT	MER7 repetitive element; Homo sapiens S104 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
9245	22173	35527	0.95	4.0E-12	AB042815.1	NT	Bos taurus Mitc2 mRNA for mitochondrial carrier homolog 2, complete cds
11521	24431	37889	4.88	4.0E-12	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and GBR1 on chromosome 21q22, segment 3/3
639	13700	26608	2.95	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
639	13700	26607	2.95	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
5315	18299	31151	0.72	3.0E-12	AL163288.2	NT	O14517 SMRP.; Homo sapiens chromosome 21 segment HS21C068
5837	18713	31614	1.35	3.0E-12	AF111682.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
7371	20365	33634	0.47	3.0E-12	BE149692.1	EST_HUMAN	RC1-HT0256-280300-017-c08 HT0256 Homo sapiens cDNA
7629	20758		0.58	3.0E-12	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
8221	21126		0.48	3.0E-12	AW654328.1	EST_HUMAN	RC3-CT0255-031089-011-h02 CT0255 Homo sapiens cDNA
9651	22577	35948	0.73	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEP SIN
11099	24030	37474	3.17	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
11099	24030	37475	3.17	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1680	14710	27672	1.83	2.0E-12	AW802131.1	EST_HUMAN	IL6-UM0071-120400-065-a05 UM0071 Homo sapiens cDNA
3527	16565	29469	0.93	2.0E-12	6754485	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4208	17225	30092	1.22	2.0E-12	J01884.1	NT	Rat U3a small nuclear RNA
4208	17225	30093	1.22	2.0E-12	J01884.1	NT	Rat U3a small nuclear RNA
4528	17637		2.47	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
5008	18004	30861	0.65	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5008	18004	30862	0.65	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5430	18512	31235	0.81	2.0E-12	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ; ENDONUCLEASE]
6751	19785		2.64	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGE resequences, MAGI Homo sapiens cDNA
7639	20478	33766	3.2	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
7730	20692	33960	1.48	2.0E-12	BE173035.1	EST_HUMAN	MRO-HT0559-200400-015-a08 HT0559 Homo sapiens cDNA
7960	20862		0.56	2.0E-12	AW842788.1	EST_HUMAN	MR2-CN0037-210200-101-b02 CN0037 Homo sapiens cDNA
8110	21022	34348	2.4	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9285	22213	35571	0.55	2.0E-12	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-JDP
9848	22865		1.98	2.0E-12	AF196884.1	NT	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
10491	23379		12.68	2.0E-12	BE165980.1	EST_HUMAN	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAC-T1)
10694	23878	37308	0.86	2.0E-12	A1334130.1	EST_HUMAN	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
12385	25163		2.32	2.0E-12	AL163283.2	NT	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
127	13232	26148	2.72	1.0E-12	AW627674.1	EST_HUMAN	q070702.x1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538
2004	15022		1.28	1.0E-12	A1871728.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN. ;
3118	16189	28063	0.94	1.0E-12	AF000991.1	NT	Homo sapiens chromosome 21 segment HS21C083
3118	16189	29064	0.94	1.0E-12	AF000991.1	NT	hh80a09.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11
3943	16971	29853	46.33	1.0E-12	AU132248.1	EST_HUMAN	MER18 repetitive element ;
3943	16971	29854	46.33	1.0E-12	AU132248.1	EST_HUMAN	wn51107.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1
6194	19250		1.65	1.0E-12	U82828.1	NT	repetitive element ;
6276	19327		1.98	1.0E-12	Q9Y2G7	SWISSPROT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6394	19442	32610	0.52	1.0E-12	BF642800.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6394	19442	32611	0.52	1.0E-12	BF642800.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
							AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
							Homo sapiens alaxia telangiectasia (ATM) gene, complete cds
							HYPOPHETICAL ZINC FINGER PROTEIN KIA0961
							EST00008 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
							EST00008 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6811	19844	33054	0.52	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
7476	20415	33693	1.9	1.0E-12	AF196884.1	NT	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
							Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7511	20450	33734	13	1.0E-12	A1248533.1	EST_HUMAN	qh66a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848614 3' similar to
							gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.11 MER10
							repetitive element ;
7511	20450	33735	13	1.0E-12	A1248533.1	EST_HUMAN	qh66a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848614 3' similar to
							gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.11 MER10
							repetitive element ;
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3,
							TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3,
							TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T,
9058	21987	35341	0.66	1.0E-12	U68059.1	NT	TCRBV13S9/13S>

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Table 4
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9263	22191	35549	1.45	1.0E-12	AA782323.1	EST_HUMAN	ac26405.s1 Stratiagene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3'
12299	25108	35576	4.45	1.0E-12	AW082164.1	EST_HUMAN	EST374237 IMAGE resequences, MAGG Homo sapiens cDNA
12493	25234		1.67	1.0E-12	AI738502.1	EST_HUMAN	w133108.x1 NCI_CGAP_Cc16 Homo sapiens cDNA clone IMAGE:2392095 3'
12636	25862		2.55	1.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
12919	25529		1.49	1.0E-12	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3' (UBE2D3) genes, complete cds
1078	14122	27059	2.27	9.0E-13	AW082714.1	EST_HUMAN	xb61f07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2580805 3' similar to contains (MER28.13 MER28 repetitive element);
3695	16727		1	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4024	17051	29942	1.04	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for carboxide sulfotransferase, exon 1, 2, 3, 4, 5
7656	20592	33890	0.42	9.0E-13	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
10128	23019		2.38	9.0E-13	N06853.1	EST_HUMAN	zz26b06.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:293651 3'
740	13798	26722	5.28	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
740	13798	26723	5.28	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1862	14894	27894	3.51	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
8680	21621	34963	0.83	8.0E-13	AB84398.1	EST_HUMAN	wm31f09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8690	21621	34964	0.83	8.0E-13	AB84398.1	EST_HUMAN	wm31f09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10644	23530		3.91	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
12187	25023	38524	2.6	8.0E-13	U68080.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV5S8A2T, TCRBV5S8A3N2T, TCRBV13S8A2T, TCRBV6S8P, TCRBV5S9A2T, TCRBV13S8P, TCRBV6S9A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P
8348	21253	34587	0.59	7.0E-13	AB84398.1	EST_HUMAN	wm31f09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8348	21253	34588	0.59	7.0E-13	AB84398.1	EST_HUMAN	wm31f09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8812	21742		0.59	7.0E-13	Q36165	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN OLF2
12737	25377		31.57	7.0E-13	BE78223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
12940	25507		2.07	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGLALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGLALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2113	15129	28131	9.96	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3397	16411		0.83	5.0E-13	R78338.1	EST_HUMAN	y82f04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3457	16498		1.9	5.0E-13	AA435773.1	EST_HUMAN	z77a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element contains element MER22 repetitive element;
7202	20202	33447	0.66	5.0E-13	P08983	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
11294	24214	37663	2.58	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1890	14911		2.05	4.0E-13	AW378814.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
2494	16486		3.04	4.0E-13	AF003526.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4881	17863		1.15	4.0E-13	AA454054.1	EST_HUMAN	z48a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
5780	18852	31957	5.23	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7572	20508	33796	1.3	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
8056	20909	34285	0.93	4.0E-13	AA431529.1	EST_HUMAN	z476g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA;
8182	21089		1.8	4.0E-13	N44291.1	EST_HUMAN	y43g05.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995 A32995 t complex sterility protein - mouse;
9400	22328	35690	1.27	4.0E-13	AL043810.1	EST_HUMAN	DKFZp434A0128_j1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434A0128 5'
10523	23410	36822	4.84	4.0E-13	AI289831.1	EST_HUMAN	qns2405.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:189945 3' similar to contains Alu repetitive element;
11608	24516	37985	1.98	4.0E-13	AA438819.1	EST_HUMAN	z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11608	24516	37988	1.98	4.0E-13	AA438818.1	EST_HUMAN	z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
12698	25354		5.02	4.0E-13	BE503023.1	EST_HUMAN	h282a05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214496 3' similar to contains MER31.1 MER31 repetitive element;
191	13289		2.94	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
850	13943		2.39	3.0E-13	AA430310.1	EST_HUMAN	z468g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2393	16398	28402	2.22	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2501	15503		3.07	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2713	15707	28702	3.37	3.0E-13	BF372862.1	EST_HUMAN	CM3-F10100-140700-242-H08 F10100 Homo sapiens cDNA
3230	16278		2.57	3.0E-13	AA745844.1	EST_HUMAN	cb18402.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
4604	17612	30472	6.13	3.0E-13	AA430310.1	EST_HUMAN	z468g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
5226	18215	31061	0.65	3.0E-13	BF372862.1	EST_HUMAN	CM3-F10100-140700-242-H08 F10100 Homo sapiens cDNA
5730	18803	31896	0.78	3.0E-13	AA134017.1	EST_HUMAN	z488h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
5730	18803	31897	0.78	3.0E-13	AA134017.1	EST_HUMAN	z488h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6223	19278	32432	0.71	3.0E-13	AW005639.1	EST_HUMAN	w288c02.x1 NCL CGAP Brn25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139
8483	21394	34735	7.8	3.0E-13	U52111.2	NT	O75139 KIAA0644 PROTEIN ; Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), ODM protein (CDM), adrenoleukodystrophy protein >
8654	21585	34920	0.78	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Rα-reactive factor
8654	21586	34921	0.78	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Rα-reactive factor
10694	23580	37010	0.7	3.0E-13	AW635487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
11119	24049		3.46	3.0E-13	AI064768.1	EST_HUMAN	HA0538 Human fetal liver cDNA library Homo sapiens cDNA
11482	24395	37845	3.05	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12028	24870	38373	1.87	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
160	13260	26178	2.22	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), ODM protein (CDM), adrenoleukodystrophy protein >
258	13355	26271	1	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1287	14330	27276	5.69	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11' and complete cds
3049	16101	29004	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3049	16101	29005	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3325	16371	29272	1.02	2.0E-13	BF431899.1	EST_HUMAN	nab7605.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3564	16601	29505	1.04	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4203	17221	31199	1.7	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5378	18360	31199	1.02	2.0E-13	M58318.1	NT	Homo sapiens ala gene
5378	18360	31200	1.02	2.0E-13	M58318.1	NT	Homo sapiens ala gene
6362	19411	32576	4.77	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6448	19494		0.44	2.0E-13	X79417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
7126	20330	33693	6.66	2.0E-13	X16912.1	NT	Human PKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7407	20108	33340	0.63	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7407	20108	33341	0.63	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10937	23822	37249	1.93	2.0E-13	6031806	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12453	25203		25.49	2.0E-13	AW892155.1	EST_HUMAN	CMO-NN0001-100300-274-911 NN0001 Homo sapiens cDNA
311	13403	26320	1.59	1.0E-13	S74129.1	NT	FGF-1 fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
913	13665	26912	5.04	1.0E-13	AJ007673.1	NT	Homo sapiens LGMD2B gene
1364	14395	27350	1.78	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2035	15052	28050	2.8	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
4704	17709	30572	1.95	1.0E-13	BF340887.1	EST_HUMAN	THR repetitive element;
6713	19749	32953	0.47	1.0E-13	AA090732.1	EST_HUMAN	602038009F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185866 5'
8489	21420	34757	1.03	1.0E-13	AA577812.1	EST_HUMAN	Y1636.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8489	21420	34758	1.03	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
10592	23478		0.93	1.0E-13	O15491	SWISSPROT	repetitive element contains element MER24 repetitive element;
10780	23676	37106	0.57	1.0E-13	AF300701.1	NT	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
11818	24739	38230	11.71	1.0E-13	BF108785.1	EST_HUMAN	repetitive element contains element MER24 repetitive element;
12292	25103		1.6	1.0E-13	AV715377.1	EST_HUMAN	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
12882	25482		2.97	1.0E-13	AJ271735.1	NT	repetitive element contains element MER24 repetitive element;
353	13440	26353	2.13	9.0E-14	AA781159.1	EST_HUMAN	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
354	13441	26354	2.16	9.0E-14	AA781159.1	EST_HUMAN	Mus musculus osteotesticular protein tyrosine phosphatase mRNA, complete cds
2523	15524		5.16	9.0E-14	AW861577.1	EST_HUMAN	7145e10.x1 Scores_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to
2632	15630	28624	1.41	9.0E-14	AJ133127.1	NT	contains MER29.b2 MER29 repetitive element;
2632	15630	28625	1.41	9.0E-14	AJ133127.1	NT	AV715377 DOB Homo sapiens cDNA clone DCBAIE03 5'
2802	15791	28790	7.93	9.0E-14	AB038162.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3157	16207	29097	6.45	9.0E-14	AW513286.1	EST_HUMAN	aj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
3284	13440	26353	1.01	9.0E-14	AA781159.1	EST_HUMAN	repetitive element;
3662	16991	29776	8.91	9.0E-14	D14547.1	NT	aj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
4870	17870	30734	1.84	9.0E-14	AJ002153.1	NT	repetitive element;
3556	16593		1.27	8.0E-14	BE468263.1	EST_HUMAN	RC4-CT0322-090100-073-409 CT0322 Homo sapiens cDNA
4039	17066		4.12	8.0E-14	R76269.1	EST_HUMAN	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
							Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
							Homo sapiens TFF gene cluster for trefoil factor, complete cds
							xo54h05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
							aj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
							repetitive element;
							Human DNA, SINE repetitive element
							Segulus oedipus gene for seminal vesicle secreted protein semenogelin I
							hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
							y72e03.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9980	21338	34674	50.26	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
10089	22882	36268	3.61	8.0E-14	AA216316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
11865	24755		1.47	8.0E-14	BE082568.1	EST_HUMAN	QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA
12944	25320	31822	3.19	8.0E-14	AI888118.1	EST_HUMAN	wc82h08.x1 NCI CGAP Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
1652	15906		5.71	7.0E-14	AW151673.1	EST_HUMAN	x87e10.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12
9476	22404		0.74	7.0E-14	AL163285.2	NT	MER10 repetitive element ; Homo sapiens chromosome 21 segment HS21C085
388	13472	26390	8.8	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10337	23226	36641	2.66	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10337	23226	36642	2.66	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
641	13702	26809	5.79	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5186	18178	31024	1.07	5.0E-14	AW073791.1	EST_HUMAN	xb03a05.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
5723	18786	31888	5.15	5.0E-14	P08547	SWISSPROT	repetitive element ;
1150	15893		1.84	4.0E-14	P04928	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1900	14921	27801	8.26	4.0E-14	AJ007079.1	NT	S-ANTIGEN PROTEIN PRECURSOR
3815	16845		0.92	4.0E-14	AA046502.1	EST_HUMAN	Homo sapiens LGMD2B gene
4394	17407	30273	1.05	4.0E-14	N46328.1	EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_Nb-HPJ Homo sapiens cDNA clone IMAGE:487858 5'
8538	21487		0.73	4.0E-14	X87344.1	NT	yw73c12.s1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:279180 3' similar to contains L1.13 L1 repetitive element ;
12949	25988		6.5	4.0E-14	AJ886224.1	EST_HUMAN	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
977	14028	26970	1.22	3.0E-14	X95466.1	NT	wvr08c03.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element ;
5036	18033	30890	0.82	3.0E-14	AW265354.1	EST_HUMAN	R.norvegicus mRNA for CP62 protein
7038	20064	33297	1.03	3.0E-14	AJ420786.1	EST_HUMAN	xp45f12.x1 NCI CGAP HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element ; contains element MER9 repetitive element ;
7038	20064	33298	1.03	3.0E-14	AJ420786.1	EST_HUMAN	fa91c12.x1 NCI CGAP Pz28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
7038	20064	33298	1.03	3.0E-14	AJ420786.1	EST_HUMAN	fa91c12.x1 NCI CGAP Pz28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7160	25666		0.58	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7379	20373	33642	0.55	3.0E-14	AA386311.1	EST_HUMAN	EST185034 Brain IV Homo sapiens cDNA
8345	22273	35635	1.04	3.0E-14	N42166.1	EST_HUMAN	Y07b10.r1 Soares melanocyte 2N1H1M Homo sapiens cDNA clone IMAGE:270523 5'
11884	18033	30880	8.35	3.0E-14	AW263354.1	EST_HUMAN	XP45F12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
12867	25838		2.9	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
411	13484	28404	2.72	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
411	13484	26405	2.72	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
714	15981	26891	6.49	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2411	15415		1.73	2.0E-14	AW372668.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
2488	15490		1.22	2.0E-14	7657528	NT	Homo sapiens rhadbold tumor deletion region protein 1 (RTDR1), mRNA
2653	15553	28560	3.95	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2871	15569		1.43	2.0E-14	BE222432.1	EST_HUMAN	h00g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.t1 OFR repetitive element;
5714	18787	31718	0.96	2.0E-14	BF380681.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5815	18887	31988	0.88	2.0E-14	AI312351.1	EST_HUMAN	ta78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element;
5922	18989	32108	2.89	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7210	20210		0.89	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-071-a06 BN0072 Homo sapiens cDNA
7664	20398	33897	1.09	2.0E-14	P58163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7930	20852	34159	20.73	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7930	20852	34160	20.73	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
10428	23317	36735	0.52	2.0E-14	AI978795.1	EST_HUMAN	hr58g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10800	23785	37211	0.61	2.0E-14	AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBBF04 5'
11219	24145	37696	4.35	2.0E-14	AW139800.1	EST_HUMAN	U1-H-B1-adv-a-10-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
11832	18989	32108	2.69	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
12864	25841		2.34	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (G6P) gene, complete cds
13071	15490		1.85	2.0E-14	7657529	NT	Homo sapiens rhadbold tumor deletion region protein 1 (RTDR1), mRNA
1094	14137	27074	1.15	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1431	14462	27414	7.47	1.0E-14	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
1431	14462	27415	7.47	1.0E-14	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
2017	15035	28029	7.34	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2200	15211	26213	4.94	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2433	15437	28437	3.4	1.0E-14	AF001688.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2986	16038	28042	1.58	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3209	16257	29155	5.6	1.0E-14	BF338227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3209	16257	29155	5.6	1.0E-14	BF338227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3955	16983	29867	2.04	1.0E-14	AA682994.1	EST_HUMAN	aa89c12.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4588	17584	30452	1.79	1.0E-14	AW275852.1	EST_HUMAN	xq38h10.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
6020	19092	32208	2.03	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6970	25660	33226	11.73	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6970	25660	33227	11.73	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1598	14629	27588	1.14	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2188	15197		1.42	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor IG-HM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
7917	20841	34143	3.98	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8595	21526	34870	1.34	9.0E-15	BE003559.1	EST_HUMAN	60187750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980158 5'
13032	25571		1.78	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2858	13573		0.94	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3184023 5'
7545	20483	33772	1.41	7.0E-15	BF033327.1	EST_HUMAN	601458631F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
10916	23801		3.03	7.0E-15	AW241958.1	EST_HUMAN	xn77d02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR_12 THR repetitive element;
12349	25141		2.12	7.0E-15	AA284465.1	EST_HUMAN	zs57d08.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gbL21934 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1.1 L1 repetitive element;
1021	14070	27013	5.98	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6142	19201	32337	1.26	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6142	19201	32338	1.26	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
13100	25815		2.17	6.0E-15	BF432200.1	EST_HUMAN	nab81c12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
493	13504	26428	9.56	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2811	15800	28799	1.5	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3528	16567		1.06	5.0E-15	AW266817.1	EST_HUMAN	UI-H-BWO-slp-g-10-0-UI.s1 NCL_CGAP_SubB8 Homo sapiens cDNA clone IMAGE:2731219 3'
450	13117	26003	2.65	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4228	17244	30112	0.73	4.0E-15	AL118596.1	EST_HUMAN	DKFZp761O0810_j1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761O0810 5'
6960	19899	33213	0.8	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0501
8365	21289	34621	0.42	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
8385	21289	34622	0.42	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11501	21289	34621	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11501	21289	34622	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4313	17327		8.61	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANFCARDIODILATIN
5038	18035		0.83	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
5160	18153	30999	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5160	18153	31000	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
7126	20329		1.41	3.0E-15	Q84625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7656	20590	33887	3.12	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7656	20590	33888	3.12	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
10436	23325		2.25	3.0E-15	AA807128.1	EST_HUMAN	cc38a07.s1 NCL_COAP_G081 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11
11234	24160	37609	1.79	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12852	25869		1.81	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
269	13364	26780	3.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
389	13473	26391	5.38	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
389	13473	26392	5.38	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1552	14593		1.2	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3568	16605	29508	1.37	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3568	16605	29509	1.37	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4155	17178	30049	0.94	2.0E-15	AW238499.1	EST_HUMAN	xp26h01.x1 NCL_COAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.13 L1 repetitive element;
4736	17741		3.24	2.0E-15	AI806335.1	EST_HUMAN	wf0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR-Q61043 Q61043 NINEIN.;

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6423	19470	32844	0.99	2.0E-15	BE562352.1	EST_HUMAN	601344233F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6423	19470	32845	0.99	2.0E-15	BE562352.1	EST_HUMAN	601344233F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7473	20413		1.28	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7647	20581	33878	2.18	2.0E-15	AA704195.1	EST_HUMAN	z77603.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7793	20722	34025	5.1	2.0E-15	W05064.1	EST_HUMAN	z978d10.r1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288675 5' similar to
8334	21239	34571	0.67	2.0E-15	AL163247.2	NT	W/P:F44F4.8 CE02227 TRANSPOSASE ;
9463	22351	35753	2.89	2.0E-15	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C047
9622	22548	35978	0.67	2.0E-15	AA397768.1	EST_HUMAN	Human DNA, SINE repetitive element
9622	22548	35979	0.67	2.0E-15	AA397768.1	EST_HUMAN	z77g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9622	22548	35979	0.67	2.0E-15	AA397768.1	EST_HUMAN	z77g08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9638	22844	36233	1.59	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9638	22844	36234	1.60	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
11278	24198		5.05	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12975	16605	29508	2.5	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12975	16605	29509	2.5	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2824	15813		3.57	1.0E-15	A1689984.1	EST_HUMAN	b228i05.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
3056	16108	29014	1.18	1.0E-15	BE043584.1	EST_HUMAN	MARINER TRANSPOSASE. ;
3186	16235	29130	1.3	1.0E-15	P08547	SWISSPROT	HK40e02.y1 NCI_OGAP_Ov44 Homo sapiens cDNA clone IMAGE:2989162 5'
5372	18354	31194	0.71	1.0E-15		NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6632	18672	32858	1.54	1.0E-15	T95763.1	EST_HUMAN	Mus musculus factor in the germline alpha (Figla), mRNA
7353	20349		1.92	1.0E-15	BE074217.1	EST_HUMAN	ye40e10.s1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains
7353	20349		1.92	1.0E-15	BE074217.1	EST_HUMAN	MER8 repetitive element ;
7390	20089	33324	0.76	1.0E-15	P09057	SWISSPROT	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
8810	21740	35089	0.86	1.0E-15	AL163280.2	NT	DYNEIN BETA CHAIN, CILIARY
8991	21920	35275	5.15	1.0E-15	A1200978.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8991	21920	35276	5.15	1.0E-15	A1200978.1	EST_HUMAN	q68h06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9591	22517	35879	0.57	1.0E-15	AL163207.2	NT	q68h06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9591	22517	35879	0.57	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9594	22520	35883	1.37	1.0E-15		NT	Homo sapiens spermidine synthase (SRM) mRNA
9789	22753	36135	1.04	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10158	23049	38449	0.88	1.0E-15	AA884653.1	EST_HUMAN	oh37d03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1
11257	24181	37631	3.1	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
13036	25717	31685	9.74	1.0E-15	AI783944.1	EST_HUMAN	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element
4431	17442		1.03	9.0E-16	BF669487.1	EST_HUMAN	602120192F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277422 5'
4625	17631	30485	1.33	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAAT displacement protein) (CUTL1) mRNA
11431	24347	37792	1.85	9.0E-16	F08888.1	EST_HUMAN	HSC23F081 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
3424	18465	29372	0.73	7.0E-16	Y10186.1	NT	Homo sapiens PHEX gene
5900	18989	32087	0.71	7.0E-16	4885120	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7727	20669	33966	1.44	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7727	20659	33957	1.44	7.0E-16	O88807	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
12994	25798		24.09	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2155	15167		8.99	6.0E-16	AW972611.1	EST_HUMAN	pe28c12.r1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
3932	16960	29843	1.05	6.0E-16	AF224689.1	NT	EST394702 MAGC resequences, MAGI, Homo sapiens cDNA
2729	15722	28718	2.6	5.0E-16	AA992176.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11952	24796	38296	3.63	5.0E-16	BF217388.1	EST_HUMAN	cl80c04.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element ;
13066	25592		14.26	5.0E-16	11418127	NT	801885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2254	16264		1.24	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2402	15407	28410	1.45	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
2402	15407	28411	1.45	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM00396-200300-115-g02 UM00396 Homo sapiens cDNA
3517	16555	29456	5.72	4.0E-16	Q16653	SWISSPROT	QV1-UM00396-200300-115-g02 UM00396 Homo sapiens cDNA
4240	17258	30122	8.21	4.0E-16	BE083876.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4240	17258	30123	8.21	4.0E-16	BE083876.1	EST_HUMAN	PM4-BT0650-010400-002-g08 BT0650 Homo sapiens cDNA
5063	18060		1.07	4.0E-16	AV730833.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5293	18278	31128	1.1	4.0E-16	P08548	SWISSPROT	AV730833 HTF Homo sapiens cDNA clone HTFAE09 5'
8172	21078	34408	35.21	4.0E-16	AL163284.2	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9835	22741	36122	0.86	4.0E-16	11423191	NT	Homo sapiens chromosome 21 segment HS21C084
11868	24572	38048	1.68	4.0E-16	AV730030.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12447	26200		12.89	4.0E-16	C05947.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
							C05947 Human pancreatic islet Homo sapiens cDNA clone hbc6355

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor:
12457	25206	31851	1.62	4.0E-16	6912459	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
137	13239	26158	1.41	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
137	13239	26159	1.41	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
488	13559		1.2	3.0E-16	AL046446.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
498	13568		2.08	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1471	14502	27463	1.15	3.0E-16	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
3017	16069	28970	4.45	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4008	17035	28926	0.74	3.0E-16	T08169.1	EST_HUMAN	EST06060 Infant Brain, Benta Soares Homo sapiens cDNA clone HIBBA13 5' and
4041	17066		0.65	3.0E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 6
4042	17069		1.07	3.0E-16	U03887.1	NT	Human BXP20 gene
5056	18053	30906	1.12	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLC5A01 3'
5480	18541		0.97	3.0E-16	AA077226.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5811	18883	31982	1.49	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
9216	22144	35498	3.69	3.0E-16	AI002836.1	EST_HUMAN	am58105.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684165 3' similar to contains
10402	23291		0.81	3.0E-16	BF690617.1	EST_HUMAN	THR.D2 THR repetitive element ;
10819	23605	36939	4.38	3.0E-16	L78810.1	NT	602246638F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
13088	25839	31374	2.1	3.0E-16	AL043268.2	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
998	14048		1.44	2.0E-16	AL163279.2	NT	DKFZp434L1623_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L1623 5'
2409	15413		1.01	2.0E-16	AA621761.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
2739	15732		1.15	2.0E-16	J03051.1	NT	af06d04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1090855 3'
4274	17288	30155	1.36	2.0E-16	X89211.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4594	17602	30458	1.32	2.0E-16	AI208733.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
7045	20071	33305	0.9	2.0E-16	Q31125	SWISSPROT	q56003.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.13
8176	21083	34415	0.85	2.0E-16	AI470723.1	EST_HUMAN	MER29 repetitive element ; HISTIDINE-RICH PROTEIN KE4
8545	21476	34818	2.1	2.0E-16	AI732837.1	EST_HUMAN	af16e11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
8736	21656	35011	0.73	2.0E-16	BE858026.1	EST_HUMAN	MER33 repetitive element ;
8736	21666	35012	0.73	2.0E-16	BE858026.1	EST_HUMAN	ncz47608.x5 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O64849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7.11 MER7 repetitive element ;
							782H08.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
							782H08.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9091	22020	35376	0.97	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA
9091	22020	35377	0.97	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-508-a01 PT0034 Homo sapiens cDNA
196	13204	26207	1.57	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
403	13516		26.08	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares fetal_fetus_Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains ORF.12 OFR repetitive element;
1987	15005	27993	3.12	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5923	18990	32109	0.88	1.0E-16	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6703	19739		21.88	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6856	18888	33102	3.03	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7985	19739		6.4	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9823	22729	38111	1.05	1.0E-16	AW875661.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
3802	16833	29719	3.35	9.0E-17	AW900048.1	EST_HUMAN	GM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
7025	20051		1.95	9.0E-17	A1392964.1	EST_HUMAN	tg22e11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109824 3' similar to contains MER28.12 MER28 repetitive element;
8686	21617		3.72	9.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains ORF.12 OFR repetitive element;
10720	23606		2.59	9.0E-17	AF200718.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1045	14089		1.76	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-195-a01 OT0032 Homo sapiens cDNA
3982	16990		0.91	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5775	25632	31951	3.95	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-080300-003-a04 HT0559 Homo sapiens cDNA
7651	20585		1.75	8.0E-17	AV730799.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
8210	21115	34445	0.47	8.0E-17	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnahe11), mRNA
1477	14508		2.48	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5508	18885		3.34	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6984	20011	33243	6.58	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
216	13315	26233	7.16	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6568	19609	32794	2.28	6.0E-17	AW662772.1	EST_HUMAN	h181d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.12 L1 repetitive element;
444	13111	25997	3.31	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
8024	20940	34255	3.01	5.0E-17	T81043.1	EST_HUMAN	yt26b04.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:106327 5'
3703	16735	29625	1.47	4.0E-17	AA643697.1	EST_HUMAN	nt96a05.e1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1068528 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9900	22888	36272	1.15	4.0E-17	AW129165.1	EST_HUMAN	x20e04.x1 NCL_CGAP_K18 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11924	24789	38286	2.06	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12381	25161		2.18	4.0E-17	A073546.1	EST_HUMAN	ov45e04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530
2110	16123	26127	1.14	3.0E-17	AW119123.1	EST_HUMAN	Q16530 PMS3 mRNA; contains MER10.12 MER10 repetitive element;
3237	16285		1.46	3.0E-17	P35410	SWISSPROT	xd89c09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3710	16742	29631	1.43	3.0E-17	BE326522.1	EST_HUMAN	MAR-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3710	16742	29632	1.43	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
8844	21774	35121	1.36	3.0E-17	N68451.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
10224	23115	36516	5.18	3.0E-17	AB028898.1	NT	z114b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292461 3' similar to contains PTR6.13 PTR5 repetitive element;
10868	23754	37180	0.71	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10868	23754	37181	0.71	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
12348	25140		3.48	3.0E-17	11417986	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
373	13460	26375	2.95	2.0E-17	AI270080.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
374	13460	26375	2.08	2.0E-17	AI270080.1	EST_HUMAN	q63a08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element
1015	14085		1.18	2.0E-17	AA722932.1	EST_HUMAN	q63a08.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element
2471	15474	28473	2.23	2.0E-17	Q28983	SWISSPROT	z931d04.s1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2471	15474	28474	2.23	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2972	16024	28924	8.35	2.0E-17	P12036	SWISSPROT	ZONADHESIN PRECURSOR
5551	18629	31506	1.75	2.0E-17	M27685.1	NT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5551	18629	31507	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5516	19580		1.76	2.0E-17	AF055066.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6766	19800		1.57	2.0E-17	AL134881.1	EST_HUMAN	Homo sapiens MHC class 1 region
8356	21281	34595	0.73	2.0E-17	AB037839.1	NT	DKFZp762J0610.1_1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
8662	21593	34932	1.39	2.0E-17	Q95156	SWISSPROT	Homo sapiens mRNA for KIAA1418 protein, partial cds
9025	21854	35312	1.13	2.0E-17	AA300640.1	EST_HUMAN	OLFATORY RECEPTOR-LIKE PROTEIN OLF3
10382	23271	36694	1.95	2.0E-17	BE299888.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10415	23304	36721	3.28	2.0E-17	AL163247.2	NT	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980615 5'
							Homo sapiens chromosome 21 segment HS21C047

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10415	23304	36722	3.28	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10752	23638	37071	5.43	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10867	23753	37178	0.84	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10867	23753	37179	0.84	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10892	23777	37203	0.73	2.0E-17	A1788902.1	EST_HUMAN	w64b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10892	23777	37204	0.73	2.0E-17	A1788902.1	EST_HUMAN	w64b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
774	13831	26764	3.41	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1737	14764		2.2	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1792	14818	27787	4.78	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2128	15141	28144	2.12	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2358	16366	28368	4.28	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3627	16663		1.21	1.0E-17	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4235	17251		9.56	1.0E-17	R09942.1	EST_HUMAN	y30e07.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:128388 5'
5397	18379		1.12	1.0E-17	AA298037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to retrovirus-related pol
6729	19785		0.97	1.0E-17	AW488468.1	EST_HUMAN	he38e05.x1 NCI_CGAP_CvML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element; contains LTR8.11 LTR8 repetitive element;
6946	19975	33197	1.67	1.0E-17	A185642.1	EST_HUMAN	q65b505.x1 Soares_fetal_lung_NHHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6946	19975	33199	1.67	1.0E-17	A185642.1	EST_HUMAN	q65b505.x1 Soares_fetal_lung_NHHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7448	20380	33659	1.21	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9154	22082	36440	1.25	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101299-072-407 BT0263 Homo sapiens cDNA
10511	23388	36810	0.94	1.0E-17	AW996538.1	EST_HUMAN	QV3-BND046-220300-128-c10 BND046 Homo sapiens cDNA
11850	24700	38192	2.05	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
10030	22930		3.62	9.0E-18	A1472167.1	EST_HUMAN	q65d03.x1 Soares_NSF_F8_9W_OT_PA_P_ST Homo sapiens cDNA clone IMAGE:2148389 3'
3852	16881	29766	1.47	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
369	13456	26369	22.74	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
369	13456	26370	22.74	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
7847	20774	34075	1.08	7.0E-18	AW887642.1	EST_HUMAN	RC3-OT0091-170300-011-403 OT0091 Homo sapiens cDNA
12818	13456	26369	6.38	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12818	13456	26370	6.38	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3338	16384	26283	1.27	6.0E-18	X71791.2	NT	RIBOSOMAL PROTEIN L4 (HUMAN); Rattus norvegicus partial Gdn/Ph-1 gene for glia-derived nexin/protease nexin I, enhancer region
4860	17862		4.52	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8825	21755		2.35	6.0E-18	11428165	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8922	21852	35207	0.77	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8835	22561	35930	0.59	6.0E-18	AI808256.1	EST_HUMAN	RC-BT168-020489-014 BT168 Homo sapiens cDNA
8835	22561	35931	0.59	6.0E-18	AI808256.1	EST_HUMAN	RC-BT168-020489-014 BT168 Homo sapiens cDNA
11772	24072	38160	1.99	6.0E-18	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12579	25281	31840	2.74	6.0E-18	U87928.1	NT	Human aconitase hydratase (ACO2) gene, exon 4
1175	14215	27154	15.33	5.0E-18	AI280214.1	EST_HUMAN	qm85g11.x1 Soares_placenta_8to6weeks_2NBHP8b9W Homo sapiens cDNA clone IMAGE:1893688 3' similar to contains Alu repetitive element
5455	18538	31378	1.08	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
9279	22207	35564	6.21	5.0E-18	BE143312.1	EST_HUMAN	MIR0-H10161-221089-002-c06 HT0161 Homo sapiens cDNA
11416	24332	37780	3.86	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11416	24332	37781	3.86	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12701	25356		11.85	5.0E-18	AW867182.1	EST_HUMAN	MIR1-SN0035-060400-001-gt11 SN0035 Homo sapiens cDNA
13006	25556		36.99	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLC00A02 3'
129	13233	26149	1.4	4.0E-18	BE044076.1	EST_HUMAN	hc06h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element
129	13233	26150	1.4	4.0E-18	BE044076.1	EST_HUMAN	hc06h04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element
1745	14772	27742	9.56	4.0E-18	AA821814.1	EST_HUMAN	nc24f11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
2216	15227	28231	1.09	4.0E-18	Q08430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2216	15227	28232	1.09	4.0E-18	Q08430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N- ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
5548	18626	31501	2.33	4.0E-18	AI017555.1	EST_HUMAN	ol23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5548	18626	31502	2.33	4.0E-18	AI017555.1	EST_HUMAN	ol23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8428	21380		0.79	4.0E-18	AA748811.1	EST_HUMAN	rx64a08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1286998 similar to contains L1.t2 L1 repetitive element ;
11443	24359	37808	0.22	4.0E-18	AA971807.1	EST_HUMAN	EST183633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
874	13927	26875	6.61	3.0E-18	AA814198.1	EST_HUMAN	cb23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
958	14008	26863	3.14	3.0E-18	BE088634.1	EST_HUMAN	P48792 40S RIBOSOMAL PROTEIN S5 ;
4030	17057	28946	1.2	3.0E-18	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7142	20250	33502	4.81	3.0E-18	BE001671.1	EST_HUMAN	PMO-BNC081-100300-001-508 BNC081 Homo sapiens cDNA
11364	24282	37725	1.52	3.0E-18	BF218650.1	EST_HUMAN	601884866F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5'
12822	25441		7.17	3.0E-18	AW022015.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
270	13365	26281	2.52	2.0E-18	AW836820.1	EST_HUMAN	QY1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
1180	14220		63.41	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
3168	16218	28108	1.39	2.0E-18	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN FLAGELLAR OUTER ARM
6596	18872		4.98	2.0E-18	AA868610.1	EST_HUMAN	af63a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577 O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ;
5998	18769	31694	3.12	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5996	18769	31695	3.12	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
6093	19164		1.94	2.0E-18	BF347228.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
6406	19454	32826	1.02	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6406	19454	32627	1.02	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6530	19574	32756	0.86	2.0E-18	BF352940.1	EST_HUMAN	IL3-HT0019-220700-222-C12 HT0019 Homo sapiens cDNA
6573	19614	32800	3.18	2.0E-18	AW66853.1	EST_HUMAN	h04g01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.t2 MER19 repetitive element ;
7840	20768	34071	0.61	2.0E-18	AA457619.1	EST_HUMAN	aa58d11.1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:836485 5' similar to TR:G61634 G61634 POLYPEPTIDE PR77 ;
8726	21856	35002	0.54	2.0E-18	BE439524.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA
10550	23436	36856	1.34	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823146 3' similar to contains MER10.t2 MER10 repetitive element ;
10550	23436	36857	1.34	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823146 3' similar to contains MER10.t2 MER10 repetitive element ;
11412	24328	37777	2.3	2.0E-18	AW470791.1	EST_HUMAN	hs33d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12154	24893	38492	3.93	2.0E-18	AW151299.1	EST_HUMAN	xg47e08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
12517	14220		8.71	2.0E-18	BE256097.1	EST_HUMAN	MER8 repetitive element ; 60114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4523	17532		0.98	1.0E-18	T95406.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ;
5540	18619	31470	2.61	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCCKE11 3'
5762	18835	31938	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5762	18835	31939	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6725	18761	32968	1.24	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9010	21839	35295	1.23	1.0E-18	AI148288.1	EST_HUMAN	oz68d09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.L1 repetitive element ;
10411	23300	36718	3.07	1.0E-18	U81328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12475	25220	31856	6.48	1.0E-18	AF003529.1	NT	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
567	13636	26547	3.3	9.0E-19	AA281961.1	EST_HUMAN	z111d06.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2
588	13636	26547	3.05	9.0E-19	AA281961.1	EST_HUMAN	MER19 repetitive element ;
8431	21363		4.15	9.0E-19	F08698.1	EST_HUMAN	z111d06.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2
9246	22174	35528	2.86	9.0E-19	AL163203.2	NT	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
9246	22174	35529	2.86	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11567	24476	37943	4.48	9.0E-19	AB032969.1	NT	Homo sapiens chromosome 21 segment HS21C003
12258	13636	26547	17.41	9.0E-19	AA281961.1	EST_HUMAN	Homo sapiens mRNA for KIAA1143 protein, partial cds
1074	14118		1.17	8.0E-19	AW974902.1	EST_HUMAN	z111d06.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2
8727	21657	35003	1.17	8.0E-19	BE158838.1	EST_HUMAN	MER19 repetitive element ;
							EST387007 IMAGE resequencing, MAGN Homo sapiens cDNA
							MRO-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA
2280	19270	28276	1.48	7.0E-19	4758139	NT	Homo sapiens DEAD/HD (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
6727	19763	32970	2.23	7.0E-19	AF092090.1	NT	Rattus norvegicus cpi151 mRNA, partial cds
7681	20615	33914	0.96	7.0E-19	P28444	SWISSPROT	BETA CRYSTALLIN A2
12388	25952		1.49	7.0E-19	AA705684.1	EST_HUMAN	z66b01.s1 Soares fetal liver spleen_1N1LS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3846	18875		1.12	6.0E-19	AW852930.1	EST_HUMAN	PMO-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4574	17582	30444	1.41	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4574	17582	30445	1.41	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M60)
4915	17914		1.28	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5157	18150	30998	0.92	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762F192.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192.5'
6072	19133	32287	6.33	5.0E-19	Q00183	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
8461	19506	32881	1.46	5.0E-19	AW653302.1	EST_HUMAN	hht7b06.y1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2968787.5'
8392	26988		0.83	5.0E-19	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10907	23792	37221	0.76	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11988	24811	38306	2.4	5.0E-19	AW183725.1	EST_HUMAN	X87b02.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2864171.3' similar to contains element MSR1 repetitive element;
13018	25721		1.44	5.0E-19	U68060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
576	13644	26551	1.08	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0501
2731	15724	28720	1.29	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674.5'
5581	18658	31535	1.19	4.0E-19	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3919	16947	29828	1.07	3.0E-19	Q28697	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3919	16947	29829	1.07	3.0E-19	Q28697	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4557	17566	30424	1.53	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11.5'
5462	18543		0.73	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7779	20708		2.01	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC83222), mRNA
9991	21349	34683	1.14	3.0E-19	X89685.1	NT	M.musculus mRNA for TPCR33 protein
12604	25300		15.12	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
2595	15593	28588	27.87	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4555	17564		1.55	2.0E-19	AI311783.1	EST_HUMAN	qc91e02.x1 NCL CGAP_Kids Homo sapiens cDNA clone IMAGE:1915898.3' similar to TR:Q69386 Q69386 POLIENV GENE
6289	19340	32508	0.62	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HITF Homo sapiens cDNA clone HITFAZ016.5'
7724	20656	33953	0.6	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8905	21835	35191	10.07	2.0E-19	AA012854.1	EST_HUMAN	ze34c09.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:380880.5'
10420	23309	36730	0.76	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLIF2
504	13575		1.98	1.0E-19	BE408611.1	EST_HUMAN	601304126F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310.5'

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2177	15189	28195	1.8	1.0E-19	H30795.1	EST_HUMAN	y97g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2768	15758		3.37	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2892	15946		7	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3461	16501	29403	1.2	1.0E-19	AA834967.1	EST_HUMAN	449b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 MER37 repetitive element;
5520	18559	31448	0.63	1.0E-19	AI890866.1	EST_HUMAN	vm91b08.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16630 Q16630 PMS3 MRNA;
6311	19361	32531	5.05	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6452	25977		0.67	1.0E-19	AA595527.1	EST_HUMAN	nr22403.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:953093 similar to contains L1.1 L1 repetitive element;
8076	20989	34306	0.88	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
8078	20989	34307	0.88	1.0E-19	U08813.1	NT	Oryctolagus cuniculus Na ⁺ /glucose cotransporter-related protein mRNA, complete cds
8284	25886		0.57	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
9018	21947	35303	1.84	1.0E-19	M64657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
9300	22228		2.52	1.0E-19	T89920.1	EST_HUMAN	y972b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element;
10269	23159		0.67	1.0E-19	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10684	23570	37000	44.92	1.0E-19	AW812259.1	EST_HUMAN	RC0-ST0174-1B1099-031-505 ST0174 Homo sapiens cDNA
10693	23579	37009	1.67	1.0E-19	N44631.1	EST_HUMAN	y91e09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272872 5'
12173	25009	38513	1.42	1.0E-19	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
6638	19867	33189	2.31	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6938	19987	33190	2.31	8.0E-20	7657288	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7941	20863	34172	1.43	8.0E-20	A1221371.1	EST_HUMAN	q96009.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7941	20863	34173	1.43	8.0E-20	A1221371.1	EST_HUMAN	q96009.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3320	16356	29288	0.7	7.0E-20	BF328455.1	EST_HUMAN	PM4-AN0036-050900-003-a04 AN0088 Homo sapiens cDNA
7336	18504	31279	5.51	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D092 5'
8314	21219	34555	0.42	7.0E-20	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
9063	21992	35345	9.3	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
9063	21992	35346	9.3	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
12139	24976		4.6	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3819	16652	29553	4.09	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4371	17386	30249	4.76	6.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4706	17711		1.6	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTC8TA01 6'
7474	20414	33692	1.63	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8524	21455	34797	5.82	5.0E-20	W90525.1	EST_HUMAN	z178408.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element ;
8524	21456	34798	5.82	5.0E-20	W90525.1	EST_HUMAN	z178408.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element ;
8892	21613	34955	1	5.0E-20	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9393	22321	35684	1.72	5.0E-20	AB028174.1	NT	Mus musculus MIMAN-g mRNA, complete cds
9393	22321	35685	1.72	5.0E-20	AB028174.1	NT	Mus musculus MIMAN-g mRNA, complete cds
9978	21336		1.13	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
1643	14674	27639	1.55	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5845	18916		0.86	4.0E-20	Q99880	SWISSPROT	HISTONE H2B C (H2B/C)
8504	21435		4.77	4.0E-20	A1874352.1	EST_HUMAN	t684903.x1 NCL_CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2293398 3'
10977	23851	37289	1.49	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
2153	15165	28167	0.99	3.0E-20	U03888.1	NT	Human BXP21 gene
4305	17319	30186	1.18	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 174
4738	17743	30604	0.92	3.0E-20	AA037616.1	EST_HUMAN	z36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1 L3 L1 repetitive element ;
9490	22418		2.55	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10810	23696	37122	1	3.0E-20	BF185284.1	EST_HUMAN	601843551F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5'
11107	24038		1.88	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12401	25173	31875	6.68	3.0E-20	BE883422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
855	13909		10.52	2.0E-20	AW303868.1	EST_HUMAN	x24e10.x1 NCL_CGAP_L14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
1138	14160	27117	2.23	2.0E-20	AA516335.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5 ;
1138	14160	27118	2.23	2.0E-20	AA516335.1	EST_HUMAN	ng69109.s1 NCL_CGAP_L12 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN ;
2864	13909		4.88	2.0E-20	AW303868.1	EST_HUMAN	ng69109.s1 NCL_CGAP_L12 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN ;
5060	18057	30909	5.5	2.0E-20	Q28983	SWISSPROT	x24e10.x1 NCL_CGAP_L14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
							P97461 40S RIBOSOMAL PROTEIN S5 ;
							ZONADHESIN PRECURSOR

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5060	18057	30910	5.5	2.0E-20	Q28983	SWISSPROT	ZONADIESIN PRECURSOR
8695	21626	34970	0.97	2.0E-20	AA309457.1	EST_HUMAN	EST180328 Liver III Homo sapiens cDNA 5' end
9732	22657	36040	1.52	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
9732	22657	36041	1.52	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12759	25707	31663	2.23	2.0E-20	H56371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
2026	15855	28038	4.78	1.0E-20	AA281981.1	EST_HUMAN	z111408.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
4548	17557	30417	1.75	1.0E-20	BF115158.1	EST_HUMAN	h164006.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
7222	20221	33469	0.77	1.0E-20	AF049867.1	EST_HUMAN	repetitive element;
9706	22631	36010	2.38	1.0E-20	11418491	NT	AF049867 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
11085	24828	38325	2.7	1.0E-20	AF223391.1	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCPC), mRNA
12513	25246		5.37	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2955	19007		1.32	9.0E-21	AJ003514.1	EST_HUMAN	rc60908.r1 NCL CGAP_Prl Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1
12261	25079		3.64	9.0E-21	AW898189.1	EST_HUMAN	repetitive element;
9370	22298		1.32	8.0E-21	AW674891.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPI112-3J21
11969	24812	36307	5.11	8.0E-21	AA809411.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
12414	25183		6.13	8.0E-21	O21330	SWISSPROT	b630a02.v1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN
2082	15096	28094	1.36	7.0E-21	P18600	SWISSPROT	O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
2082	15096	28095	1.36	7.0E-21	P18600	SWISSPROT	cb71f06.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
3766	16798	29686	0.68	7.0E-21	AL163300.2	NT	ATP SYNTHASE A CHAIN (PROTEIN 6)
4353	17367		6.58	7.0E-21	AA046502.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
6702	19738	32940	1.03	7.0E-21	AL163218.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
8959	21889	35247	1.67	7.0E-21	AJ277557.1	NT	Homo sapiens chromosome 21 segment HS21C100
9234	22162	35518	8.52	7.0E-21	D14718.1	NT	z67a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
10614	25600	36933	1.04	7.0E-21	AW856922.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
11138	24067	37512	1.91	7.0E-21	AA723404.1	EST_HUMAN	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
11713	24615	38091	1.91	7.0E-21	7706668	NT	Human chromosomal protein HMGT related gene
							RC0-C10301-271199-031-F03 C10301 Homo sapiens cDNA
							zg73d03.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to
							gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR.13 OFR
							repetitive element;
							Homo sapiens PTD013 protein (PTD013), mRNA

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4195	17215	30081	0.75	6.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9679	22605		0.89	6.0E-21	BE162737.1	EST_HUMAN	PM1-H10454-080100-002-H09 HT0454 Homo sapiens cDNA
952	14002	26947	1	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
2299	15307	28313	0.98	5.0E-21	AA928194.1	EST_HUMAN	om23g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541908 3' similar to TR:002711
4470	17481	30340	3.73	5.0E-21	BE568839.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN;
4789	14002	26947	0.75	5.0E-21	5902031	NT	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4917	17816	30782	5.93	5.0E-21	4885474	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
7068	20274		0.88	5.0E-21	AW440864.1	EST_HUMAN	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
7362	20357	33626	0.97	5.0E-21	BE859505.1	EST_HUMAN	he05e10.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918154 3'
12338	25133		1.74	5.0E-21	AA393574.1	EST_HUMAN	763d11.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303579 3' similar to contains OFR.11
1763	14789	27759	2.09	4.0E-21	AA907013.1	EST_HUMAN	OFR repetitive element;
7197	20197	33443	2.34	4.0E-21	AB019576.1	NT	z172c04.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
							oo86c03.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530
10289	23189	36600	0.66	4.0E-21	U91328.1	NT	PMS3 mRNA ;contains OFR.11 OFR repetitive element;
1861	14883	27863	1.11	3.0E-21	AA218891.1	EST_HUMAN	Raf1us norvegicus mRNA for r1TM, complete cds
2293	15301	28307	1.58	3.0E-21	AL163201.2	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3129	16179	29073	4.01	3.0E-21	AJ007973.1	NT	zq15d06.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:6297771 3'
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens LGMD2B gene
5889	18762	31686	0.86	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5889	18762	31687	0.86	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5941	19008		0.89	3.0E-21	AV661044.1	EST_HUMAN	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
6420	19467		28.39	3.0E-21	BF184799.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLCGOAT0 3'
7423	20122	33359	6.84	3.0E-21	BF361093.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
10215	23109	36506	1.28	3.0E-21	AW897760.1	EST_HUMAN	RC1-OT0093-100800-019-g08 OT0093 Homo sapiens cDNA
12859	25882	31478	3.03	3.0E-21	AL163213.2	NT	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
166	13265		12.2	2.0E-21	BE163247.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
1242	14278		1.69	2.0E-21	BE084410.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
2885	15679	28678	2.58	2.0E-21	Q28983	SWISSPROT	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2885	15679	28679	2.58	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4979	17977		1.08	2.0E-21	AW151673.1	EST_HUMAN	x87e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
5672	18748	31657	2.04	2.0E-21	A1624592.1	EST_HUMAN	MER10 repetitive element ;
5768	18841	31942	0.67	2.0E-21	AA027211.1	EST_HUMAN	ts30f03.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5768	18841	31943	0.67	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
6266	19317	32482	0.59	2.0E-21	W44493.1	EST_HUMAN	ze97a12.1 Scarses fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8848	21778	35125	0.61	2.0E-21	AJ010770.1	NT	ze97a12.1 Scarses fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8935	21865	35223	7.76	2.0E-21	BE141785.1	EST_HUMAN	ze28h02.1 Scarses senescent fibroblasts NbHSF Homo sapiens cDNA clone IMAGE:323687 5'
9362	22310	35671	3.96	2.0E-21	AU136779.1	EST_HUMAN	Homo sapiens hyperion gene, exons 1-50
11498	24409		1.64	2.0E-21	BE350127.1	EST_HUMAN	QVC-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
11763	24664	38149	1.4	2.0E-21	BE973829.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005082 5'
11763	24664	38150	1.4	2.0E-21	BE973829.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12612	25304		7.32	2.0E-21	AF176815.1	NT	MER29 repetitive element ;
1283	14316	27265	1.25	1.0E-21	AA557667.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1428	14459		2.24	1.0E-21	A1601284.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
5176	18167	31012	0.67	1.0E-21	O76013	SWISSPROT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
5276	18262		0.91	1.0E-21	AF224693.1	NT	nl46c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
6762	19796		2.57	1.0E-21	AL079752.1	EST_HUMAN	MER29 repetitive element ;
7556	20493	33783	4.73	1.0E-21	A1223104.1	EST_HUMAN	ar68d12.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
11057	23941		1.57	1.0E-21	6730038	NT	KERATIN, TYPE I CUTICULAR HA6 (HAIR KERATIN, TYPE I HA6)
12973	25535		1.46	1.0E-21	AF046133.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4517	17626	30392	1.89	9.0E-22	A1702438.1	EST_HUMAN	DKFZp434D830.j1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D830 5'
11231	24157	37608	3.17	9.0E-22	A1761874.1	EST_HUMAN	qq47e05.x1 Scarses testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM
976	14027		5.48	8.0E-22	BE144748.1	EST_HUMAN	PROTEIN (HUMAN);
6676	19713	32907	0.5	8.0E-22	BF373321.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6876	19713	32908	0.5	8.0E-22	BF373321.1	EST_HUMAN	Homo sapiens chromosome Xp22 410-8
8476	21407		3.46	8.0E-22	AA046502.1	EST_HUMAN	tz94a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286204 3' similar to TR:Q15408 Q15408
688	13749	26664	6.19	7.0E-22	AL163246.2	NT	NEUTRAL PROTEINASE LARGE SUBUNIT ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4381	17395	30260	3.42	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
9248	22176		1.38	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9390	22318	35680	2.29	7.0E-22	M78560.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#636208) Homo sapiens cDNA clone HFBCF07
10129	23020	36415	2.86	7.0E-22	AF009860.1	NT	Homo sapiens T cell receptor beta locus, TORBV753A2 to TORBV12S2 region
4146	17167	30041	1.02	6.0E-22	AA405040.1	EST_HUMAN	z165d10.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742867 5'
8818	21748		2.19	6.0E-22	AW029123.1	EST_HUMAN	wz05g07.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2542812 3'
6795	19828	33038	4	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10808	23694	37121	6.02	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12824	25443		2.77	5.0E-22	BF476511.1	EST_HUMAN	nee27b05.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255888 3' similar to contains Alu repetitive element
3704	19736		1.17	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8984	25989		2.42	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11165	24093	37541	2.39	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085434 5'
12979	25539		3.07	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
985	14036		1.2	3.0E-22	A1469679.1	EST_HUMAN	tm1410.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:U19563 HIGH AFFINITY INTERLEUKIN-3 RECEPTOR B (HUMAN); contains L1.11 L1 repetitive element
2605	15603	28597	1.11	3.0E-22	A1859038.1	EST_HUMAN	w158b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21.;
3740	16772		1.6	3.0E-22	D14718.1	NT	Human chromosomal protein HM/G1 related gene
4910	17915	30781	9.05	3.0E-22	A1090125.1	EST_HUMAN	qb2b07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697560 3' similar to contains MER12.12 MER12 repetitive element
8808	21738		1.04	3.0E-22	BE156613.1	EST_HUMAN	QV0-HT0368-090200-099-f12 HT0368 Homo sapiens cDNA
8813	21743	35091	2.29	3.0E-22	BE089841.1	EST_HUMAN	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8932	21862	35217	1.17	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
8932	21862	35218	1.17	3.0E-22	X60660.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
1987	14985		3.78	2.0E-22	N24942.1	EST_HUMAN	R.rattus RY2G5 mRNA for a potential ligand-binding protein
2550	15556	28548	1.78	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3481	16521	29420	5.75	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKA G3), mRNA
4325	17339	30204	1.49	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-261199-007-412 ST0262 Homo sapiens cDNA
6065	25638	32257	1.42	2.0E-22	W39456.1	EST_HUMAN	zad001.1 Soares_gonocent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322879 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6418	19465	32639	3.65	2.0E-22	BF092116.1	EST_HUMAN	RC0-TN0078-150900-025-H12 TN0078 Homo sapiens cDNA
10225	23116	36517	1.14	2.0E-22	A1276522.1	EST_HUMAN	q17h06.x1 Soares_NHT-MPp_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains MER28.13 MER28 repetitive element

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10313	23202	36811	0.88	2.0E-22	AA716315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
10313	23202	36812	0.88	2.0E-22	AA716316.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
12174	26010	39514	2	2.0E-22	AW418980.1	EST_HUMAN	he24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
12232	25526	31746	2.75	2.0E-22	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1901	14922	27902	3.28	1.0E-22	AW865517.1	EST_HUMAN	PM4-SN020-010400-009-102 SN020 Homo sapiens cDNA
2621	15619	28612	2.77	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (S-TM2) gene, complete cds
3471	16511	29412	1.55	1.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
8206	21112	34443	1.65	1.0E-22	BE084687.1	EST_HUMAN	MRO-BT0659-220200-002-107 BT0659 Homo sapiens cDNA
11030	23914	37356	1.09	1.0E-22	AI365435.1	EST_HUMAN	qz08b07.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
11030	23914	37357	1.09	1.0E-22	AI365435.1	EST_HUMAN	MER29 repetitive element;
13016	26562		10.07	9.0E-23	AW802801.1	EST_HUMAN	qz08b07.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
3631	16667	29584	0.87	8.0E-23	AF198349.1	NT	MER29 repetitive element;
3356	16400		2	7.0E-23	AV647246.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
11476	24390	37839	4.28	7.0E-23	5031852	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3495	16534		1.88	6.0E-23	AF198333.1	NT	AV647246 GLC Homo sapiens cDNA clone GLCAW007 3'
4367	17381	30245	0.91	5.0E-23	AL163249.2	NT	Homo sapiens Not56 (D. melanogaster)-like protein (NOT56L) mRNA
							Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
							Homo sapiens chromosome 21 segment HS21C049
							qz58c03.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to
12535	25258	31832	4.89	6.0E-23	AI209130.1	EST_HUMAN	SW.MV10_MOUSE_P23249 PROTEIN MOV-10. ;
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
5629	18705	31604	3.35	5.0E-23	U82871.2	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6487	26849	32710	4.17	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7841	25849	32710	3.31	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6708	18744	32946	0.86	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6708	18744	32947	0.86	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8421	21363	34691	3.67	3.0E-23	AA130165.1	EST_HUMAN	z35g09.r1 Soares, pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:5039688 5' similar to contains MER29.12 MER29 repetitive element ;
9791	22765	36138	3.55	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9791	22765	36139	3.55	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10806	23692		2.67	3.0E-23	AW897927.1	EST_HUMAN	RC3-NN0066-270400-011-H01 NN0066 Homo sapiens cDNA
689	13760	26665	3.22	2.0E-23	AI288880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1FL1 gene
1170	15848		3.25	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2843	15832	28828	1.46	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2843	15832	28828	1.46	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3429	16470		1.19	2.0E-23	A1201488.1	EST_HUMAN	qp/3111.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3780	16811		6.02	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
4061	17087	28971	3.88	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4061	17087	28972	3.88	2.0E-23	H59931.1	EST_HUMAN	y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
							y16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
8453	21385		7.43	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
9402	22330	35692	1.35	2.0E-23	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12345	25138		5.2	2.0E-23	M32658.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12832	25448		2.72	2.0E-23	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
12946	25895		1.53	2.0E-23	AU133931.1	EST_HUMAN	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4879	17878		5.48	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7021	20047		3.5	1.0E-23	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608663 5'
8929	21859	35214	4.78	1.0E-23	AA448097.1	EST_HUMAN	z402c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:762898 5' similar to contains PTR5.12
11116	24046	37492	1.55	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
11116	24046	37493	1.55	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
							ab75a08.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852798 3' similar to
574	13842		1.94	9.0E-24	AA663213.1	EST_HUMAN	TR-E19822 E19822 CA PROTEIN. ;
4758	17763	30625	1.43	8.0E-24	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
4758	17763	30626	1.43	8.0E-24	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
6719	19755	32861	1.1	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
8393	21296	34627	0.47	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3941	16969		1.03	7.0E-24	AW937954.1	EST_HUMAN	QV0-DT0047-170200-122-a08 DT0047 Homo sapiens cDNA
5317	18301		2.6	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A2311 5'
729	13787		1.96	6.0E-24	AB001421.1	NT	Macaca fasciata mRNA for Testis-Specific Protein Y (TSPY), complete cds
863	13917	26861	9.62	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
4442	17453	30312	0.73	6.0E-24	P21440	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 2 (P-GLYCOPROTEIN 2)
4054	17081	28967	11.38	5.0E-24	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8225	21130	34461	0.88	5.0E-24	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6154	19212	32352	3.15	4.0E-24	AA594178.1	EST_HUMAN	nm31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVRK
9239	22167	35520	1.09	4.0E-24	AW813711.1	EST_HUMAN	P31785 POL POLYPROTEIN ;
11623	24530	37999	2.08	4.0E-24	BE54822.1	EST_HUMAN	RC3-ST0197-130100-014-08 ST0197 Homo sapiens cDNA
12694	25351	31828	4.93	4.0E-24	AB029016.1	NT	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:348498 5'
12849	25706	31682	1.6	4.0E-24	M20707.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
7439	20181	33424	0.77	3.0E-24	U66061.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
7439	20181	33425	0.77	3.0E-24	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
8993	21922		2.99	3.0E-24	AW614871.1	EST_HUMAN	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
9048	21977		0.64	3.0E-24	AW962076.1	EST_HUMAN	h168c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2367950 3' similar to contains MER29.b2
9998	22815	36204	4.73	3.0E-24	AL163282.2	NT	MER29 repetitive element ;
12769	25398	31809	3.49	3.0E-24	BF127762.1	EST_HUMAN	EST374149 IMAGE resequences, MAGG Homo sapiens cDNA
2369	15375	28377	2.69	2.0E-24	AA167539.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C032
3863	16892		0.81	2.0E-24	AW698189.1	EST_HUMAN	601810440F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053398 5'
7750	25983		0.58	2.0E-24	AL163206.2	NT	zp11f09.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
7894	20820	34126	0.95	2.0E-24	AF086824.1	NT	RC3-NN0088-090500-021-b03 NN0088 Homo sapiens cDNA
7899	20825	34129	0.54	2.0E-24	AJ003538.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
9299	22227	35598	4.11	2.0E-24	AL119198.1	EST_HUMAN	Mus musculus rho/rae-interacting citron kinase (Crik) mRNA, complete cds
9337	22266		0.92	2.0E-24	H69214.1	EST_HUMAN	Mus musculus Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPI12-5H13
10388	23257	36678	1.22	2.0E-24	AI521759.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
10388	23257	36679	1.22	2.0E-24	AI521759.1	EST_HUMAN	ye2b09.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:212728 5' similar to contains
12621	25923		14.01	2.0E-24	M28877.1	NT	MER28 repetitive element ;
1722	14750	27718	2	1.0E-24	7708340	NT	Human O family dispersed repeat element
2722	15715		2.54	1.0E-24	AW820194.1	EST_HUMAN	Homo sapiens OGI-127 protein (LOC51046), mRNA
3086	16118	29019	0.81	1.0E-24	D86423.1	NT	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
							Mus musculus mRNA for HGT keratin, partial cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4369	17383		2.52	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
6666	19704	32868	1.03	1.0E-24	7106336	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
7979	20900	34215	5.06	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8193	21100	34430	0.8	1.0E-24	BE144528.1	EST_HUMAN	MRO-HT0166-271199-005-409 HT0166 Homo sapiens cDNA
8523	21454	34796	3.02	1.0E-24	AW901164.1	EST_HUMAN	OMD-NN1010-130300-281-407 NN1010 Homo sapiens cDNA
12121	24962	38465	1.87	9.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5117	18114	30958	5	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element;
8797	21727	35076	7.33	7.0E-25	AA486646.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
12124	24955	38470	3.08	7.0E-25	AA583540.1	EST_HUMAN	nt25h08.s1 NCI_CGAP_Fr1 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST
7332	18600		4.99	6.0E-25	W87623.1	EST_HUMAN	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA ;
8183	21090	34422	11.36	6.0E-25	7306380	NT	zh65h07.r1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416889 5'
1678	14708	27671	1.99	5.0E-25	AW850271.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
11761	24692	38147	2.97	5.0E-25	AW978707.1	EST_HUMAN	IL3-CT0219-161199-031-D04 CT0219 Homo sapiens cDNA
1466	14497	27458	2.85	4.0E-25	T98107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
3462	16502		3.81	4.0E-25	AW887671.1	EST_HUMAN	ye56h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3977	17005	28893	1.52	4.0E-25	AF000388.1	NT	PM3-OT0083-280200-001-g07 OT0083 Homo sapiens cDNA
4421	17432		4.88	4.0E-25	BE170957.1	EST_HUMAN	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
10449	23338	36755	0.62	4.0E-25	AA383873.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
3365	16409	29310	4.59	3.0E-25	8923321	NT	EST87317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat
3365	16409	29311	4.59	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5002	18001	30858	0.83	3.0E-25	P29622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
6374	18366	31198	1	3.0E-25	H52187.1	EST_HUMAN	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
5991	19098	32183	0.48	3.0E-25	U53212.1	NT	ye06b11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208661 5' similar to contains MER8 repetitive element ;
6902	19932	33150	0.58	3.0E-25	AA603690.1	EST_HUMAN	Human degenerate channel MDEG mRNA, partial cds
8912	21842	35195	4.08	3.0E-25	AL16210.2	NT	np27b02.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb.M61866 ZINC FINGER PROTEIN 85 (HUMAN);
11473	24386	37836	2.04	3.0E-25	AA579013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1376	14408	27362	2.4	2.0E-25	5032158	NT	nt30h10.s1 NCI_CGAP_Fr1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.L1 L1 repetitive element ;
2329	15337	26341	7.65	2.0E-25	BE888016.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA 601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2878	15572	28599	3.22	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4286	17300	30167	1.93	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4286	17300	30168	1.93	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
10285	23175	36587	1.69	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
385	13489	26387	0.83	1.0E-25	AL040228.1	EST_HUMAN	DKFZp434H0313_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1276	14310		2.3	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
4969	17897	30826	2.68	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
6848	19890		0.99	1.0E-25	AA189080.1	EST_HUMAN	zq45b06.s1 Stratiogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element
7108	25697	33574	2.81	1.0E-25	AA582690.1	EST_HUMAN	rm54h11.s1 NCJ CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
8144	21053	34385	0.49	1.0E-25	Q0JL58	SWISSPROT	ZINC FINGER PROTEIN 215 (BWSR2 ASSOCIATED ZINC-FINGER PROTEIN BAZ2)
8493	21424	34764	6	1.0E-25	AA709079.1	EST_HUMAN	z06g04.s1 Soares Fetal heart_NH119W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element;
10075	22950	36385	6.69	1.0E-25	X60660.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
10075	22950	36386	6.69	1.0E-25	X60660.1	NT	R. rattus RY2G5 mRNA for a potential ligand-binding protein
11408	24324	37774	3.18	1.0E-25	U83193.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12358	25147	38170	1.65	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12358	25147	38171	1.65	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2505	15508	28508	1.67	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
12233	25725		1.52	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5892	18981		2.09	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1599	14630	27589	3.97	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anthratic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4065	17091	28976	1.29	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4256	17272	30138	1.96	7.0E-26	AW340153.1	EST_HUMAN	hd02a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808368 3'
5834	18905	32020	1.05	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
12094	24635		8.16	7.0E-26	AA115895.1	EST_HUMAN	zn30408.r1 Stratiogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12874	25474		10.79	7.0E-26	AW954559.1	EST_HUMAN	EST368629 MAGE resequences, MAGC Homo sapiens cDNA
2238	15248	28255	3.72	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3395	18437	29341	1.1	6.0E-26	AA206131.1	EST_HUMAN	zq52h04.r1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
12108	24949	38452	2.01	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1205	14244	27185	2.37	5.0E-26	AI708235.1	EST_HUMAN	es38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;
1205	14244	27188	2.37	5.0E-26	AI708235.1	EST_HUMAN	es38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;
9946	22851		2.84	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
11103	24034	37479	3.09	4.0E-26	BE266187.1	EST_HUMAN	60T1191345F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3535210 5'
1783	14809	27777	1.27	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2019	15037	28031	0.97	3.0E-26	AL045855.2	EST_HUMAN	DKFZp434I086.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I086 5'
2045	15062		10.66	3.0E-26	AA115895.1	EST_HUMAN	zn30408.11 Stratagene neurospithellum NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3846	16874	28757	1.75	3.0E-26	AA152464.1	EST_HUMAN	zn30T10.11 Stratagene colon (9637204) Homo sapiens cDNA clone IMAGE:388427 5' similar to TR:G685374
3845	16874	28758	1.75	3.0E-26	AA152464.1	EST_HUMAN	zn30T10.11 Stratagene colon (9637204) Homo sapiens cDNA clone IMAGE:388427 5' similar to TR:G685374
7239	20148	33388	11.15	3.0E-26	BF245458.1	EST_HUMAN	G685374 THYROID RECEPTOR INTERACTOR ;
12000	24842	38338	2.25	3.0E-26	AW875651.1	EST_HUMAN	G685374 THYROID RECEPTOR INTERACTOR ;
12000	24842	38339	2.25	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-605 PT0012 Homo sapiens cDNA
12032	24874	38379	6.6	3.0E-26	AA688173.1	EST_HUMAN	nr37406.st NCL_CGAP_GCS Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1
12225	25059	38557	1.59	3.0E-26	AF228925.1	NT	OFR repetitive element ;
13037	25574		1.62	3.0E-26	AW073434.1	EST_HUMAN	Mus musculus harmanin isoform b3 (Ush1c) mRNA, complete cds, alternatively spliced
705	13784	26681	4.64	2.0E-26	AL163282.2	NT	xe57b09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2570873 3' similar to contains MER30.11
1891	14912		3.43	2.0E-26	AL038088.2	EST_HUMAN	Home sapiens chromosome 21 segment HS21C082
3278	16326	28232	6.59	2.0E-26	X86694.1	NT	DKFZp668L171.st 568 (synonym: hfxd2) Homo sapiens cDNA clone DKFZp668L171 3'
11194	24120		2.8	2.0E-26	D87675.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
11666	24571	38047	2.9	2.0E-26	AI801412.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
11851	24701		2.02	2.0E-26	AF055066.1	NT	to89a01.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185418 3' similar to contains Alu
12454	25204		2.34	2.0E-26	AB037859.1	NT	repetitive element; contains element MER20 MER20 repetitive element ;
12640	25876	31475	2.85	2.0E-26	11435947	NT	Homo sapiens MHC class 1 region
141	13243	26161	8.54	1.0E-26	BE170371.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2061	15077	28077	1.62	1.0E-26	AL039363.2	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2598	15596	28591	1.04	1.0E-26	BE814895.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
							QV4-H10538-020300-125-402 HT0558 Homo sapiens cDNA
							DKFZp434H1910.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
							MR2-BIN0114-240600-030-g07 BIN0114 Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2736	15729		5.44	1.0E-26	AF261085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
4058	17084		7.92	1.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21 C002
7155	20263		2.7	1.0E-26	BE165080.1	EST_HUMAN	MR3-H10487-150200-113-g01 HT0487 Homo sapiens cDNA
11331	24250		2.15	1.0E-26	AL038487.1	EST_HUMAN	DKFZp666C2146_r1 566 (synonym: hfkx2) Homo sapiens cDNA clone DKFZp666C2146 5'
12682	25947		2.96	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
8020	20936		1.2	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9843	22951		4.28	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
12236	28065		4.92	9.0E-27	BF445656.1	EST_HUMAN	naa03c07.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.t1 OFR repetitive element;
11	13126	26012	2.93	8.0E-27	AI831482.1	EST_HUMAN	wf49c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408160 3' similar to contains THR.b2 THR repetitive element;
679	13647		5.38	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21 C027
1439	14470	27426	7.31	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1439	14470	27427	7.31	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2180	15191	28198	0.93	8.0E-27	AW864776.1	EST_HUMAN	PM2-SN0018-220300-002-g07 SN0018 Homo sapiens cDNA
3228	16276	29177	1.44	8.0E-27	P12236	SWISSPROT	ADP.ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3402	18444	29351	0.73	8.0E-27	AF181997.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5893	18962	32080	0.58	8.0E-27	AF732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBC06 5'
7318	18486		3.29	8.0E-27	BE926560.1	EST_HUMAN	MR4-BT0398-250800-204-006 BT0398 Homo sapiens cDNA
7399	20098	33332	2.38	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
9750	22674	36058	1.99	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
9750	22674	36059	1.99	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
707	13766		1.29	7.0E-27	Z70684.1	NT	Human endogenous retroviral element HC2
6224	18213		2.47	7.0E-27	AW626172.1	EST_HUMAN	h51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975979 3' similar to TR:076040
6310	19360	32530	0.58	7.0E-27	X65747.1	NT	ORF040 ORF2: FUNCTION UNKNOWN.;
9416	22344		0.93	7.0E-27	D86984.1	NT	R.norvegicus gnat-3 mRNA for gustducin
24116	24116		4.48	7.0E-27	AJ271735.1	NT	Human mRNA for KIAA0231 gene, partial cds
11168	24058	37543	2.67	6.0E-27	M26697.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11168	24058	37543	2.67	6.0E-27	M26697.1	NT	Human nuclear protein (B23) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12201	25036	38537	1.39	6.0E-27	U63163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
8249	21154		18.36	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10731	23817	37044	3.95	5.0E-27	BF686614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
10731	23617	37045	3.65	5.0E-27	BF686614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
2405	15410	28413	1.44	4.0E-27	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
7048	20074	33307	1.55	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
8518	21449		1.05	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8593	21494		1.45	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10284	23154	36564	0.68	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
12033	24875	36380	1.99	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2055	15072	28073	4.43	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4370	17394	30248	1.48	3.0E-27	BE071624.1	EST_HUMAN	PM0-BT0527-060100-001-411 BT0527 Homo sapiens cDNA
5530	18609	31459	6.41	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
8294	21198	34534	0.91	3.0E-27	BE070351.1	EST_HUMAN	7e3302x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9845	22953	36342	4.43	3.0E-27	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
44	13160	26051	10.46	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1913	14934		18.23	2.0E-27	AA565345.1	EST_HUMAN	rk01b10.s1 NCL_CGAP_P411 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3155	16205		17.02	2.0E-27	AW629172.1	EST_HUMAN	hi51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976979 3' similar to TR:076040
3271	16319	29222	1.28	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3271	16319	29223	1.28	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6972	19998	33229	0.64	2.0E-27	H026355.1	EST_HUMAN	y39a01.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8669	21600	34940	0.94	2.0E-27	AU886347.1	EST_HUMAN	SP:HMGC_MOUSE_Q02861 HOMEOBOX PROTEIN ;
9809	22715		2.52	2.0E-27	AA651627.1	EST_HUMAN	w128g07.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426268 3'
10310	23199	36609	0.81	2.0E-27	X60658.1	NT	repetitive element ;
10538	23424	36840	1.06	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
10538	23424	36841	1.06	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stragene (cat#836206) Homo sapiens cDNA clone HFBCF07
11393	24309	37755	3.01	2.0E-27	AU121685.1	EST_HUMAN	EST00738 Fetal brain, Stragene (cat#836206) Homo sapiens cDNA clone HFBCF07
							AU121885 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 6'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11919	14934		8.23	2.0E-27	AA689346.1	EST_HUMAN	rt01b10.s1 NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17883 60S
469	13631		1.19	1.0E-27	AL163246.2	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); Homo sapiens chromosome 21 segment HS21CD46
1024	14073	27014	1.05	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1724	14762	27720	1.37	1.0E-27	4827059	NT	Homo sapiens xylulokinase (H. influenzae) homolog (XYLB) mRNA
4168	17189		1.22	1.0E-27	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
6823	19856	33068	6.79	1.0E-27	6005855	NT	MER29 repetitive element;
7198	20196	33441	1.81	1.0E-27	F30158.1	EST_HUMAN	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7196	20196	33442	1.81	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
9171	22089	35460	1.14	1.0E-27	AB007923.1	NT	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
9537	22464		1.76	1.0E-27	BE079780.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
10243	23134	36538	3.02	1.0E-27	D87449.1	NT	RC8-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA
12128	24969	38473	3.74	1.0E-27	AF111063.1	NT	Human mRNA for KIAA0260 gene, partial cds
147	13246		1.86	9.0E-28	BE348399.1	EST_HUMAN	Bos taurus latrophilin 3 splice variant bbaa mRNA, complete cds
331	13421	26337	2.38	9.0E-28	AU126260.1	EST_HUMAN	hw17c11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
12307	25114		7.03	9.0E-28	BF377859.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313;
12605	25806		4.27	8.0E-28	AW157571.1	EST_HUMAN	AU126260 NT2RPT1 Homo sapiens cDNA clone NT2RP1000443 5'
1209	14248	27189	8.25	7.0E-28	AU142750.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
11632	24538	38009	2.12	7.0E-28	11417866	NT	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
12288	25085		4.39	7.0E-28	AV735348.1	EST_HUMAN	TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
9475	22403		1.48	6.0E-28	AF016062.1	NT	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
12848	25460		6.74	6.0E-28	AA504582.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
338	13428		2.24	5.0E-28	A021003.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFACA12 5'
4054	17119	29096	1.51	5.0E-28	R79762.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
2871	15667	28667	2.17	4.0E-28	AW195068.1	EST_HUMAN	aa60603.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
7714	20846	33943	2.02	4.0E-28	A198941.1	EST_HUMAN	repetitive element/contains element PTR5 repetitive element;
							w018c07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455892 3' similar to contains THR.b1
							TH-R repetitive element;
							y69f10.1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
							xn33c09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
							Q08379 GOLGIN-95;
							q06f10.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
							REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11300	24219		3.24	4.0E-28	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
11444	24360		29.1	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
11465	20646	33943	4.95	4.0E-28	A198941.1	EST_HUMAN	q66f10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:U19503 LINE-1
12654	25327		1.71	4.0E-28	AW854244.1	EST_HUMAN	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
1309	14342		2.17	3.0E-28	AF155382.1	NT	RC3-CT0254-240400-210-112 CT0254 Homo sapiens cDNA
5267	18283		1.32	3.0E-28	AF008660.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
9386	22314	35676	2.31	3.0E-28	BF354030.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11374	24280	37734	1.65	3.0E-28	U33588.1	NT	MR3-HT0713-280500-013-009 HT0713 Homo sapiens cDNA
12680	25340		3.12	3.0E-28	A1831981.1	EST_HUMAN	Homo sapiens MHC class 1 region
12797	25423		2.7	3.0E-28	BE082801.1	EST_HUMAN	wj98f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element ;
91	13204	26117	6.06	2.0E-28	BE082187.1	EST_HUMAN	RC2-BT0842-210200-013-f03 BT0842 Homo sapiens cDNA
1192	14231	27170	9.59	2.0E-28	Y11107.3	NT	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
2499	15501	28502	2.03	2.0E-28	A348634.1	EST_HUMAN	Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41
3417	18459	29365	0.71	2.0E-28	AL163209.2	NT	qo35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element ;
6562	19603	32769	1.36	2.0E-28	BF224402.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
6567	19628		4.16	2.0E-28	BF212805.1	EST_HUMAN	hr76d03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LCR1 repetitive element ;
8622	21553	34895	0.75	2.0E-28	AF005273.1	NT	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
10113	23004		4.86	2.0E-28	AW972305.1	EST_HUMAN	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
12662	25333		2.45	2.0E-28	H06376.1	EST_HUMAN	EST384394 IMAGE resequences, MAGL Homo sapiens cDNA
1497	14528	27491	2.43	1.0E-28	D38044.1	NT	y79c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
2234	15244	28252	2.84	1.0E-28	BF333238.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
8442	21374		4.03	1.0E-28	11429885	NT	QV1-BT0821-120900-350-b03 BT0821 Homo sapiens cDNA
8597	21526		3.55	1.0E-28	8922793	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC83091), mRNA
9818	22724	36107	4.34	1.0E-28	AA308744.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
10368	23277	36698	5.69	1.0E-28	4758431	NT	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' and similar to similar to retroviral LTR
10368	23277	36699	5.69	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12273	25089		7.93	1.0E-28	AA054192.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
							z61c01.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:380448 5'

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12972	25710		1.89	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
13057	25898	31361	3.13	9.0E-29	AW663987.1	EST_HUMAN	h17g008.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12787	26396		3.07	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1625	14855	27819	1.18	7.0E-29	AW908447.1	EST_HUMAN	EST378521 MAGe resequences, MAGI Homo sapiens cDNA
3612	16648		0.98	7.0E-29	BE254708.1	EST_HUMAN	601114980F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355387 5'
13095	25611		9.49	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
616	13681	26584	7.99	6.0E-29	AI836748.1	EST_HUMAN	wp69601.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2469885 3' similar to TR:O15475
12549	25284		8.83	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
5119	18116		1.25	5.0E-29	AL163203.2	NT	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
9290	22218		8.41	5.0E-29	AW887541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
3279	16327		3.19	4.0E-29	AI762367.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
6242	19286		7.81	4.0E-29	BE164930.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8659	21550	34927	0.65	4.0E-29	AI678101.1	EST_HUMAN	QV1-FT0471-280300-121-a05 FT0471 Homo sapiens cDNA
8659	21550	34928	0.65	4.0E-29	AI678101.1	EST_HUMAN	wd35g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
9304	22232	35592	3.98	4.0E-29	J04988.1	NT	MER29.12 MER29 repetitive element ;
2394	15359	28403	2.03	3.0E-29	U07847.1	NT	Human 90 kD heat shock protein gene, complete cds
4522	17531	30394	1.85	3.0E-29	AB042287.1	NT	Human beta-galactoside alpha2,6-sialyltransferase (SIAT1) mRNA, exon U
4845	17846	30714	1.07	3.0E-29	BF333236.1	EST_HUMAN	Homo sapiens PIS gene for 6-pyruvyltetrahydropterin synthase, complete cds
6155	19213	32353	0.88	3.0E-29	BE314018.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
9292	22220	35577	2.21	3.0E-29	D38044.1	NT	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
9840	22745	36127	1.38	3.0E-29	AW303317.1	EST_HUMAN	Human gene for Ah-receptor, exon 7-9
10061	22877		1.82	3.0E-29	AL163246.2	NT	xv17603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
10465	23353		0.62	3.0E-29	BE350127.1	EST_HUMAN	repetitive element; contains MER19.12 MER19 repetitive element ;
11338	24257	37656	3.97	3.0E-29	P23266	SWISSPROT	Homo sapiens chromosome 21 segment HS21C046
13027	25907		1.75	3.0E-29	D63882.1	NT	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
515	13585	26497	1.13	2.0E-29	AF084869.1	NT	MER29 repetitive element ;
515	13585	26498	1.13	2.0E-29	AF084869.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
						NT	Human HsLIM15 mRNA for HsLIM15, complete cds
						NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
						NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1556	14587	27545	6.77	2.0E-29	A1963604.1	EST_HUMAN	wr65d10.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1556	14587	27546	6.77	2.0E-29	A1963604.1	EST_HUMAN	wr65d10.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
4378	17302	30256	2.7	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6037	19089	32227	0.89	2.0E-29	A1082459.1	EST_HUMAN	cs71e04.x1 NCI CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.L2 L1 repetitive element ;
6421	19468	32641	1.58	2.0E-29	A1806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER8 repetitive element ;
7991	19468	32641	1.32	2.0E-29	A1806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER8 repetitive element ;
8555	21486	34827	1.06	2.0E-29	BE867157.1	EST_HUMAN	601442206F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5'
9141	22039	35430	0.59	2.0E-29	10667821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
9141	22039	35431	0.59	2.0E-29	10667821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
10039	22939	36327	3.67	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10039	22939	36328	3.67	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10733	23619	37047	4.45	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10733	23619	37048	4.45	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8388	21252	34624	0.46	1.0E-29	AV700745.1	EST_HUMAN	AV700745 GK0 Homo sapiens cDNA clone GKCALE08 3'
9390	22278	35640	10.42	1.0E-29	AW993880.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA nc20c07.s1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 repetitive element ;
6884	19896	33111	3.5	9.0E-30	AA761215.1	EST_HUMAN	MER4 repetitive element ;
12346	25139		1.68	9.0E-30	11422745	NT	Homo sapiens zinc/ferritin regulated transporter-like (ZIRT), mRNA
6574	19815		10.01	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8846	21776	35123	1.37	8.0E-30	AA383873.1	EST_HUMAN	EST97317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat
9241	22163	35521	3.59	8.0E-30	AI667072.1	EST_HUMAN	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'
1536	14596		1	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-160400-004-d11 BT0724 Homo sapiens cDNA
1798	14824	27782	1.66	6.0E-30	D25303.1	NT	Human mRNA for Integrin alpha subunit, complete cds
3233	16281	29181	2.66	6.0E-30	BE009026.1	EST_HUMAN	QV0-BND147-290400-214-F12 BND147 Homo sapiens cDNA
4871	10261	29181	0.97	6.0E-30	BE009026.1	EST_HUMAN	QV0-BND147-290400-214-F12 BND147 Homo sapiens cDNA
							tg92g03.x1 NCI CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element ;
4099	17124	30001	48.68	5.0E-30	A1396992.1	EST_HUMAN	Human aconitase hydratase (ACO2) gene, exon 7
5419	25744		4.71	5.0E-30	U87931.1	NT	Homo sapiens chromosome 21 segment HS21C078
11324	24243		1.71	5.0E-30	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11595	24504	37971	2.33	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11595	24504	37972	2.33	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2158	15170	28172	2.19	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2158	15170	28173	2.19	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c09 DT0043 Homo sapiens cDNA
7176	18448	31317	0.49	4.0E-30	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9462	22390	35752	1.66	4.0E-30	AW812488.1	EST_HUMAN	GM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
1179	14219		1.67	3.0E-30	AI338551.1	EST_HUMAN	qq93c05.x1 Soares_t01a_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element ;
3821	16851	29735	0.8	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
7629	20564	33858	0.49	3.0E-30	T18862.1	EST_HUMAN	b12056t Testis 1 Homo sapiens cDNA clone b12056
8530	21461		0.68	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10915	23800	37229	0.98	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
11655	24561	38032	1.63	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
698	13757	26674	1.06	2.0E-30	AW857315.1	EST_HUMAN	CMQ-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1111	14153		2.49	2.0E-30	F08888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1498	14529	27492	4.84	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2764	15756	28751	9.26	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2962	16014	28912	6.53	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3954	16883	29768	2.7	2.0E-30	AW206581.1	EST_HUMAN	UI-H-B11-afic-c-12-Q-U.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4860	17889	30754	2.53	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4890	17889	30755	2.53	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
7063	20087	33321	0.9	2.0E-30	BF306337.1	EST_HUMAN	601893208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138993 5'
9046	21975	35333	0.56	2.0E-30	AA019103.1	EST_HUMAN	ze58c10.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5'
9101	22030	35385	5.93	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-570C01 5'
9194	22122	35477	3.05	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW-DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
9194	22122	35478	3.05	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW-DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
10502	23390	36801	4.23	2.0E-30	AW971588.1	EST_HUMAN	EST333657 IMAGE resequences, MAGI Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10584	23470	36886	9.11	2.0E-30	AW470791.1	EST_HUMAN	hs33406.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THRLb3
306	13398	26317	9.63	1.0E-30	C18939.1	EST_HUMAN	THR repetitive element ; C18939 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-570C01 5'
561	13630	26539	3.28	1.0E-30	AW468897.1	EST_HUMAN	hd30b04.x1 Scores_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE:2910891 3' similar to contains MER1.13 MER1 MER1 repetitive element ;
739	13797	26721	1.74	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2227	15237	26244	9.85	1.0E-30	AA684977.1	EST_HUMAN	ae77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868609 3'
2486	15488	26489	2.37	1.0E-30	BF34726.1	EST_HUMAN	602022660.F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4157991 5'
3102	16163	29049	1.38	1.0E-30	AA315045.1	EST_HUMAN	EST186868 HCC cell line (matelastis to liver in mouse) II Homo sapiens cDNA 5' end
8188	21093	34424	22.54	1.0E-30	BF183230.1	EST_HUMAN	601809932.F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
12907	25826		6.4	1.0E-30	H55593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3830	16860	29742	0.73	9.0E-31	T73025.1	EST_HUMAN	yc65406.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3830	16860	29743	0.73	9.0E-31	T73025.1	EST_HUMAN	yc65406.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8899	21829	35181	0.91	9.0E-31	R18214.1	EST_HUMAN	yf89b08.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30665 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8899	21829	35182	0.91	9.0E-31	R18214.1	EST_HUMAN	yf89b08.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:30565 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
9184	22112		1.57	9.0E-31	Z38263.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
9186	22114	35472	0.63	9.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
13091	25608	31733	1.57	9.0E-31	6755441	NT	Mus musculus syndecan 4 (Sdc4), mRNA
1104	14147	27096	2.21	8.0E-31	8923399	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2438	16442		11.81	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5027	18024	30882	1	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
5027	18024	30883	1	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
734	13762		1.21	7.0E-31	AA372637.1	EST_HUMAN	EST64555 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end
2717	15710	26707	1.62	7.0E-31	BE328517.1	EST_HUMAN	hw05a1.1.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2717	15710	26708	1.62	7.0E-31	BE328517.1	EST_HUMAN	hw05a1.1.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8971	21901	35255	0.67	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8971	21901	35256	0.67	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9809	22712		1.18	7.0E-31	BE406611.1	EST_HUMAN	601304125.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12765	25395	31808	2.38	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3746	16778		3.23	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8732	21662		3.32	6.0E-31	AF056066.1	NT	Homo sapiens MHC class 1 region

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8806	21836	35192	0.79	6.0E-31	BE360127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kir13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
11179	24105	37552	1.74	6.0E-31	AU119105.1	EST_HUMAN	MER29 repetitive element;
12397	25170	31874	3.28	6.0E-31	AW372888.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12512	25761		1.97	6.0E-31	BE894488.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
205	13304	26220	1.58	5.0E-31	M60694.1	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
205	13304	26221	1.58	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
							Homo sapiens type I DNA topoisomerase gene, exon 8
9013	21942		0.57	5.0E-31	BF058540.1	EST_HUMAN	7k0604.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13637 Q13637
617	13882		4.99	4.0E-31	AJ271735.1	NT	SIMILAR TO POGO ELEMENT, contains L1.11 L1 repetitive element;
							Homo sapiens Xq pseudautosomal region; segment 1/2
1634	14664	27626	1.18	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP
1840	14863		2.67	4.0E-31	AL163280.2	NT	ACETYL GALACTOSAMINYL TRANSFERASE (UDP-GALNAc:POLYPEPTIDE, N-
2837	15826		2.03	4.0E-31	5730038	NT	ACETYL GALACTOSAMINYL TRANSFERASE (GALNAc-T1)
12551	26267		1.55	4.0E-31	AJ230126.1	NT	Homo sapiens chromosome 21 segment HS21C080
12888	25488		1.49	4.0E-31	AB008881.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							Homo sapiens GGT1 gene, exon 1
2637	16634	26631	2.8	3.0E-31	6008871	NT	Homo sapiens gene for activin receptor type IIB, complete cds
							Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
7725	20657	33954	12.5	3.0E-31	4826833	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8) mRNA
7815	20839	34142	1.42	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8271	21176	34511	0.47	3.0E-31	AW893062.1	EST_HUMAN	GM3-NN0006-300300-132-e07 NN0006 Homo sapiens cDNA
8271	21176	34512	0.47	3.0E-31	AW893062.1	EST_HUMAN	GM3-NN0006-300300-132-e07 NN0006 Homo sapiens cDNA
8739	21689		1.97	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
10109	23000	36396	9.6	3.0E-31	D14623.1	NT	Horse mRNA for ferritin L-chain, complete cds
11077	24009	37451	3.26	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11693	24502		3.99	3.0E-31	BF035327.1	EST_HUMAN	601458331F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1933	14954	27931	1.39	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-280300-111-f03 LT0051 Homo sapiens cDNA
2229	15239	26246	2	2.0E-31	A1393988.1	EST_HUMAN	tg44g05.x1 Scerree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2363	15369	26373	2.94	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513.1 1761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761G1513 5'
							aa8811.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
2484	15487	26466	5.87	2.0E-31	AA458824.1	EST_HUMAN	THR12 THR repetitive element;
5457	18538	31380	0.78	2.0E-31	AW444496.1	EST_HUMAN	UHHB13-akb-f-09-0-UJ.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5911	18980	32098	3.09	2.0E-31	BE360127.1	EST_HUMAN	h103g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 b3 MER29 repetitive element ;
9824	22550			2.0E-31	AA877764.1	EST_HUMAN	m06804.s1 NCI_CGAP_Cor10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9748	22572	36056	3.52	2.0E-31	7681635	NT	Homo sapiens B9 protein (B9), mRNA
10417	23305	36725	0.99	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 5'
10417	23303	36726	0.99	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CUAALB07 5'
10577	23463	36888	3.42	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
10577	23463	36887	3.42	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12486	25229		3.14	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12619	25667		4.65	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
17	13132	26019	6.9	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1690	14720	27681	1.32	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1690	14720	27682	1.32	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1690	14720	27683	1.32	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4748	17753	30611	1.98	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547B235 5'
4748	17753	30612	1.98	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547B235 5'
5475	18556	31398	3.52	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151288-028-a08_1 ST0220 Homo sapiens cDNA
6373	19422	32587	2.19	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ccb1 repeat region
7669	20602	33900	0.84	1.0E-31	AF126145.1	NT	Bos taurus xenodictic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
8355	21260	34594	0.81	1.0E-31	BE972818.1	EST_HUMAN	601662052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:39355293 5'
11354	24272	37714	3.49	1.0E-31	AI086434.1	EST_HUMAN	q121h03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRAXIN. ;
2907	15960		0.96	9.0E-32	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
6930	19569	33180	2.38	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAA301 5'
7765	20695	33694	0.5	9.0E-32	L31770.1	NT	Bos taurus vacuolar H ⁺ -ATPase subunit mRNA, complete cds
8032	20948		1.02	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2091	15105	28106	9.97	8.0E-32	AI056770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5670	18744	31654	0.71	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA
4970	17969	30827	3.02	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12467	25213		3.51	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphion and neighbouring non-empilled region
2781	15772	28767	0.94	6.0E-32	A1478104.1	EST_HUMAN	hm34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159894 3' similar to contains MER29.13
7758	20888		1.16	6.0E-32	BE888016.1	EST_HUMAN	MER29 repetitive element ;
12853	25950		2.14	6.0E-32	AA884653.1	EST_HUMAN	601511330F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
1060	14104	27042	25.76	5.0E-32	AF116627.1	NT	ch37c03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459872 3' similar to contains L1.t3 L1 repetitive element ;
959	14009		2.03	4.0E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
8047	20950	34274	3.28	4.0E-32	11432574	NT	Homo sapiens chromosome 21 segment HS21C046
8047	20950	34275	3.28	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
478	13549	26469	2.66	3.0E-32	Y17263.1	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
1473	14504	27466	11.44	3.0E-32	AV731500.1	EST_HUMAN	Homo sapiens FLI-1 gene, partial
9930	22835	36224	9.8	3.0E-32	AV758634.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone H1FAK07 5'
9930	22835	36225	9.8	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFB8B12 5'
11363	24281	37724	3.36	3.0E-32	AA777621.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFB8B12 5'
12489	25231		5.74	3.0E-32	BE279086.1	EST_HUMAN	z95a07.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.t3 THR repetitive element ;
12851	18423	31346	4.39	3.0E-32	5174574	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12831	18423	31347	4.39	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology); translocated to, 4 (MLLT4) mRNA
12978	25538		4.9	3.0E-32	BE279086.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology); translocated to, 4 (MLLT4) mRNA
4991	17990	30847	0.97	2.0E-32	BE298613.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6501	19545	32721	0.76	2.0E-32	M35418.1	NT	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529169 5'
6753	19767	32999	5.02	2.0E-32	Z38133.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6753	19767	33000	5.02	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8854	21784	35132	4.45	2.0E-32	AA114294.1	EST_HUMAN	H. sapiens mRNA for myosin
8854	21784	35133	4.45	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
7408	20107	33342	6.17	1.0E-32	11496780	NT	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
9158	22086	35445	0.56	1.0E-32	AA720574.1	EST_HUMAN	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
3540	16578		5.3	9.0E-33	BE327112.1	EST_HUMAN	THR repetitive element ;
							hwo7c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O86539 O86539 WW DOMAIN BINDING PROTEIN 11. ;

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6887	19723		3.62	9.0E-33	AF23391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8349	22274	35636	1.78	9.0E-33	BF347229.1	EST_HUMAN	602021764F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
11238	24194		4.48	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
64	13180	26085	2.59	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
64	13180	26086	2.59	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2174	15186	28181	2.13	7.0E-33	AI590116.1	EST_HUMAN	to12609.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element;
2697	15891		9.74	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE08 5'
3288	16335		17.96	7.0E-33	AW971307.1	EST_HUMAN	EST383396 MAGE resequences, MAGL Homo sapiens cDNA
9601	22429		0.93	7.0E-33	X54890.1	NT	Human ILRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
11268	24190	37639	2.15	7.0E-33	BF347229.1	EST_HUMAN	602021764F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
11694	24696	36073	2.08	7.0E-33	AW971668.1	EST_HUMAN	EST383687 MAGE resequences, MAGL Homo sapiens cDNA
12472	26218	31854	10.74	7.0E-33	AA601416.1	EST_HUMAN	no16h0.1.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.H1.L1 repetitive element;
3799	16830		0.92	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6302	19353	32522	1.06	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
6302	19353	32523	1.08	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
9142	22070	35432	5.23	6.0E-33	JD4038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
9260	22188	35545	2.64	6.0E-33	11428198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
10515	23402	36813	1.57	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10515	23402	36814	1.57	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1802	14828		1.58	5.0E-33	BF373616.1	EST_HUMAN	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA
1903	14924		1.12	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1916	14937	27913	1.27	5.0E-33	4607208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1916	14937	27914	1.27	5.0E-33	4607208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2291	15269		3.09	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6982	19990	33216	0.67	5.0E-33	AA180080.1	EST_HUMAN	zq45b06.s1 Strazagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element
10742	23628	37038	0.92	5.0E-33	AW264678.1	EST_HUMAN	xq33f11.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2762461 3'
10742	23628	37039	0.92	5.0E-33	AW264678.1	EST_HUMAN	xq33f11.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2762461 3'
1155	14156		2.61	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2139	15162	28133	1.24	4.0E-33	4759937	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2444	15448		2.75	4.0E-33	AA628621.1	EST_HUMAN	ab51b11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element ;
2576	15575	28571	7.3	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4597	17605	30462	1.78	4.0E-33	AW293349.1	EST_HUMAN	UHH-B12-ah1-c-03-0-J1.st NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5588	18685	31541	20.44	4.0E-33	AA053053.1	EST_HUMAN	z71a08.11 Stratagene cdon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671.1ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6856	19695	32890	0.73	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6856	19695	32891	0.73	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1116	14158		4.65	3.0E-33	BE350127.1	EST_HUMAN	ht09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
1117	14158		2.57	3.0E-33	BE350127.1	EST_HUMAN	ht09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
2474	15924		3.3	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLC8CF09 3'
10920	23805	37232	0.97	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407847 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE. ;
108	13133		3.44	2.0E-33	A1160189.1	EST_HUMAN	qb67g03.x1 Soares fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
1399	14430	27384	1.52	2.0E-33	AA010242.1	EST_HUMAN	z09e08.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430214 5'
1399	14430	27385	1.52	2.0E-33	AA010242.1	EST_HUMAN	z09e08.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430214 5'
4526	17635		3.75	2.0E-33	BE150039.1	EST_HUMAN	MR0-HT0405-160300-202-08 HT0405 Homo sapiens cDNA
5107	18104	30851	2.21	2.0E-33	AA628683.1	EST_HUMAN	ab51g11.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734.cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5228	18217	31063	1.77	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5228	18217	31064	1.77	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6681	19727	32927	1.07	2.0E-33	A127492.1	EST_HUMAN	q08d01.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1880181 3'
9645	22571		1.77	2.0E-33	A1052256.1	EST_HUMAN	cc21d03.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1875973 3' similar to gb:M29636 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
9	13124		1.05	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5762	18854	31950	0.59	1.0E-33	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
7806	20735	34038	1.09	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
10524	25993		1.04	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11765	24666	38152	1.81	1.0E-33	AW066818.1	EST_HUMAN	QV3-BN0047-230200-102-503 BN0047 Homo sapiens cDNA
12089	24930	38435	2.78	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12739	25379		1.45	1.0E-33	A1927191.1	EST_HUMAN	wc88c06.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462410 3'
12899	13124		3.59	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12927	25501	31770	2.44	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
4724	17729		0.97	9.0E-34	BE155575.1	EST_HUMAN	PM4-HT0352-181189-001-D02 HT0352 Homo sapiens cDNA
13078	25600		14.65	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2184	15195	28200	0.99	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
8276	21181	34519	0.56	8.0E-34	BE069882.1	EST_HUMAN	MR4-BT0399-200100-001-n03 BT0399 Homo sapiens cDNA
1463	14494	27455	3.68	7.0E-34	T70845.1	EST_HUMAN	y415605.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:108320 5'
10505	14484	27455	0.58	7.0E-34	T70845.1	EST_HUMAN	y415605.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:108320 5'
12534	25257		2.38	7.0E-34	H12856.1	EST_HUMAN	y14c10.r1 Soares placenta N02HP Homo sapiens cDNA clone IMAGE:148722 5'
493	13563	26481	1.4	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
493	13563	26482	1.4	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
5288	18274	31122	0.97	6.0E-34	AW998611.1	EST_HUMAN	PMO-BN0055-100300-001-c06 BN0055 Homo sapiens cDNA
12368	25152	31888	1.9	8.0E-34	U03688.1	NT	Mus musculus DAB2J hair-specific (hac1-1) gene
1902	14923		1.91	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5196	18189	31029	5.67	5.0E-34	U30883.1	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
9424	22382	38718	1.68	5.0E-34	AF078779.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
11098	24029	37473	2.34	5.0E-34	AB037856.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11701	24603		1.72	5.0E-34	AL163208.2	NT	Homo sapiens mRNA for KIAA1495 protein, partial cds
2014	15032	28026	2.07	4.0E-34	A1804667.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
3215	16263	29162	0.99	4.0E-34	5803168	NT	tf04c06.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2249194 3'
6075	19136	32270	0.49	4.0E-34	AA661773.1	EST_HUMAN	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
9590	22516	35878	1.26	4.0E-34	BF209778.1	EST_HUMAN	ak35c01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407836 3'
6479	19524	32702	0.8	3.0E-34	M37277.1	NT	601874950FT NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
11592	24501		3.29	3.0E-34	BF035327.1	EST_HUMAN	Human Ig germline H-chain D-region genes, partial cds
							601458531FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
9506	22433	35796	0.86	2.0E-34	A1678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element;
9506	22433	35797	0.86	2.0E-34	A1678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element;
11601	24510	37976	1.51	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
11601	24510	37977	1.51	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1524	14555	27516	5.3	1.0E-34	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3741	16773	29699	1.87	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4158	17179	30051	1	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4168	17179	30052	1	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4593	17601		7.12	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0508-240400-016-h08 BT0508 Homo sapiens cDNA
6378	19427	32593	2.35	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
6378	19427	32594	2.35	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
9869	22781	36170	0.59	1.0E-34	P23286	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
10219	23110	36511	10.5	1.0E-34	AL038635.1	EST_HUMAN	DKF2p664A1563_J1 564 (synonym: hbr2) Homo sapiens cDNA clone DKF2p664A1563 5'
11628	24534	38003	1.58	1.0E-34	BE781790.1	EST_HUMAN	601470582F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11628	24534	38004	1.56	1.0E-34	BE781790.1	EST_HUMAN	601470582F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
12708	25902		2.49	1.0E-34	AA807097.1	EST_HUMAN	oc31c11.s1 NCI CGAP_G031 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203
12918	25528		7.96	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
3714	16746	29634	2.2	8.0E-35	AW663302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
242	13339		10.64	8.0E-35	6031190	NT	hnr7506.y1 NCI CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2988787 5'
1766	14792	27762	4.72	8.0E-35	BF589937.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1766	14792	27763	4.72	8.0E-35	BF589937.1	EST_HUMAN	nae33a08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4975	17973	30834	3.13	8.0E-35	BF183105.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
11132	24081	37508	2.21	8.0E-35	BE378480.1	EST_HUMAN	nae33a08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
12466	25212		5.01	8.0E-35	BF569282.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
6769	19793	33007	1.63	7.0E-35	11425417	NT	601609588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
1983	15001	27986	1.35	6.0E-35	6005979	NT	601236498F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
4137	17168	30034	0.73	8.0E-35	AW297191.1	EST_HUMAN	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
5310	18294	31147	0.78	6.0E-35	AW753589.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
8477	21408	34749	4.62	6.0E-35	6005921	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
9267	22195	35552	0.58	6.0E-35	X94232.1	NT	UHL-BWO-qld-4-09-0-U1.e1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
9267	22195	35553	0.58	6.0E-35	X94232.1	NT	PM1-C70297-091299-004-h08 C70297 Homo sapiens cDNA
10191	23082	36483	0.79	6.0E-35	AB002364.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10414	23303	36720	2.76	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for novel T-cell activation protein
13088	25594	31726	7.58	6.0E-35	11417871	NT	H. sapiens mRNA for novel T-cell activation protein
13088	25594	31727	7.58	6.0E-35	11417871	NT	H. sapiens mRNA for novel T-cell activation protein
13088	25594	31727	7.58	6.0E-35	11417871	NT	Human mRNA for KIAA0368 gene, partial cds
13088	25594	31727	7.58	6.0E-35	11417871	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
13088	25594	31727	7.58	6.0E-35	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
13088	25594	31727	7.58	6.0E-35	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
151	13251	26169	38.71	5.0E-35	AF154830.1	NT	Homo sapiens carboxyl phosphate synthetase mRNA, complete cds
1738	14765	27735	5.09	5.0E-35	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
3052	16105	29009	1.46	5.0E-35	6912339	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4516	17525	30391	1.58	5.0E-35	AF023298.1	NT	Homo sapiens cdk2 kinase (CLK2), protein1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; melaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
8762	21892		5.28	5.0E-35	BE990992.1	EST_HUMAN	601431084F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8788	21718	35066	2.81	5.0E-35	A1208765.1	EST_HUMAN	q338c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.
8788	21718	35067	2.81	5.0E-35	A1208765.1	EST_HUMAN	q338c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.
11620	24527		3.16	5.0E-35	AA001786.1	EST_HUMAN	z84f12.1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1454	14496	27447	6.73	4.0E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1841	14864	27845	11.9	4.0E-35	H91193.1	EST_HUMAN	y488a07.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element;
4920	17919		0.72	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5245	18232		1.01	4.0E-35	BE409102.1	EST_HUMAN	601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'
7575	20511		1.75	4.0E-35	BE350127.1	EST_HUMAN	H09g01.x1 NCL_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146288 3' similar to contains MER29.b3 MER29 repetitive element;
9083	22012	35369	9.88	4.0E-35	AL046596.1	EST_HUMAN	DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
1601	14632	27592	17.44	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2353	15361		4.16	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5524	18603	31451	23.63	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2.;
5524	18603	31452	23.63	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2.;
10021	22921		1.52	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10671	23557	36989	0.97	3.0E-35	AW003063.1	EST_HUMAN	wr3a05.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10286 RETROVIRUS-RELATED POL. POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
112	15866	26135	0.91	2.0E-35	N88985.1	EST_HUMAN	K632F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K632 5' similar to REPETITIVE ELEMENT

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1216	14254	27195	1.08	2.0E-35	T11909.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
2232	15242	28260	3.94	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
2732	15725	28721	1.13	2.0E-35	AW665005.1	EST_HUMAN	h189a12.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12;
3357	16401	29301	0.79	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA00571), mRNA
3357	16401	29302	0.79	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA00571), mRNA
3618	16654		0.94	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3984	17012	28900	0.88	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3984	17012	28901	0.88	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4781	17788	31230	3.68	2.0E-35	H49239.1	EST_HUMAN	y19a12.r1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:274079 5'
5412	18393	31230	1.08	2.0E-35	AW291061.1	EST_HUMAN	UI-H-BI2-agg-b-10-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2723682 3'
5412	18393	31231	1.08	2.0E-35	AW291061.1	EST_HUMAN	UI-H-BI2-agg-b-10-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2723682 3'
5774	18847	31950	1.77	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA
7463	20403	33678	0.73	2.0E-35	BE832636.1	EST_HUMAN	GM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7463	20403	33679	0.73	2.0E-35	BE832636.1	EST_HUMAN	GM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11237	24163	37610	2.88	2.0E-35	X59417.1	NT	H sapiens PROS-27 mRNA
12208	18847	31950	1.51	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA
12901	25489		8.38	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
49	13166	26060	4.55	1.0E-35	AA631949.1	EST_HUMAN	f1nc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	13166	26061	4.55	1.0E-35	AA631949.1	EST_HUMAN	f1nc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
776	13633	26766	32.39	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
776	13633	26766	32.39	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-008-412 ST0162 Homo sapiens cDNA
934	13986		1.78	1.0E-35	T87947.1	EST_HUMAN	y093a01.r1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN;
2573	15571	28568	2.29	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2818	15807	28806	2.11	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
2818	15807	28806	2.11	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
3206	16254	29150	1.73	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFF08 3'
3206	16254	29151	1.73	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEFF08 3'
4629	17638	30399	5.72	1.0E-35	7696906	NT	Mus musculus activin receptor interacting protein 1 (Anip1-pending), mRNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4529	17638	30400	5.72	1.0E-35	7659305	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5700	18773	31702	1.44	1.0E-35	11528236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7337	18505	31280	0.97	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-407 ST0111 Homo sapiens cDNA
7337	18505	31281	0.97	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-407 ST0111 Homo sapiens cDNA
7903	20828	34131	0.82	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
8090	21002	34325	1.02	1.0E-35	11418002	NT	Homo sapiens KIAA0845 gene product (KIAA0845), mRNA
10071	25692	36380	1.86	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10071	25692	36381	1.86	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
11050	23934	37373	0.83	1.0E-35	BF589594.1	EST_HUMAN	naa06d06.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
11050	23934	37374	0.83	1.0E-35	BF589594.1	EST_HUMAN	naa06d06.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
12172	25008	38511	1.57	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12172	25008	38512	1.57	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12180	25016		1.89	1.0E-35	AI525119.1	EST_HUMAN	prom1a-7.D01.r btumor Homo sapiens cDNA 5'
12275	25867		1.95	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12800	25426		2.23	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838985 5'
6240	19284	32453	0.67	8.0E-36	X78479.1	NT	B.bovis BBSr mRNA for scinderin
9771	22695	36081	0.9	8.0E-36	AA348480.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
2973	16025	28025	2.11	7.0E-36	AW857579.1	EST_HUMAN	GM1-CT0315-091298-063-407 CT0315 Homo sapiens cDNA
3163	16213		6.32	7.0E-36	4687498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
8103	21015	34341	6.04	7.0E-36	U06872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
8103	21015	34342	6.04	7.0E-36	U06872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
12610	25303	31814	1.95	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
2020	15038	28032	1.45	6.0E-36	7706622	NT	Homo sapiens ninjurin 2 (NINJ2), mRNA
2443	15447		10.07	6.0E-36	AB035346.1	NT	Homo sapiens TOL8 gene, exon 12
3707	16739	28628	0.84	6.0E-36	BF515101.1	EST_HUMAN	ULH.BW1.amv.c-12.0-JL.st NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5077	18074	30923	0.98	6.0E-36	AB030501.1	NT	Rattus norvegicus mRNA for DLG6 gamma, complete cds
5514	18503	31441	8.6	6.0E-36	AI435169.1	EST_HUMAN	th83b06.x1 Soares NSF FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126185 3' similar to
7468	20408	33685	3.1	6.0E-36	AW780143.1	EST_HUMAN	db:MI1949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
9211	22139	35498	2.81	6.0E-36	AF208161.1	NT	hcd06h02.x1 NCI CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN
							P62292 IMPORTIN ALPHA-2 SUBUNIT ;
							Homo sapiens syncytin precursor, mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11980	24823	38318	2.78	6.0E-36	AJ380499.1	EST_HUMAN	tf95c09.x1 NCJ CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
142	13244	26182	9.93	5.0E-36	AJ271735.1	NT	MER9 repetitive element;
2800	15789	26786	7.59	5.0E-36	BE388436.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3676	16709	29589	2.47	5.0E-36	AL163209.2	NT	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
4900	17859	30765	1.16	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4900	17859	30766	1.16	5.0E-36	5729729	NT	Homo sapiens AP15-like 1 (AP15L1), mRNA
8284	21188	34503	0.76	5.0E-36	11079227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12246	13244	26182	7.07	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12511	25245	31886	2.53	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1252	14288	27231	2.41	4.0E-36	BE010038.1	EST_HUMAN	PM3-BND176-100400-001-g04 BND176 Homo sapiens cDNA
1672	14702	27663	1.63	4.0E-36	BE3882574.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2236	15246	29352	0.67	4.0E-36	AW247772.1	EST_HUMAN	2820020 SpHms NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3403	16445	29352	0.67	4.0E-36	BE388299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3403	16445	29353	0.67	4.0E-36	BE388299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4867	17867	30731	0.92	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5281	18267	31115	0.84	4.0E-36	AA905361.1	EST_HUMAN	dk05b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1506909 3' similar to
5917	18955		0.86	4.0E-36	R64023.1	EST_HUMAN	SW:D3HL RAT P28268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
6290	19341	32509	2.46	4.0E-36	11497041	NT	y19106.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:139713 5'
8102	21014	34340	1.89	4.0E-36	M33320.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
9118	22046	36403	1.4	4.0E-36	D87675.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
9118	22046	36404	1.4	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11426	24342	37787	1.6	4.0E-36	AA400370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
12528	25252		2.02	4.0E-36	11420518	NT	z089c10.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
12568	25765		3.64	4.0E-36	AV753629.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
720	13778	26700	5.9	3.0E-36	AF099810.1	NT	AV753629 TP Homo sapiens cDNA clone TPGABH01 5'
4823	17650	30494	8.32	3.0E-36	10181139	NT	Homo sapiens neuroxin III-alpha gene, partial cds
3211	16259	29158	1.03	2.0E-36	BE269267.1	EST_HUMAN	Homo sapiens myosin VIIa (Jp1-pending), mRNA
5073	18070	30919	2.71	2.0E-36	AW880376.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5674	18748	31659	2.46	2.0E-36	AF267747.1	NT	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
6062	19124	32252	4.78	2.0E-36	T08756.1	EST_HUMAN	Mus musculus p47-phox gene, complete cds
6868	19890	33104	11.42	2.0E-36	T086229.1	EST_HUMAN	Mus musculus p47-phox gene, complete cds
9925	22830	36216	0.87	2.0E-36	BF12794.1	EST_HUMAN	ESTU06648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBB128 5' end
							ye44a07.r1 Stragene liver (#837224) Homo sapiens cDNA clone IMAGE:83508 5'
							UIH-BW1-amu-a-11-0-U1.s1 NCJ CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10078	22871	36280	0.73	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10078	22871	36281	0.73	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
910	13962	26909	2.47	1.0E-36	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2217	15228	28233	1.64	1.0E-36	BF673761.1	EST_HUMAN	602130493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 6'
3393	16436		1.98	1.0E-36	AF156982.1	NT	Homo sapiens human endogenous retrovirus W provirus 19 protease (pro) gene, partial cds
5931	18998	32118	0.62	1.0E-36	AL044446.1	EST_HUMAN	DKFZp34343022_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp34343022 5'
6118	19177	32312	1.07	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6424	19471		4.02	1.0E-36	AI867714.1	EST_HUMAN	w637612.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6653	19692	32885	1.46	1.0E-36	R25012.1	EST_HUMAN	y938g10.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6653	19692	32886	1.46	1.0E-36	R25012.1	EST_HUMAN	y938g10.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6978	20005	33237	0.7	1.0E-36	AL120542.1	EST_HUMAN	DKFZp781A228_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781A228 5'
8538	21469	34808	3.87	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590388 5'
8538	21469	34809	3.87	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590388 5'
8631	21662	34899	1.3	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8631	21662	34900	1.3	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
9580	22507	35871	2.58	1.0E-36	AW103659.1	EST_HUMAN	xe82b07.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10815	23501	36934	4.83	1.0E-36	BF584189.1	EST_HUMAN	QV6-NN1023-010600-169-h01 NN1023 Homo sapiens cDNA
10817	23703	37130	1.29	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0278-040500-017-a10 CT0278 Homo sapiens cDNA
10817	23703	37131	1.29	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0278-040500-017-a10 CT0278 Homo sapiens cDNA
11387	24303	37750	2.92	1.0E-36	AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11820	24741	38232	3.56	1.0E-36	AW504143.1	EST_HUMAN	UI-HF-BN0-ale-c-03-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12410	25179		3.83	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12826	25444		5.38	1.0E-36	AL163243.2	NT	Homo sapiens chromosome 21 segment HS21C013
13053	26594		2.46	1.0E-36	AF20723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7774	20704	34004	2.32	9.0E-37	AW009277.1	EST_HUMAN	w805007.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7774	20704	34005	2.32	9.0E-37	AW009277.1	EST_HUMAN	w805007.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
12631	25326		1.58	9.0E-37	W22618.1	EST_HUMAN	79D4 Human retina cDNA Tsp509I-cloned sublibrary Homo sapiens cDNA not directional
3405	16447	26355	1.23	8.0E-37	4757979	NT	Homo sapiens chimerin (ghimaein) 2 (CHN2) mRNA
5429	18511		1.54	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
6040	19102	32229	3.98	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.B3 MER29 repetitive element ;

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6040	19102	32230	3.98	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
6092	19153	32289	5.86	8.0E-37	AW840940.1	EST_HUMAN	MER29 repetitive element ;
8464	21395	34736	7.32	8.0E-37	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1311	14344		2.02	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
11197	24123	37569	3.84	7.0E-37	AIB17700.1	EST_HUMAN	PTR5 repetitive element ;
11333	24252	37689	2.04	7.0E-37	AIS68702.1	EST_HUMAN	Im87g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1
5275	18261		4.44	6.0E-37	R10039.1	EST_HUMAN	repetitive element ;
8007	21836	35262	0.66	6.0E-37	AF160899.1	NT	Y25a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127850 5'
12847	25459		1.5	6.0E-37	U78308.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12847	25512		4.27	6.0E-37	AF202723.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
6330	19380	32547	5.64	6.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6330	19380	32548	5.54	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8316	22244	35805	1.33	5.0E-37	AV750211.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
11357	24275		4.86	6.0E-37	7657117	NT	AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'
12405	25176		5.01	5.0E-37	AF149773.1	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCA1), mRNA
2447	15451	28447	4.71	4.0E-37	AA702794.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6540	19683	32767	0.61	4.0E-37	AW794502.1	EST_HUMAN	ZB90B04.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
9894	22809	36198	0.82	4.0E-37	AA843806.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
2030	15047	28043	2.37	3.0E-37	AL048956.1	EST_HUMAN	ak03a02.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2030	15047	28044	2.37	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2538	15538		1.69	3.0E-37	AW961150.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
3006	16058		4.1	3.0E-37	AW961150.1	EST_HUMAN	EST1737222 MAGG resequences, MAGF Homo sapiens cDNA
6079	19140	32276	0.65	3.0E-37	AL138274.1	EST_HUMAN	EST1737222 MAGG resequences, MAGF Homo sapiens cDNA
7864	20791	34094	0.53	3.0E-37	T03080.1	EST_HUMAN	DKFZp547G087_r1 547 (synonym: htrf1) Homo sapiens cDNA clone DKFZp547G087 5'
7987	20906	34222	0.9	3.0E-37	A1749952.1	EST_HUMAN	FB23B1 Fetal brain, Stralagene Homo sapiens cDNA clone FB23B1 3' end similar to Human somatic cytochrome c (HCS) gene
402	13515	26436	0.67	2.0E-37	D89790.1	NT	at34c05.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
402	13515	26437	0.67	2.0E-37	D89790.1	NT	Q13537 SIMILAR TO POGO ELEMENT ;
							Homo sapiens mRNA for AML1, complete cds
							Homo sapiens mRNA for AML1, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1108	14150	27090	1.86	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1108	14150	27091	1.86	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1979	14997	27982	1.21	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3983	16991	29875	7.1	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
5573	18651		0.57	2.0E-37	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
6825	19658	33070	0.64	2.0E-37	11990617	NT	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
6953	19982	33208	3.43	2.0E-37	AA346720.1	EST_HUMAN	EST52831 Fetal heart II Homo sapiens cDNA 5' and
8575	21506	34850	0.67	2.0E-37	BE637764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8575	21508	34851	0.67	2.0E-37	BE637764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8615	21546	34887	2.9	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
11992	24934	38332	10.6	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDPT1) mRNA, complete cds
13083	25604		5.52	2.0E-37	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2100	15114	28119	5.86	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3241	16289		1.23	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-270400-016-h03 CT0347 Homo sapiens cDNA
4260	17276	30145	1.09	1.0E-37	BE872365.1	EST_HUMAN	601448619F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852662 5'
5053	18050	30903	2.8	1.0E-37	BF371716.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6238	19290		0.97	1.0E-37	7305380	NT	Mus musculus otogelin (Otog), mRNA
8793	21723	35070	0.89	1.0E-37	BE546032.1	EST_HUMAN	601072419F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
9204	22222	35580	3.18	1.0E-37	AA171406.1	EST_HUMAN	z21b02.r1 Stratiotes neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to
11071	23955	37391	0.51	1.0E-37	AV730743.1	EST_HUMAN	contains L1.12 L1 repetitive element:
11141	24070	37516	2.19	1.0E-37	M22878.1	NT	Human somatic cytochrome c (Hc1) processed pseudogene, complete cds
12696	25352		3.76	1.0E-37	BE771814.1	EST_HUMAN	GM3-FT0098-140700-243-d07 FT0098 Homo sapiens cDNA
5986	19051	32176	2.07	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56769), mRNA
1260	14266	27229	1.68	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2521	15522	28526	1.44	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153992 5'
2197	15208	28212	1.39	7.0E-38	AW672825.1	EST_HUMAN	EST384920 MAGE rescues, MAGI Homo sapiens cDNA
3089	16140	29038	1.66	6.0E-38	BF033033.1	EST_HUMAN	601465722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856248 5'
5763	18855	31961	1.38	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5783	18855	31962	1.38	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7713	20645	33942	0.56	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7780	20709	34011	0.54	6.0E-38	AJ010969.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
7780	20709	34012	0.54	6.0E-38	AJ010969.1	NT	Homo sapiens mRNA for potassium channel Kv4.2

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12278	25091		4.75	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12729	25372	31803	10.22	6.0E-38	AB002050.1	NT	Homo sapiens DNA for Human P2XM1, complete cds
750	13907	28732	1.22	5.0E-38	AW671819.1	EST_HUMAN	EST333908 MAGE resequences, MAGL Homo sapiens cDNA
2478	15480	28481	1.46	5.0E-38	AJ237740.1	NT	Homo sapiens RIBLR gene (partial), exon 8
4014	17041	29930	1.12	5.0E-38	T83107.1	EST_HUMAN	yd40h07.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to SP:OLF3 MOUSE P23275 OLFACTORY RECEPTOR ;
4014	17041	29931	1.12	5.0E-38	T83107.1	EST_HUMAN	yd40h07.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110749 5' similar to SP:OLF3 MOUSE P23275 OLFACTORY RECEPTOR ;
7378	20372	33841	1.47	5.0E-38	BE871610.1	EST_HUMAN	601450149F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3854074 5'
123	13229	26143	3.02	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
123	13229	26144	3.02	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1184	14224	27162	0.83	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2112	15125		5.04	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3761	16783		1.32	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRP4), mRNA
3922	16950	29833	2.25	3.0E-38	P53538	SWISSPROT	SSUJ72 PROTEIN
3922	16950	29834	2.25	3.0E-38	P53538	SWISSPROT	SSUJ72 PROTEIN
7058	25662	33316	6.82	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7614	20549	33941	0.84	3.0E-38	AW302461.1	EST_HUMAN	xw04d01.x1 NCJ_OGAP_Brn63 Homo sapiens cDNA clone IMAGE:2827009 3'
8015	20932		0.87	3.0E-38	AA378327.1	EST_HUMAN	EST81188 Synovial sarcoma Homo sapiens cDNA 6' end
8028	20944	34260	6.71	3.0E-38	BF373664.1	EST_HUMAN	CM3-FT10181-140700-241-407 FT10181 Homo sapiens cDNA
9209	22137	35484	2.29	3.0E-38	H85494.1	EST_HUMAN	yw85b04.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:249775 5'
9209	22137	35495	2.29	3.0E-38	H85494.1	EST_HUMAN	yw85b04.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:249775 5'
10478	23566		1.74	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
53	13170	26068	1.86	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1407	14438	27382	1.44	2.0E-38	5802097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1673	14703	27664	2.29	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 6' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1673	14703	27665	2.29	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 6' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
2432	15436	28436	1.05	2.0E-38	W76571.1	EST_HUMAN	zdf6g09.r1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:345684 5'
4695	17700	30565	2.75	2.0E-38	4557987	NT	Homo sapiens Keratin 18 (KRT18) mRNA
5252	18238	31089	0.94	2.0E-38	AA437181.1	EST_HUMAN	zvf1d09.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR:G817957 GB17957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
5270	18256	31106	0.76	2.0E-38	BE296224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532680 5'

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5270	18266	31107	0.76	2.0E-38	BE296224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
5280	18238	31089	0.76	2.0E-38	AA437181.1	EST_HUMAN	z61d09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:768128 5' similar to TR:G817957
5920	18987	32105	0.84	2.0E-38	Z26634.2	NT	G817967 GLYCINE RECEPTOR SUBUNIT ALPHA 4;
5920	18987	32106	0.84	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
8180	21087	34421	1.5	2.0E-38	AV721103.1	EST_HUMAN	Homo sapiens mRNA for ankyrin B (440 kDa)
9053	21982		4.83	2.0E-38	BE165980.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
9452	22380	35742	0.53	2.0E-38	F08450.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9517	22444	35807	1.72	2.0E-38	AF069755.1	NT	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
9762	22686		1.63	2.0E-38	BE222256.1	EST_HUMAN	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
10929	23914	37243	1.81	2.0E-38	D63479.2	NT	hu09g02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710
11683	24587	38064	4.61	2.0E-38	AA595480.1	EST_HUMAN	GAG POLYPROTEIN. ;
11683	24587	38064	4.61	2.0E-38	AA595480.1	EST_HUMAN	Homo sapiens mRNA for KIAA0145 protein, partial cds
11683	24587	38065	4.61	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.s1 NCL_CGAP_P223 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
11922	24767	38264	4.98	2.0E-38	BE712790.1	EST_HUMAN	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
12065	24906	38407	3.96	2.0E-38	AF190501.1	NT	nc34g03.s1 NCL_CGAP_P223 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
12065	24906	38408	3.96	2.0E-38	AF190501.1	NT	E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE. ;
12327	25126		6.26	2.0E-38	AV726988.1	EST_HUMAN	QV2-HT0698-080800-283-a05 HT0698 Homo sapiens cDNA
12329	25127		2.08	2.0E-38	AB012723.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12590	25287		2.05	2.0E-38	M55630.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12601	25287	31845	3.76	2.0E-38	H55641.1	EST_HUMAN	Homo sapiens gene for khesin-like protein, complete cds
12663	25334		2.34	2.0E-38	S74906.1	NT	Human topoisomerase I pseudogene 2
1120	14162		2.31	1.0E-38	AA401570.1	EST_HUMAN	CH2202580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
2015	15033	28027	1.5	1.0E-38	4885288	NT	E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
2033	15050	28047	1.07	1.0E-38	7601969	NT	zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
2517	15518	28522	2.35	1.0E-38	AF270831.1	NT	MER19 repetitive element ;
2658	15654	28654	17.84	1.0E-38	4758371	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
4430	17441	30301	3.04	1.0E-38	AL163203.2	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4430	17441	30302	3.04	1.0E-38	AL163203.2	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
							Homo sapiens fibronogen-like 1 (FGL1), mRNA
							Homo sapiens chromosome 21 segment HS21C003
							Homo sapiens chromosome 21 segment HS21C003

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4707	17712	30575	1.16	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
6260	18311	32475	4.54	1.0E-38	7305380	NT	Mus musculus ologelin (Olog), mRNA
6260	18311	32476	4.54	1.0E-38	7305380	NT	Mus musculus ologelin (Olog), mRNA
7803	20732	34034	2.59	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9686	22621	35989	0.71	1.0E-38	11422280	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9944	22849	36238	6.24	1.0E-38	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12465	25705		2.48	1.0E-38	AL163284.2	NT	MER29 repetitive element ;
57	13174	26074	4.39	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C084
1421	14452	27408	1.67	8.0E-39	4789229	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar, proton pump) 16kD (ATP6C) mRNA
1853	14875		2	8.0E-39	AB23404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
2106	15120	28123	8.87	7.0E-39	AL163227.2	NT	wh5310.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
11248	24172	37619	1.99	6.0E-39	BF331829.1	EST_HUMAN	POL PROTEIN ;
13007	25557		2.04	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1036	14082	27022	1.52	5.0E-39	AF003528.1	NT	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
3027	16079	28981	8.45	6.0E-39	AJ750154.1	EST_HUMAN	7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP.R151.8
12743	25383		2.33	6.0E-39	11420289	NT	CE00828 ;
572	13640	25549	15.64	4.0E-39	AB015610.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
3633	18699	29568	0.92	4.0E-39	AL163210.2	NT	al36b04.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
4584	17592		0.88	4.0E-39	AL163209.2	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.11 LTR7 repetitive element ;
6041	18103	32231	0.63	4.0E-39	11422113	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
6041	19103	32232	0.63	4.0E-39	11422113	NT	Chlorococcus aestivus mRNA for ribosomal protein S4X, complete cds
8653	21894	34919	0.68	4.0E-39	AA682949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
9869	22784	36172	0.61	4.0E-39	D84116.1	NT	Homo sapiens chromosome 21 segment HS21C009
9869	22784	36173	0.61	4.0E-39	D84116.1	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
12760	25393		6.23	4.0E-39	11418177	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
12862	25467		3.9	4.0E-39	BE593482.1	EST_HUMAN	ae92g04.x1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
50	13167	28062	10.7	3.0E-39	AA631949.1	EST_HUMAN	OFR.b1 OFR repetitive element ;

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
50	13167	26063	10.7	3.0E-39	AA631949.1	EST_HUMAN	hmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
50	13167	26064	10.7	3.0E-39	AA631949.1	EST_HUMAN	hmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12319	25120	38157	5.05	3.0E-39	A084557.1	EST_HUMAN	ox63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
12319	25120	38158	5.05	3.0E-39	A084557.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12360	25149		8.33	3.0E-39	H37903.1	EST_HUMAN	ox63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
922	13974		8.72	2.0E-39	BE409203.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
937	13889		41.15	2.0E-39	A1525119.1	EST_HUMAN	ox63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
1057	14101		3.78	2.0E-39	AF000573.1	NT	pp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
1553	14584		17.9	2.0E-39	AW372318.1	EST_HUMAN	801301607F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3636289 5'
1989	15007	27996	3.94	2.0E-39	AA720574.1	EST_HUMAN	prmmra-7.D01.r bvtumor Homo sapiens cDNA 5'
2675	15671	28670	2.37	2.0E-39	AL163248.2	NT	Homo sapiens homogenizate 1,2-dioxygenase gene, complete cds
4509	17519	30365	1.77	2.0E-39	BF370207.1	EST_HUMAN	PVO-BT0340-211289-003-d02 BT0340 Homo sapiens cDNA
5679	18753	31674	4.28	2.0E-39	AA509880.1	EST_HUMAN	THR repetitive element ;
7761	20891	33990	2.1	2.0E-39	AA080887.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
7958	20880	34191	0.75	2.0E-39	AL163202.2	NT	RC4-FN0037-280700-011-e10 FN0037 Homo sapiens cDNA
7958	20880	34192	0.75	2.0E-39	AL163202.2	NT	ng86f03.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693
8377	21281	34612	1.41	2.0E-39	A1638173.1	EST_HUMAN	zn06f02.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:546651 5'
8885	21815	35166	0.65	2.0E-39	AF078779.1	NT	Homo sapiens chromosome 21 segment HS21C002
10027	22927		0.55	2.0E-39	AA984531.1	EST_HUMAN	H75f09.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2137885 3' similar to TR:Q13537 Q13537
10152	23043		0.89	2.0E-39	A1686860.1	EST_HUMAN	MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
11864	24754	38249	3.66	2.0E-39	D86964.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
12228	25062	38560	1.67	2.0E-39	11526976	NT	am88c11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'
1534	14564	27524	3.13	1.0E-39	AJ006345.1	NT	Human mRNA for KIAA0209 gene, partial cds
1534	14564	27525	3.13	1.0E-39	AJ006345.1	NT	Homo sapiens GIOT-2 for gonadotropin inducible transcription repressor-2 (GIOT-2), mRNA
1554	14565	27542	6.17	1.0E-39	7857020	NT	Homo sapiens KVLQ11 gene
1754	14781	27751	1.02	1.0E-39	H55224.1	EST_HUMAN	Homo sapiens KVLQ11 gene
4033	17060	29949	1.15	1.0E-39	AB020684.1	NT	Homo sapiens KVLQ11 gene
4212	17229	30096	1.13	1.0E-39	11430303	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4212	17229	30097	1.13	1.0E-39	11430303	NT	CHR220163 Chromosome 22 exon Homo sapiens cDNA clone C22_205 5'
4725	17730	30563	0.99	1.0E-39	AW286073.1	EST_HUMAN	Homo sapiens mRNA for KIAA0877 protein, partial cds
							Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
							Homo sapiens catenin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
							UI-H-BWO-alu-h-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730850 3'

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4770	17775	30642	1.35	1.0E-39	AW951995.1	EST_HUMAN	EST364065 IMAGE resequences, MAGB Homo sapiens cDNA
4770	17775	30643	1.35	1.0E-39	AW051995.1	EST_HUMAN	EST364065 IMAGE resequences, MAGB Homo sapiens cDNA
4815	17816	30683	9.43	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
5543	18621	31496	0.84	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5543	18621	31497	0.84	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5824	18895	32008	1.77	1.0E-39	T80876.1	EST_HUMAN	Alu repetitive element; contains LTR1 repetitive element;
5861	18932	32050	5.55	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5861	18932	32051	5.55	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
7139	20247	31723	1.83	1.0E-39	11495736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7766	20696	33086	2.13	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
9127	22055	35415	1.08	1.0E-39	O46630	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
11362	24280	37723	1.48	1.0E-39	4750051	NT	Homo sapiens ribosomal protein S6 kinase, 60kD, polypeptide 5 (RPS6KA5) mRNA
577	13846	26552	2.46	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1263	14297	27242	12	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1263	14297	27243	12	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
3851	16880	28765	0.78	9.0E-40	4503784	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4037	18402	29888	4.69	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4620	17466	30323	0.72	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3088	16139	29037	0.92	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 Hela cDNA Library Homo sapiens cDNA clone 7H15A04
3998	17025		1.48	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
8177	21084	34416	2.02	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
8177	21084	34417	2.02	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11335	24254	37692	2.49	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2775	15766	28760	5	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2775	15766	28761	5	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6164	19221		2	6.0E-40	BE504768.1	EST_HUMAN	h240g01.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:3210480 3'
6387	19436		1.28	6.0E-40	7661999	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7265	20174	33415	3.95	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7265	20174	33416	3.95	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10483	23371	36784	9.8	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
10483	23371	36785	9.8	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2647	15643	28642	3.38	6.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1899	14920	27900	4.03	4.0E-40	AI686005.1	EST_HUMAN	h91b01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN. ;
2120	15133		5.66	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4496	17506	30372	12.55	4.0E-40	7682117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8468	21397	34738	0.6	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8571	21502	34945	4.56	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.1 NCL_CGAP_B14 Homo sapiens cDNA clone IMAGE:1222122
9607	22633	35902	5.67	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070600-002-H12 BN0167 Homo sapiens cDNA
9607	22633	35903	5.67	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070600-002-H12 BN0167 Homo sapiens cDNA
4230	17246	30115	1.04	3.0E-40	AI925949.1	EST_HUMAN	wt1207.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6738	19770	32980	0.61	3.0E-40	4506738	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6831	19880	33181	7.22	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8952	21882	35241	3.77	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9521	22448	35811	1.3	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9752	22676	36060	1.79	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11105	24036	37481	1.57	3.0E-40	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
11711	24613	38089	10.95	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
345	13434		7.41	2.0E-40	AI223036.1	EST_HUMAN	qg52h08.x1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
821	13876		8.11	2.0E-40	AW303888.1	EST_HUMAN	x724e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:1838847 3'
1948	14870		9.06	2.0E-40	AV731601.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S6. ;
1949	14969	27949	1.3	2.0E-40	4506188	NT	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1949	14969	27950	1.3	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2085	15099	28098	1.02	2.0E-40	AI688562.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2182	15193	28199	1.48	2.0E-40	5453592	NT	w80a11.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN. ;
							Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2740	15733		0.97	2.0E-40	BE275932.1	EST_HUMAN	601121507F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3171	16221	28112	5.08	2.0E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
5009	18007	30806	1.59	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5009	18007	30867	1.59	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5344	18327	31176	1.89	2.0E-40	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
12210	25044	38547	1.74	2.0E-40	A1377428.1	EST_HUMAN	tc35d11.x1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:2066613 3' similar to contains element L1 repetitive element;
12210	25044	38548	1.74	2.0E-40	A1377428.1	EST_HUMAN	tc35d11.x1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:2066613 3' similar to contains element L1 repetitive element;
908	13960		1.6	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2667	16663	28663	1.68	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
2735	15728		2.75	1.0E-40	BE018348.1	EST_HUMAN	b679a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17.;
2786	15776	28771	1.09	1.0E-40	BF541030.1	EST_HUMAN	602086804F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
2786	15776	28772	1.09	1.0E-40	BF541030.1	EST_HUMAN	602086804F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
3341	16387		2.04	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4720	17725	30688	2.82	1.0E-40	4508072	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6504	19548	32726	0.75	1.0E-40	W92708.1	EST_HUMAN	zh70f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
6504	19548	32727	0.75	1.0E-40	W92708.1	EST_HUMAN	zh70f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7446	20387	33656	2.17	1.0E-40	AA673201.1	EST_HUMAN	rl42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7446	20387	33657	2.17	1.0E-40	AA673201.1	EST_HUMAN	rl42f04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7602	20637	33826	0.6	1.0E-40	P26808	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
12712	25832		9.64	1.0E-40	BF334112.1	EST_HUMAN	MR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA
8500	21431	34772	1.79	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
853	15886	26850	1.4	7.0E-41	A1894384.1	EST_HUMAN	wp04f04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
853	15886	26851	1.4	7.0E-41	A1894384.1	EST_HUMAN	wp04f04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5446	18527	31253	1.12	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6241	19295	32454	3.07	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6611	19652	32836	0.88	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7334	18502	31277	0.76	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11866	24756	38250	2.03	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
12057	24898	39403	1.73	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13081	25829		8.62	7.0E-41	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
300	13393	26312	1.92	6.0E-41	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
2123	15136	28142	1.68	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSGR1), mRNA
8540	21480	34821	1.38	6.0E-41	BF513783.1	EST_HUMAN	UI-H-BW1-amp-b-03-Q-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
1824	14847	27823	1.1	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:79626 3'
4202	17220		1.23	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6827	19850		2.49	5.0E-41	BE087042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
412	13485		2.25	4.0E-41	BE156318.1	EST_HUMAN	QV0-H10367-150200-114-g09 HT0367 Homo sapiens cDNA
1125	14167	27104	1.03	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005983 5'
1433	14464	27418	15.71	4.0E-41	A027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1433	14464	27419	15.71	4.0E-41	A027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1445	14476	27435	5.91	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1661	14691	27651	6.9	4.0E-41	A1500406.1	EST_HUMAN	tm86c04.x1 NCI CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
2930	15983	28881	5.42	4.0E-41	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2930	15983	28882	5.42	4.0E-41	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4242	17258	30124	2.16	4.0E-41	X92685.1	NT	H sapiens DNase I hypersensitive site (HSS-3) enhancer element
6797	19820		1.5	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
10218	23107	36507	7.78	4.0E-41	BF304663.1	EST_HUMAN	601888065F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
12097	24938		6.55	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAAC007 5'
12873	25734		1.65	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
975	14026	26969	1.79	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4444	17455	30314	2.6	3.0E-41	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5680	18754	31675	8.05	3.0E-41	X87689.1	NT	H sapiens mRNA for putative p64 CLCP protein
6842	19681	32872	1.23	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1987 protein, partial cds
7632	20567	33862	0.64	3.0E-41	AA355168.1	EST_HUMAN	EST64683 Jurkat T-cells V1 Homo sapiens cDNA 5' end
8268	21171	34505	0.46	3.0E-41	RS4765.1	EST_HUMAN	Y75c08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154575 5'
12150	24989	38489	1.49	3.0E-41	AJ29041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
12282	25086		2.71	3.0E-41	AA609768.1	EST_HUMAN	af17f10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1847	14612	27575	12.06	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1972	14990	27973	1.69	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2233	15243	28251	1.27	2.0E-41	D66962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2285	15293	28301	5.57	2.0E-41	X99631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2876	14612	27575	5.54	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
4735	17740	30602	2.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4735	17740	30603	2.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
5729	18802	31895	0.55	2.0E-41	AA594575.1	EST_HUMAN	no1207.s1 NCL CGAP_Pher1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb.X52851_ma1
6917	19947	33187	0.68	2.0E-41	4504778	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
7944	20866	34178	0.57	2.0E-41	11439575	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
8125	21035	34384	7.09	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
8351	21255	34616	0.47	2.0E-41	11422047	NT	Homo sapiens tryptophan hydroxylase (tryptophan 5-monooxygenase) (TPH), mRNA
8846	21577	34914	1.73	2.0E-41	M86944.1	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L), mRNA
8646	21577	34915	1.73	2.0E-41	M86944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8675	21506	34948	1.42	2.0E-41	AA328285.1	EST_HUMAN	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8628	22453	35816	1.8	2.0E-41	P52742	SWISSPROT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
9951	22856	36243	0.62	2.0E-41	11417118	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
9951	22856	36244	0.62	2.0E-41	11417118	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
11917	24764	38261	2.55	2.0E-41	AA372637.1	EST_HUMAN	ZINC FINGER PROTEIN 135
12789	25417	31790	2.57	2.0E-41	AB011399.1	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
3250	16298	28202	0.93	1.0E-41	BE869735.1	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
3250	16298	29203	0.93	1.0E-41	BE869735.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
4682	17687	30554	2.78	1.0E-41	6678468	NT	Homo sapiens gene for AF-6, complete cds
7167	18439	31341	0.56	1.0E-41	H99079.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
9952	22857	36245	1.73	1.0E-41	AI217868.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
12404	25175		2.43	1.0E-41	11526291	NT	Mus musculus tubulin alpha 6 (Tubae6), mRNA
9085	22014		1.27	9.0E-42	BE179191.1	EST_HUMAN	Homo sapiens hyaluronate synthase 1 (HAS1) Homo sapiens cDNA
9716	22041	36021	2.86	9.0E-42	11530161	NT	RCO-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9716	22641	36022	2.86	9.0E-42	11530161	NT	Homo sapiens hyaluronate synthase 1 (HAS1) Homo sapiens cDNA
485	13556	26472	5.02	8.0E-42	AF003530.1	NT	Homo sapiens hyaluronate synthase 1 (HAS1) Homo sapiens cDNA
2121	15134	28140	2.62	8.0E-42	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12441	25835		61.24	8.0E-42	AA493886.1	EST_HUMAN	nt07c02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:949586 similar to TR:G434304 G434304
12459	25726						3678P EXPRESSED SEQUENCE TAG mRNA;
960	14010		2.16	8.0E-42	AW088082.1	EST_HUMAN	xc97a04.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2692174 3' similar to contains OFR.12
9040	21989		2.25	7.0E-42	AL163285.2	NT	OFR repetitive element;
9786	22750		0.65	7.0E-42	R10963.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
11616	24524	37983	1.58	7.0E-42	A1204398.1	EST_HUMAN	y33g04.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:1729174 5'
11616	24524	37994	1.44	7.0E-42	AA569592.1	EST_HUMAN	qf58g12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1764278 3'
11833	24777		1.44	7.0E-42	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1880	14901	27883	1.45	7.0E-42	AA640560.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1880	14901	27894	2.07	6.0E-42	AF012872.1	NT	nt98j06.s1 NCI_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1206635
			2.07	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
							Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2308	15316		2.49	6.0E-42	AW238656.1	EST_HUMAN	xc2803.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.L1 L1
5654	18728	31633	1.43	6.0E-42	AB028990.1	NT	repetitive element;
5918	18728	31633	1.26	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
140	13242		5.66	5.0E-42	AJ271735.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
461	13533	26453	1.77	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
509	13580		2.7	5.0E-42	5730038	NT	h3g1e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
510	13581		2.08	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6963	20010	33241	1.09	6.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6963	20010	33242	1.09	6.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
7112	20316	33580	3.11	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
							Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7568	20604	33782	2.33	6.0E-42	AF071569.1	NT	
8326	21231	34566	0.44	6.0E-42	4926977	NT	Homo sapiens reelin (RELN) mRNA
9336	22266	35629	2.5	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
11070	23954	37389	0.94	6.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11070	23954	37390	0.94	6.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11436	24352	37800	2.75	6.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
12205	25040	38543	2.03	6.0E-42	X98411.1	NT	H sapiens mRNA for myosin-II
12205	25040	38544	2.03	6.0E-42	X98411.1	NT	H sapiens mRNA for myosin-II

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
777	13834	26767	6.96	4.0E-42	AF05086.1	NT	Homo sapiens MHC class 1 region
777	13834	26768	6.96	4.0E-42	AF05086.1	NT	Homo sapiens MHC class 1 region
1083	14136	27073	1.14	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4200	17304	30173	1.25	4.0E-42	X69417.1	NT	H sapiens PROS-27 mRNA
4927	17341	30207	1.11	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4347	17361	30226	5.79	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4697	17702	30566	13.24	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
10862	23846	37272	0.78	4.0E-42	AW371201.1	EST_HUMAN	CMO-BT0282-171299-127-503 BT0282 Homo sapiens cDNA
11083	24024	37468	2.94	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-H11 ST0278 Homo sapiens cDNA
11093	24024	37467	2.94	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-H11 ST0278 Homo sapiens cDNA
1601	14532	27497	2.85	2.0E-42	BF376834.1	EST_HUMAN	RCO-TN0079-110900-024-907 TN0079 Homo sapiens cDNA
2437	15441		4.27	2.0E-42	AW993344.1	EST_HUMAN	RC3-NN0070-270400-011-H10 NN0070 Homo sapiens cDNA
2449	15453	28449	4.09	2.0E-42	AW250059.1	EST_HUMAN	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2816233 3'
5963	19030	32150	19.97	2.0E-42	AW953368.1	EST_HUMAN	EST387438 MAGE resequences, MAGEC Homo sapiens cDNA
5963	19030	32151	19.97	2.0E-42	AW953368.1	EST_HUMAN	EST387438 MAGE resequences, MAGEC Homo sapiens cDNA
6764	19798	33010	0.56	2.0E-42	M29145.1	NT	Human hepatocyte growth factor (hHGF) mRNA, complete cds
7057	20083	33315	0.91	2.0E-42	A052588.1	EST_HUMAN	ow83d05.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 3'
10356	23245	36664	1.27	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10557	23443	36864	0.58	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
10557	23443	36865	0.58	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
757	13813	26742	1.28	1.0E-42	X67147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1088	14112	27052	1.1	1.0E-42	AW285909.1	EST_HUMAN	U1-HB1-afh-e-04-Q-U1.st NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1128	14170	27107	12.36	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1128	14170	27108	12.36	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1270	15895	27254	13.15	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene
1270	15895	27255	13.15	1.0E-42	AF067166.1	NT	encoding mitochondrial protein, complete cds
1270	15895	27255	13.15	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene
1727	14754	27724	0.95	1.0E-42	11423219	NT	encoding mitochondrial protein, complete cds
2044	15061	28062	1.28	1.0E-42	AF110286.1	NT	Homo sapiens rec (LOC51201), mRNA
2575	15574	28570	1.77	1.0E-42	5174458	NT	Homo sapiens PDNPF1 gene, exon 17
3005	16057	28961	8.99	1.0E-42	4505524	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
3771	16803	28690	2.39	1.0E-42	7662027	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3771	16803	28690	2.39	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3859	16888	29773	0.99	1.0E-42	5031610	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
4000	17027	29916	1.64	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4344	17358	30223	2.1	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4859	17861	30726	1.82	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4859	17861	30727	1.82	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4891	17890	30756	6.88	1.0E-42	4506788	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5074	18071	30920	0.67	1.0E-42	Z46120.1	EST_HUMAN	HSCOFF071 normalized infant brain cDNA Homo sapiens cDNA clone c-0607
10588	23474	36801	5.15	9.0E-43	4757089	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
675	13737	26849	14.25	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
675	13737	26850	14.25	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
724	13782	26704	3.77	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
724	13782	26705	3.77	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
724	13782	26706	3.77	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5897	18966	32084	0.95	8.0E-43	H13952.1	EST_HUMAN	YC9e11.1r1 Soares placenta NB2-HP Homo sapiens cDNA clone IMAGE:148172 5'
3709	16741	29630	10.56	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
9328	22256		3.22	7.0E-43	A1936748.1	EST_HUMAN	wp69b01.x1 NCI CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2468985 3' similar to TR:O15475
1372	14404		5.64	6.0E-43	AA491890.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN; contains LTR7.b1 LTR7 repetitive element;
2633	15631		3.13	6.0E-43	AV708201.1	EST_HUMAN	ne72408.x1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:809803 similar to gb:L05095 60S
6666	19607	32792	2.69	6.0E-43	9955973	NT	RIBOSOMAL PROTEIN L30 (HUMAN);
7236	20145	33385	2.3	6.0E-43	AW468897.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
10365	23254	36674	2.34	6.0E-43	AA195164.1	EST_HUMAN	h330b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810991 3' similar to contains
11545	24454		1.91	6.0E-43	AL119186.1	EST_HUMAN	MER1.13 MER1 repetitive element;
148	13248		1.86	5.0E-43	AL163213.2	NT	z35606.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529641
526	13595	26506	3.69	5.0E-43	AA382780.1	EST_HUMAN	G529641 DB1, COMPLETE ODS; contains element P TR7 repetitive element;
2891	15845	28846	1.9	5.0E-43	AV732578.1	EST_HUMAN	DKFZp761L1712.r1 781 (synonym: harny2) Homo sapiens cDNA clone DKFZp761L1712 5'
6560	20140	33379	0.96	5.0E-43	A1613509.1	EST_HUMAN	EST98033 Testis I Homo sapiens cDNA 5' end
7231	20140	33378	0.84	5.0E-43	A1613509.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
8765	21695	35037	0.67	5.0E-43	AA442271.1	EST_HUMAN	tw22e07.x1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260462 3'
8765	21695	35038	0.67	5.0E-43	AA442271.1	EST_HUMAN	tw22e07.x1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2260462 3'
8765	21695	35039	0.67	5.0E-43	AA442271.1	EST_HUMAN	z54a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
8765	21695	35038	0.67	5.0E-43	AA442271.1	EST_HUMAN	z54a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9436	22364		0.8	5.0E-43	H74277.1	EST_HUMAN	yu49g12.r1 Scores fetal liver spleen 1N1L3 Homo sapiens cDNA clone IMAGE:229510 5'
9902	22890	36274	4.55	5.0E-43	AA465288.1	EST_HUMAN	aa33d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
10883	23768	37193	2.79	5.0E-43	AI733244.1	EST_HUMAN	co62c10.x5 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1669810 3' similar to TR:P00591 P00591 PV14 GENE.
10917	23802	37230	1.14	5.0E-43	AL049110.1	EST_HUMAN	DKFZp434D0119_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D0119
11202	24128	37575	5.3	5.0E-43	AW653007.1	EST_HUMAN	MIR2-SN0007-280400-004-c02 SN0007 Homo sapiens cDNA
999	15847	26992	3.43	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 end flanking repeat regions
5440	18522	31247	1.13	4.0E-43	AI056338.1	EST_HUMAN	oy47h03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1669013 3'
6528	19669	32854	0.76	4.0E-43	6989009	NT	Homo sapiens glycol-RNA synthetase (GARS), mRNA
7490	20430		2.01	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
8756	21685	35029	6.4	4.0E-43	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
8756	21688	35030	6.4	4.0E-43	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
10804	23680	37118	1.48	4.0E-43	6005967	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
12384	25162		3.73	4.0E-43	R20950.1	EST_HUMAN	yu08b05.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element;
1241	14277		2.63	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1721	14749	27717	0.96	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autoantigen
3632	16668	29565	1.58	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) (human, leukemic cell line SKH1, mRNA Mutant, 5938 nt)
4390	17404	30272	0.96	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
5535	18614	31463	0.5	3.0E-43	M59259.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
5535	18614	31464	0.5	3.0E-43	M59259.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
6111	19171	32303	0.79	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6616	19557	32840	1.94	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6616	19557	32841	1.94	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
7030	20056	33289	4.08	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8741	21671		5.67	3.0E-43	AA458824.1	EST_HUMAN	aa88f11.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element;
9379	22307	35688	0.82	3.0E-43	7861721	NT	Homo sapiens hypothetical protein (HSA011616), mRNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
195	13293		9.69	2.0E-43	A190764.1	EST_HUMAN	q661c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733988 3' similar to contains PTR7.13
6749	19783	32906	1.03	2.0E-43	BE222778.1	EST_HUMAN	PTR7 PTR7 repetitive element;
6749	19783	32906	1.03	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173760 3' similar to contains element
7652	20588	33882	1.13	2.0E-43	AW207390.1	EST_HUMAN	MER40 repetitive element;
8883	21813		7.74	2.0E-43	U43701.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173760 3' similar to contains element
11845	24551		3.5	2.0E-43	T03007.1	NT	MER40 repetitive element;
1676	14706	27688	3.36	1.0E-43	AF164836.1	EST_HUMAN	U11-B1-af-a-09-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
1676	14706	27688	3.36	1.0E-43	AF164836.1	NT	Human ribosomal protein L23a mRNA, complete cds
1732	14759	27730	3.31	1.0E-43	AL163284.2	NT	FB1G5 Fetal brain, Stragelene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
2771	15763	28755	4.57	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
5595	18671	31550	0.64	1.0E-43	4895544	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
6896	19928	33141	9.3	1.0E-43	4507188	NT	Homo sapiens chromosome 21 segment HS21C084
6896	19928	33142	9.3	1.0E-43	4507188	NT	602022313F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157666 5'
7304	18473	31294	1.42	1.0E-43	R19751.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8511	21442	34784	0.76	1.0E-43	AF175285.1	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
8843	21574		2.98	1.0E-43	AF198490.1	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
8995	22323	35686	31.07	1.0E-43	AW963678.1	EST_HUMAN	Y040e01.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to
10781	23667	37096	0.65	1.0E-43	AW953229.1	EST_HUMAN	SP-BD38_MOUSE P28656 BRAIN PROTEIN DN38 :
11401	24317	37764	7.46	1.0E-43	A1984961.1	EST_HUMAN	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
11804	24725	38217	4.22	1.0E-43	11424378	NT	Homo sapiens 8q22.1 region and MTG8 (GBFA2T1) gene, partial cds
12331	25129		2.53	1.0E-43	AL137894.1	EST_HUMAN	EST1375749 MAGE resequences, MAGH Homo sapiens cDNA
12584	25280	31843	4.37	1.0E-43	A1675416.1	EST_HUMAN	EST1365299 MAGE resequences, MAGB Homo sapiens cDNA
12799	25426	31794	2.19	9.0E-44	11418322	NT	w87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
915	13967	26914	7.98	8.0E-44	A1222865.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
915	13967	26915	7.98	8.0E-44	A1222865.1	EST_HUMAN	DKFZp761D1015.1 761 (synonym: harny2) Homo sapiens cDNA clone DKFZp761D1015 5'
9103	22031	35386	1.34	8.0E-44	X94354.1	NT	w69b04.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313775 3'
11350	24268	37710	1.67	8.0E-44	11423553	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
11605	24514	37883	4.61	8.0E-44	Y10498.2	NT	ch23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
12112	24983	38457	1.43	8.0E-44	L29139.1	NT	ch23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
12553	25268	31836	2.48	8.0E-44	11627389	NT	H. sapiens DNA for Cone cGMP-PDE gene
						NT	Homo sapiens similar to phosphoglucomutase 1 (H. sapiens) (LOC63246), mRNA
						NT	Homo sapiens mRNA for thymidine kinase, partial
						NT	Homo sapiens myosin mRNA, partial cds
						NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12589	25592	31739	1.51	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIH-FB2122), mRNA
12915	25753	31570	1.67	8.0E-44	11418090	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
682	13744		0.88	7.0E-44	RO6035.1	EST_HUMAN	y989e0.1.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:124920 5'
2249	15259	28287	2.16	7.0E-44	9031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3007	16059	28982	2.27	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3007	16059	28983	2.27	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3929	16957	29840	3.77	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4340	17354	30217	1.04	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4340	17354	30218	1.04	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8763	21693	35035	3.71	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
6341	19391	32560	0.73	6.0E-44	Z20946.1	EST_HUMAN	HSAADDEYU P, Human foetal Brain Whole tissue Homo sapiens cDNA
12189	26026	38626	1.7	6.0E-44	AW054060.1	EST_HUMAN	EST366120 MAGE resequences, MAGEC Homo sapiens cDNA
323	13415		2.68	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
352	13439		2.24	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
8498	21399	34739	4.6	5.0E-44	AI58523.1	EST_HUMAN	tr40d02.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9921	22909		1.7	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element;
3475	16515	29414	2.37	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
3871	16900		0.92	4.0E-44	BE165980.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
5140	18135		1.89	4.0E-44	AI435225.1	EST_HUMAN	MR3-HT0487-160200-113-g01 HT0487 Homo sapiens cDNA
7890	20816	34122	0.62	4.0E-44	BE883178.1	EST_HUMAN	tr11d02.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8847	21777	35124	0.82	4.0E-44	L21948.1	NT	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
9435	22363		0.6	4.0E-44	BE176618.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11685	24588	38068	12.08	4.0E-44	U90878.1	NT	RC3-HT0585-010400-023-d08 HT0585 Homo sapiens cDNA
2569	15558	28556	1.3	3.0E-44	BE880626.1	EST_HUMAN	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
3145	16195	29068	7.34	3.0E-44	AA169851.1	EST_HUMAN	601491529F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5'
3980	16998	29874	2.48	3.0E-44	AA337234.1	EST_HUMAN	zp18b05.1r1 Striatagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
8266	21173	34508	0.6	3.0E-44	BE884820.1	EST_HUMAN	EST42289 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
10049	22983	30354	0.65	3.0E-44	AF005273.1	NT	601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
1075	14119	27056	1.99	2.0E-44	4826683	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1075	14119	27057	1.99	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1235	14271	27214	4.6	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1235	14271	27215	4.6	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1235	14271	27215	4.6	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1338	14371	27323	2.45	2.0E-44	AF133588.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1395	14426	27380	1.25	2.0E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN
2168	15178	28184	1.68	2.0E-44	AF070851.1	NT	P22059 OXYSTEROL-BINDING PROTEIN.;
2570	15568		1.85	2.0E-44	4507592	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2612	15610	28605	1.59	2.0E-44	D25303.1	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
2653	15848		1.05	2.0E-44	5901933	NT	Human mRNA for integrin alpha subunit, complete cds
4685	17690	30557	1.83	2.0E-44	AW864378.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4901	17800	30787	1.07	2.0E-44	7706128	NT	PM4-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA
4901	17800	30788	1.07	2.0E-44	7706128	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA
6332	19382	32550	1.53	2.0E-44	11449901	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA
7178	18450	31319	1.12	2.0E-44	AF038988.1	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
7814	20743	34047	3.51	2.0E-44	11419226	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds
7814	20743	34048	3.51	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8998	21927	35281	0.82	2.0E-44	7706370	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8998	21927	35282	0.82	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
9178	22108	35484	1.61	2.0E-44	BE388058.1	EST_HUMAN	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
12243	25067		3.54	2.0E-44	BE244802.1	EST_HUMAN	601286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813586 5'
55	13172	26071	4.62	1.0E-44	7657334	NT	TCBAP1E2785 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
55	13172	26072	4.62	1.0E-44	7657334	NT	cDNA clone TCBAP2795
602	13668	26571	2.93	1.0E-44	AW853132.1	EST_HUMAN	Homo sapiens Missheper/NIK-related kinase (MINK), mRNA
1225	14262		1.53	1.0E-44	AW994803.1	EST_HUMAN	Homo sapiens Missheper/NIK-related kinase (MINK), mRNA
1595	14626		7.72	1.0E-44	AL163303.2	NT	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
2237	15247	28253	5.03	1.0E-44	AA434554.1	EST_HUMAN	RC1-EN0039-110300-012-501 EN0039 Homo sapiens cDNA
2237	15247	28254	5.03	1.0E-44	AA434554.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2810	15799	28798	2.11	1.0E-44	AF198779.1	NT	zW53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to
3789	16820		2.83	1.0E-44	AA455868.1	EST_HUMAN	contains THR13 THR repetitive element;
8841	21771	35117	1.02	1.0E-44	AW987073.1	EST_HUMAN	contains THR13 THR repetitive element;
							Homo sapiens transcription factor (GHM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein Q, and synaptophysin genes, complete cds; and L-type calcium channel a2
							aa01c09.e1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
							EST379147 IMAGE resequences, MAGJ Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	21771	35118	1.02	1.0E-44	AW967073.1	EST_HUMAN	EST376147 MAGC resequences, MAGJ Homo sapiens cDNA
9206	22134	35491	0.93	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9577	22504	35868	0.89	1.0E-44	AI337183.1	EST_HUMAN	q88g07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009628 3'
11452	24368		3.65	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11981	24804	38303	4.28	1.0E-44	10092864	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK6546.2), mRNA
12020	24862	38362	2.2	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
12020	24862	38363	2.2	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
6941	19970	33193	1.28	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2551	15551	28549	3.7	8.0E-45	6174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5217	18207	31052	10.51	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
6784	19817	33029	0.4	8.0E-45	AW892763.1	EST_HUMAN	CM4-NN0005-130300-283-b09 NN0005 Homo sapiens cDNA
8885	21616	34959	0.92	8.0E-45	AA377985.1	EST_HUMAN	EST190893 Synovial sarcoma Homo sapiens cDNA 5' end
1575	14605		1.15	6.0E-45	AI675425.1	EST_HUMAN	wb99c06.x1 NCI_CGAP_PT28 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.L1 L1 repetitive element;
4063	17089		1.03	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to SW-R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
12884	25924		1.51	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
917	13669		0.95	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2018	15036	28030	3.85	5.0E-45	BF333627.1	EST_HUMAN	CM4-CH0044-180200-515-f01 CN0044 Homo sapiens cDNA
3256	16304	29210	2.68	5.0E-45	AI623766.1	EST_HUMAN	tg94f07.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2110453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1 ;
5702	18775	31703	8.55	5.0E-45	AA397781.1	EST_HUMAN	z172d03.g1 Scores, testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
6252	18305	32467	1.25	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6252	18305	32468	1.25	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6300	19351	32519	0.95	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6300	19351	32520	0.95	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6430	19477	32653	1.15	5.0E-45	11466268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6430	19477	32654	1.15	5.0E-45	11466268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8852	21782	35129	0.82	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9593	22519	35882	1.81	5.0E-45	4759223	NT	Homo sapiens programmed cell death 3 (PDCD3), mRNA
12119	24960	38463	2.67	6.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1171	14211	27149	7.57	4.0E-45	X85826.1	NT	H. sapiens ART4 gene
2310	16318	28319	2.48	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4628	17634	30498	0.68	4.0E-45	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
9511	22438		0.98	4.0E-45	AA228220.1	EST_HUMAN	repetitive element;
3379	16422		1.33	3.0E-45	T71480.1	EST_HUMAN	y33507.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
4175	18422		1.17	3.0E-45	T71480.1	EST_HUMAN	y33507.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6484	18529	32707	1.24	3.0E-45	6753651	NT	Mus musculus dynein, exon, heavy chain 11 (Dnahe11), mRNA
6484	18529	32708	1.24	3.0E-45	6753651	NT	Mus musculus dynein, exon, heavy chain 11 (Dnahe11), mRNA
9019	21948		1.85	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
9349	22277	35639	3.43	3.0E-45	4758461	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10797	23683	37111	13.79	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10797	23683	37112	13.79	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12992	25868		2.28	3.0E-45	X99211.1	NT	H. sapiens DNA for endogenous retroviral like element
2528	15527		3.49	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3079	16130	29026	0.91	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6800	19833	33044	5.42	2.0E-45	L01685.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
8054	20967	34282	1.35	2.0E-45	BE782184.1	EST_HUMAN	601467793FT NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3970838 5'
8986	21915	35271	0.91	2.0E-45	AW834834.1	EST_HUMAN	RC0-LT0001-150200-032-d11 LT0001 Homo sapiens cDNA
11242	25697	37614	8.83	2.0E-45	BE934350.1	EST_HUMAN	MRO-HT0923-190800-201-e02 HT0923 Homo sapiens cDNA
11619	24526	37695	3.41	2.0E-45	AA458770.1	EST_HUMAN	ae87f12.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11937	24781	38277	1.76	2.0E-45	AW270280.1	EST_HUMAN	TR-G1144569 G1144569 R-SL Y1.1
11937	24781	38278	1.76	2.0E-45	AW270280.1	EST_HUMAN	x672803.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
13022	25595		4.02	2.0E-45	11418157	NT	x72803.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
128	13503		1.78	1.0E-45	BE388855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
432	13503		2.04	1.0E-45	BE388855.1	EST_HUMAN	601284360FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36006183 5'
495	13565	28484	0.97	1.0E-45	4506412	NT	601284360FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36006183 5'
1202	14241	27182	1.62	1.0E-45	7657280	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3150	16200	29092	10.58	1.0E-45	U32109.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3551	16589	29495	0.91	1.0E-45	9659558	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3634	16670	29567	0.78	1.0E-45	AB046811.1	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4590	17698	30466	7.63	1.0E-45	BE366633.1	EST_HUMAN	Homo sapiens mRNA for KIAA1591 protein, partial cds
4839	17840		1.36	1.0E-45	H57443.1	EST_HUMAN	601288116FT NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
8608	21540	34881	0.75	1.0E-45	11422236	NT	y05b02.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5'
							Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8809	21540	34882	0.75	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
9168	22098	35455	0.95	1.0E-45	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9865	22591	35984	4.71	1.0E-45	BE887843.1	EST_HUMAN	601611226F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912535 5'
10052	22968	36357	0.99	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
12435	25193	31880	3.16	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12803	26239		16.13	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12808	25302		4.79	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12887	25550	31755	3.18	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8806	21736	35086	1.96	9.0E-46	5910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9193	22121		8.32	9.0E-46	AL163209.2	NT	Homo sapiens chondrosome 21 segment HS21C009
10958	23842	37268	8.76	9.0E-46	AW246964.1	EST_HUMAN	2822449.5pifme NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822449 5'
2468	15469	28468	6.19	8.0E-46	AK33261.1	EST_HUMAN	132208.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_rna2
2468	15469	28469	6.19	8.0E-46	AK33261.1	EST_HUMAN	132208.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_rna2
8832	21563		3.52	8.0E-46	BE167244.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
4894	17699		1.67	7.0E-46	BE386185.1	EST_HUMAN	RC6-HT0508-280200-012-C12 HT0506 Homo sapiens cDNA
4821	17920		1.05	7.0E-46	BE064386.1	EST_HUMAN	601277292F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3618119 5'
6277	19328	32494	5.01	7.0E-46	8922708	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6770	19804	33015	2.69	7.0E-46	BF105845.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
12731	25373		1.73	7.0E-46	AL163246.2	NT	601822635F1 NIH_MGC 77 Homo sapiens cDNA clone IMAGE:4042736 5'
2803	15792	28791	6.23	6.0E-46	AB84381.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
2803	15792	28792	6.23	6.0E-46	AB84381.1	EST_HUMAN	WM31f08.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
5190	18182		0.79	6.0E-46	BE536440.1	EST_HUMAN	MER19 repetitive element ;
6369	19418	32584	10.85	6.0E-46	AB35448.1	EST_HUMAN	601058602F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3445177 5'
7565	20521	33808	0.85	6.0E-46	AW61244.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_K168 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
7776	20703	34008	0.41	6.0E-46	BF509740.1	EST_HUMAN	SA GENE ;
11828	23963		2.25	6.0E-46	BE784971.1	EST_HUMAN	xc42e04.x1 NCI_CGAP_U41 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:L08069 DNAJ
217	13318		5.9	5.0E-46	AL163210.2	NT	PROTEIN HOMOLOG 2 (HUMAN);
3990	16627	29630	1.56	5.0E-46	BE677194.1	EST_HUMAN	U1-H-B14-apg-b-06-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087288 3'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3590	16627	29531	1.56	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupsid_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
7039	20065	33299	1.7	5.0E-46	BF590442.1	EST_HUMAN	naa38f07.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3259757 3' similar to TR:O75202 O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
7272	20225	33473	4.46	5.0E-46	BF347229.1	EST_HUMAN	602021184f1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
7454	20394	33665	0.78	5.0E-46	AW582253.1	EST_HUMAN	QV4-ST0212-120100-075-409 ST0212 Homo sapiens cDNA
7781	20710	34013	0.48	5.0E-46	BE549744.1	EST_HUMAN	7b3b05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
684	13726		1.5	4.0E-46	AA601143.1	EST_HUMAN	no54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1731	14758	27728	2.74	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008896 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
1731	14758	27729	2.74	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008896 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
2788	15778	28774	6.51	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
4525	17534	30396	1.19	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0822 protein, partial cds
4525	17534	30397	1.19	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0822 protein, partial cds
5292	18277	31128	0.66	4.0E-46	BE044260.1	EST_HUMAN	ho42a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5292	18277	31127	0.66	4.0E-46	BE044260.1	EST_HUMAN	ho42a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5622	18698	31595	3.17	4.0E-46	M36852.1	NT	Human Ig gamma1b heavy-chain gene V region, partial cds
5622	18698	31596	3.17	4.0E-46	M36852.1	NT	Human Ig gamma1b heavy-chain gene V region, partial cds
2463	16457	28454	1.46	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
9309	22237	35598	12.37	3.0E-46	AI931492.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
12004	24848	38343	2.23	3.0E-46	D31765.1	NT	Human mRNA for KIAA0061 gene, partial cds
862	13918	28980	7.03	2.0E-46	AA488646.1	EST_HUMAN	ne08a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
1582	14613		3.73	2.0E-46	AA678246.1	EST_HUMAN	z127a1.1.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'
1667	14697	27657	6.29	2.0E-46	U79027.1	NT	Homo sapiens Bruton's tyrosine Kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
5095	18092	30940	1.72	2.0E-46	AA399286.1	EST_HUMAN	z159e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN ;
7904	20829	34132	7.26	2.0E-46	9810569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
8437	21678		1.84	2.0E-46	BE899151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12633	25314		1.86	2.0E-46	AA001788.1	EST_HUMAN	z184f12.1 Soares fetal_liver spleen_INF.S S1 Homo sapiens cDNA clone IMAGE:428015 5'
12604	25740	31670	4.32	2.0E-46	AW27214.1	EST_HUMAN	xq78h03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2756789 3'
1261	14295	27241	4.49	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
1594	14825	27585	0.98	1.0E-46	7692177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
1594	14825	27586	0.98	1.0E-46	7692177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2301	15309	28315	4.24	1.0E-46	AW978516.1	EST_HUMAN	EST390625 MAGe resequences, MAGP Homo sapiens cDNA
2422	15426	28427	5.47	1.0E-46	H97330.1	EST_HUMAN	EST488095 WATM1 Homo sapiens cDNA clone 488095
3284	16341	29243	7.22	1.0E-46	AA631912.1	EST_HUMAN	np78b02.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-11 mRNA. (HUMAN);
4981	17979		3.75	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5998	18967	32085	7.4	1.0E-46	BF194707.1	EST_HUMAN	7692501.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6206	25643	32410	5.23	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6206	25643	32411	5.23	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6938	19928	33145	0.55	1.0E-46	BF198247.1	EST_HUMAN	7n48e07.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567652 3' similar to contains element MER22 repetitive element;
11297	18967	32085	4.47	1.0E-46	BF194707.1	EST_HUMAN	7692501.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
792	13847		4.57	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
5043	18040	30898	2.99	9.0E-47	AW770928.1	EST_HUMAN	h183e04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN. ;
6637	19677	32865	0.84	9.0E-47	11425439	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
12857	25828	31488	3.56	9.0E-47	11417966	NT	Homo sapiens SEG14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1830	14853	27831	20.02	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
1830	14853	27832	20.02	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2765	15757	28752	1.39	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3069	16121	29022	2.41	8.0E-47	AJ228043.1	NT	Homo sapiens 959 kb contig between ANL1 and CBR1 on chromosome 21q22, segment 3/3
3690	16723	29616	0.68	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
3690	16723	29617	0.68	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
6371	18363	31193	0.92	8.0E-47	7682421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
12929	25739		1.76	7.0E-47	AV693284.1	EST_HUMAN	AV693284 GSK Homo sapiens cDNA clone GKASH11 5'
2579	15578	28572	4.46	6.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C946
9250	22178	35632	0.53	6.0E-47	U77054.1	EST_HUMAN	HSU77054 Human Homo sapiens cDNA clone N7
9816	22722	36105	7.41	6.0E-47	AI695189.1	EST_HUMAN	z98h02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296659 3'
10234	23125	36526	0.64	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10234	23125	36527	0.84	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6859	19891	33105	7.46	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11236	24162		3.62	5.0E-47	M78590.1	EST_HUMAN	EST007038 Fetal brain, Stratagene (cds#38206) Homo sapiens cDNA clone HFBCF07
1425	14456	27410	2.84	4.0E-47	4557656	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
7145	20253	33505	0.77	4.0E-47	BE938896.1	EST_HUMAN	MIR4-TN0108-280800-201-d04 TN0108 Homo sapiens cDNA
9050	21979	35335	2.12	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
9050	21979	35336	2.12	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
9177	22105	35463	0.83	4.0E-47	AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-005 BN0034 Homo sapiens cDNA
12063	24904		2.46	4.0E-47	AW515509.1	EST_HUMAN	xx66b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
566	13635	26545	1.77	3.0E-47	BE907634.1	EST_HUMAN	Q84292 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]:
566	13635	26546	1.77	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
843	13998	26836	3.47	3.0E-47	NS7483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
973	14024	26968	0.13	3.0E-47	AL163264.2	NT	y54b04.s1 Soares multiple sclerosis 2NblMSP Homo sapiens cDNA clone IMAGE:277827 3'
3348	16394	29295	1.59	3.0E-47	4504116	NT	Homo sapiens chromosome 21 segment HS21C084
4049	17076		6.31	3.0E-47	U93181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
6245	19299	32457	4.63	3.0E-47	AW408800.1	EST_HUMAN	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
6245	19299	32458	4.63	3.0E-47	AW408800.1	EST_HUMAN	U1-HF-BMO-adv-d-07-Q-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6845	19877		1.81	3.0E-47	A1222413.1	EST_HUMAN	U1-HF-BMO-adv-d-07-Q-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7775	20705	34006	0.67	3.0E-47	A1819755.1	EST_HUMAN	qh04e07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7775	20705	34007	0.67	3.0E-47	A1819755.1	EST_HUMAN	W11Th08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9391	22319	35061	0.73	3.0E-47	AW963786.1	EST_HUMAN	W11Th08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
9391	22319	35062	0.73	3.0E-47	AW963786.1	EST_HUMAN	EST375869 MAGe resequences, MAG1 Homo sapiens cDNA
158	13258	26176	1.28	2.0E-47	4505318	NT	EST375869 MAGe resequences, MAG1 Homo sapiens cDNA
994	14044	26966	1.85	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
994	14044	26967	1.85	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1587	14618		1	2.0E-47	A189279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1616	14646	27608	1.39	2.0E-47	7662109	NT	Homo sapiens chromosome 21 segment HS21C009
1704	14733	27689	3.63	2.0E-47	AA524514.1	EST_HUMAN	wq96b02.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2478851 3'
2247	16267	28263	1.12	2.0E-47	AF060588.1	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
4456	17467	30324	2.07	2.0E-47	4504866	NT	hg43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
4491	17602	30365	2.02	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
4491	17602	30366	2.02	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4627	17633	30497	3.41	2.0E-47	5174648	NT	nf23g07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914652
							nf23g07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914652
							Homo sapiens Reu1Rex activation domain binding protein-related (RAB-R) mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5954	18059	32186	0.84	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6205	19261	32408	1.39	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6205	19261	32409	1.39	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
8163	26684		1.43	2.0E-47	LC0731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8404	21307	34639	0.4	2.0E-47	11410317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
8542	21473	34814	0.85	2.0E-47	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8542	21473	34815	0.95	2.0E-47	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9277	22205	35562	1.35	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
10022	22822	36310	0.88	2.0E-47	11528138	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
12424	25866	31472	2.43	2.0E-47	R42423.1	EST_HUMAN	y92808.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29968 3' similar to contains OFR repetitive element ;
1430	14401	27413	3.11	1.0E-47	A533428.1	EST_HUMAN	qb99103.x1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:1631189 3'
3895	16924	29800	0.98	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3895	16924	29801	0.98	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
6210	18200	31044	3.06	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
7395	20094	33328	27.78	1.0E-47	A880886.1	EST_HUMAN	at19e08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995
9426	22354		2.21	1.0E-47	AW664648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10842	23728	37151	2.62	1.0E-47	L30115.1	NT	h84a11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M26326
1635	14685	27627	4.36	9.0E-48	AF223391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3617	16653	29554	0.73	9.0E-48	BF359947.1	EST_HUMAN	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
5877	18946	32062	0.74	9.0E-48	BE888196.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5877	18946	32063	0.74	9.0E-48	BE888196.1	EST_HUMAN	CM2-MT0100-310700-290-005 MT0100 Homo sapiens cDNA
6338	19388	32557	0.49	9.0E-48	A833168.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
6470	19515	32690	0.73	9.0E-48	AU123240.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
11556	24465	37830	3.65	9.0E-48	BE393813.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844
1278	14312		2.99	8.0E-48	4501900	NT	O60844 HOMOLOG OF RAT ZMOGEN GRANULE MEMBRANE PROTEIN. ;
1279	14312		2.87	8.0E-48	4501900	NT	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
							601370478F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							H661b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3180	16230	29124	4.26	8.0E-48	AW768477.1	EST_HUMAN	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3180	16230	28125	4.26	8.0E-48	AW768477.1	EST_HUMAN	hK61b03.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb.X64707
513	13584		1.61	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
514	13584		12.95	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1663	14693	27653	5	7.0E-48	5730038	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
6838	19668	33082	24.59	7.0E-48	11416831	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
3660	16395	29591	0.69	6.0E-48	A1761111.1	EST_HUMAN	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
4802	17803	30670	0.91	6.0E-48	AA746867.1	EST_HUMAN	w69h03.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:23988613 3'
6293	19344	32512	0.98	6.0E-48	AB006955.1	NT	h64d04.s1 NCI CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1267015
7093	20299	33560	0.81	6.0E-48	11420995	NT	Homo sapiens mRNA for ALE-75, complete cds
7877	25678	34105	0.6	6.0E-48	AB046844.1	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7877	25678	34106	0.6	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1924 protein, partial cds
9668	22594	35969	1.83	6.0E-48	AF026816.1	NT	Homo sapiens mRNA for KIAA1924 protein, partial cds
10070	22985	36378	1.91	6.0E-48	11427428	NT	Homo sapiens putative oncogene protein mRNA, partial cds
10212	23103	36504	3.65	6.0E-48	AA189080.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
2267	15277	28283	1.09	5.0E-48	4827059	NT	zq45b08.s1 Striatogene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element;
2277	15283	28294	0.91	5.0E-48	4827059	NT	Homo sapiens xylokinase (H. Influenzae) homolog (XYLB) mRNA
3355	18400	29300	2.09	5.0E-48	4826991	NT	Homo sapiens xylokinase (H. Influenzae) homolog (XYLB) mRNA
11395	24311	37757	3.3	4.0E-48	A1820420.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
1412	14443	27396	1.26	3.0E-48	AV690954.1	EST_HUMAN	Iu47a02.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2264154 3'
1992	15010	27969	7.65	3.0E-48	4885170	NT	AV690954 GKG Homo sapiens cDNA clone GKCDRE12 5'
1992	15010	28000	7.65	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3479	16519	29418	1.04	3.0E-48	AF172453.1	NT	Homo sapiens oploid growth factor receptor mRNA, complete cds
3698	16730	29621	1.22	3.0E-48	AW664531.1	EST_HUMAN	h14b12.x1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872265 3' similar to SW:DCRB_HUMAN
6112	19172	32304	2.29	3.0E-48	BE084571.1	EST_HUMAN	P93555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
7364	20358	33627	1.04	3.0E-48	AF087913.1	NT	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
8962	21892		3.97	3.0E-48	AA659990.1	EST_HUMAN	Human endogenous retrovirus HERV-P-147D
11309	24228	37674	7.05	3.0E-48	BF514170.1	EST_HUMAN	nv03f05.s1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
5	13121	26008	1.1	2.0E-48	AA465007.1	EST_HUMAN	PTR5 repetitive element ;
48	13165	28059	1.64	2.0E-48	AA631940.1	EST_HUMAN	U1-H-BW1-enl-a-10-0-U1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
							z80c03.r1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
							fmc67 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone OR17-28

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4648	17654	30520	1.34	2.0E-48	BE240085.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia BAYLOR-HQSC project=TCBA Homo sapiens cDNA clone TCBAP3842
6025	19087	32212	0.69	2.0E-48	AA613171.1	EST_HUMAN	nc18g01.s1 NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1101072 3'
6025	19087	32213	0.69	2.0E-48	AA613171.1	EST_HUMAN	nc18g01.s1 NCI_CGAP_Phet Homo sapiens cDNA clone IMAGE:1101072 3'
7942	20864	34174	3.76	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7942	20864	34175	3.76	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7959	20881	34193	4.86	2.0E-48	11496238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8928	21858	35213	1.38	2.0E-48	AV743451.1	EST_HUMAN	AV743451 OB Homo sapiens cDNA clone CBCOG10 5'
12393	13121	26008	3.07	2.0E-48	AA465007.1	EST_HUMAN	z80c03.r1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:810052 5'
12700	25794	31580	2.02	2.0E-48	BE737154.1	EST_HUMAN	601305064f1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
59	13175	26076	46.78	1.0E-48	7706634	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
898	13951	26898	4.8	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1103	14146	27084	2.39	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kd) (p100), mRNA
1103	14146	27085	2.39	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kd) (p100), mRNA
1322	14356	27303	2.88	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1934	14955	27932	25.02	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
3547	16585	29480	0.95	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21G046
6541	19584	32768	0.94	1.0E-48	AI889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14589 SIMILARITY TO U73941 ;
6541	19584	32769	0.94	1.0E-48	AI889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14589 SIMILARITY TO U73941 ;
6778	19810		0.91	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6880	19910	33125	0.56	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6880	19910	33126	0.56	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7630	20565	33859	2.99	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9754	22678	36063	1.03	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9808	22714	36097	7.14	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
10111	23002	36398	4.69	1.0E-48	BF304683.1	EST_HUMAN	60188098f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10568	23744	37167	4.48	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10568	23744	37168	4.48	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
2022	15040	28034	1.25	8.0E-49	AB026497.1	NT	Mus musculus MyoPDZ mRNA for myosin containing PDZ domain, complete cds
6288	19339	32506	3.39	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6288	18339	32507	3.39	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
7156	20264	33518	0.57	8.0E-49	AA642035.1	EST_HUMAN	nc18103.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184021 5'
8871	21801	35155	4.49	8.0E-49	U23850.1	NT	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10495	23333	36795	1.43	8.0E-49	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
144	13488	26407	2.05	7.0E-49	6729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
144	13488	26408	2.05	7.0E-49	6729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
415	13488	26407	2.48	7.0E-49	6729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
415	13488	26408	2.48	7.0E-49	6729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
416	13488	26407	2.71	7.0E-49	6729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
416	13488	26408	2.71	7.0E-49	6729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
1249	14285	27228	1.88	7.0E-49	AL163284.2	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
4759	17764	30627	1.02	7.0E-49	O80811	SWISSPROT	Homo sapiens chromosome 21 segment HS21C084
5645	18719	31623	1.71	7.0E-49	AI807191.1	EST_HUMAN	HYPOTHETICAL PROTEIN DJ816O24.3
5656	18730	31636	1.09	7.0E-49	AL120937.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23566683 3' similar to TR:O54923
6016	18719	31623	1.07	7.0E-49	AI807191.1	EST_HUMAN	OS4923 RSEC15 ;
210	13309	26226	29.3	6.0E-49	AW731740.1	EST_HUMAN	DKFZp762C033_s1 762 (synonym: hme12) Homo sapiens cDNA clone DKFZp762C033 3'
6045	19107	32237	0.49	6.0E-49	AW511225.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:U17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
6710	19746	32949	0.69	6.0E-49	AI140742.1	EST_HUMAN	hd44a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
7815	20744	34049	0.56	6.0E-49	AW511225.1	EST_HUMAN	hd44a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
11725	24627	38107	4.36	6.0E-49	AW452218.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'
12088	24929	38433	3.13	6.0E-49	AA366556.1	EST_HUMAN	hd44a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95636
12088	24928	38434	3.13	6.0E-49	AA366556.1	EST_HUMAN	O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
12695	25723	26716	9.03	6.0E-49	AA707587.1	EST_HUMAN	UI-H-B13-elo-a-05-0-UJ.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088048 3'
735	13793	26717	6.77	5.0E-49	AL163210.2	NT	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
735	13793	26717	6.77	5.0E-49	AL163210.2	NT	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
735	13793	26717	6.77	5.0E-49	AL163210.2	NT	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
1817	14841	27816	6.22	5.0E-49	AA172121.1	EST_HUMAN	z29c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN ; contains LTR7.3 LTR7 LTR7 repetitive element ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2799	15788	28787	6.37	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3317	16364	29264	2.42	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metalloprotein 1) (H. sapiens) (LOC33362), mRNA
548	13617	26524	26.58	4.0E-49	AW189533.1	EST_HUMAN	x08b01.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2875593 3' similar to WP:B0350.2B
7616	20551	33843	0.56	4.0E-49	Z28834.2	NT	CE08703;
7616	20551	33844	0.56	4.0E-49	Z28834.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7648	20582	33879	0.64	4.0E-49	11525737	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7648	20582	33880	0.64	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
7908	20833	34135	0.45	4.0E-49	AB002354.2	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
8925	21230	34565	0.7	4.0E-49	7682209	NT	Homo sapiens mRNA for KIAA0356 protein, partial cds
12565	25918		4.86	4.0E-49	AA210798.1	EST_HUMAN	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
12648	25323		12.03	4.0E-49	AF240786.1	NT	z8005.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682977 5'
582	13650	28556	1.04	3.0E-49	X68968.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2896	15690		3.49	3.0E-49	AA016131.1	EST_HUMAN	H. sapiens mRNA for acetyl-CoA carboxylase
5105	18102	30950	2.73	3.0E-49	U46999.1	NT	z831cd5.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1 repetitive element;
7820	20749	34054	9.14	3.0E-49	H39479.1	EST_HUMAN	Human type IV collagen (COL4A6) gene, exon 40
11748	24649	38130	1.84	3.0E-49	AA337561.1	EST_HUMAN	EST25612 WATM1 Homo sapiens cDNA clone 25e12
684	13746		2.4	2.0E-49	BE165980.1	EST_HUMAN	EST42672 Endometrial tumor Homo sapiens cDNA 5' end
3269	16317	29220	1.4	2.0E-49	N28446.1	EST_HUMAN	MR3-H10487-150200-113-g01 H10487 Homo sapiens cDNA
3629	18655	29563	0.95	2.0E-49	AF026564.1	NT	yc23d06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262571 5'
4924	17923	30787	0.71	2.0E-49	BF511846.1	EST_HUMAN	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
7040	20066	33300	1.16	2.0E-49	AV717938.1	EST_HUMAN	U1-H-B14-aps-d-02-Q-U1.s1 NCI_CGAP_Sut88 Homo sapiens cDNA clone IMAGE:3088638 3'
8678	21809		3.33	2.0E-49	M86033.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DCBALB01 5'
12326	25801		1.83	2.0E-49	Y10776.1	NT	EST02558 Fetal brain, Siralagene (cat#938206) Homo sapiens cDNA clone HFBCEY60
12857	25811		2.85	2.0E-49	AF163884.1	NT	H. sapiens mRNA for CAP-binding protein complex interacting protein 1
924	13976		4.83	1.0E-49	BF033327.1	EST_HUMAN	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
1578	14806	27566	13.36	1.0E-49	4557887	NT	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1823	14846	27822	2.37	1.0E-49	BE255216.1	EST_HUMAN	Homo sapiens keratin 18 (KRT18) mRNA
5544	18622	31498	5.98	1.0E-49	BF131007.1	EST_HUMAN	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
							601820053F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4052052 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6314	19364	32534	0.89	1.0E-49	H18291.1	EST_HUMAN	yn48h04.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
6320	19370	32539	1.54	1.0E-49	AW964940.1	EST_HUMAN	EST376713 MAGE resequences, MAGH Homo sapiens cDNA
7586	20522	33809	0.51	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCV11 5'
7586	20522	33810	0.51	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCV11 5'
7592	20528	33818	2.76	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3620863 5'
7592	20528	33819	2.76	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3620863 5'
7682	20616	33915	2.16	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta 81c6weeks 2NbHP8t9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X66873 KINESIN HEAVY CHAIN (HUMAN);
7682	20616	33916	2.16	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta 81c6weeks 2NbHP8t9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X66873 KINESIN HEAVY CHAIN (HUMAN);
8656	21587	34923	1.14	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8656	21587	34924	1.14	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9233	22161		0.71	1.0E-49	9694184	NT	Homo sapiens RNA binding motif protein 7 (LOC81120), mRNA
8544	22471	35829	1.35	1.0E-49	BE403340.1	EST_HUMAN	601300392F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3635398 5'
10626	23512	36945	1.34	1.0E-49	AL043128.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5'
11487	24339	37849	1.49	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDWAE04 5'
11755	24656	38139	5.93	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12560	25272		2.1	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6669	25979		0.86	9.0E-50	BE298768.1	EST_HUMAN	601176250F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3531588 5'
180	13280	26195	2.73	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
742	13800	26724	1.67	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
742	13800	26725	1.67	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1058	14102		14.95	8.0E-50	AF000573.1	NT	Homo sapiens homogenitase 1 2-dioxygenase gene, complete cds
1788	14814	27783	2.7	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1), mRNA
2780	15741	28736	1.28	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
4199	17218	30084	0.98	8.0E-50	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
642	13703	28810	2.14	7.0E-50	BE089591.1	EST_HUMAN	QY0-B10703-280400-211-e08 B10703 Homo sapiens cDNA
7092	20258	33558	0.76	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150600-011-A12 TN0073 Homo sapiens cDNA
7092	20258	33559	0.76	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150600-011-A12 TN0073 Homo sapiens cDNA
							nc89e12.s1 NCL CGAP_C09 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X69391 60S
7688	20621	33921	0.73	7.0E-50	AA627822.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
11186	24122	37568	16.2	7.0E-50	A1872137.1	EST_HUMAN	wm56g11.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:2439908 3'
4452	17462		0.79	6.0E-50	BE784381.1	EST_HUMAN	601589565F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3943577 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8792	21722		6.08	6.0E-50	BE044076.1	EST_HUMAN	ho36h04.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28.b3 MER28 repetitive element;
11254	24178	37626	2.63	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
11254	24178	37627	2.63	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1816	14840	27814	1.17	6.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
1816	14840	27815	1.17	6.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
9638	22664		4.38	6.0E-50	AA557683.1	EST_HUMAN	n45h10.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043883 similar to contains PTR5.3 PTR5 repetitive element;
942	13993		1.64	4.0E-50	AA601143.1	EST_HUMAN	no54e09.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104620 3' similar to gb.X63741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3509	16547	29447	1.19	4.0E-50	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
6921	19661	32846	0.53	4.0E-50	11440683	NT	Homo sapiens cytochrome P-450 2C8 (CYP2C8), mRNA
7804	20339	33828	0.94	4.0E-50	BE087536.1	EST_HUMAN	QV1-BT0681-260300-127-f12 BT0681 Homo sapiens cDNA
13089	25945		1.54	4.0E-50	AA769866.1	EST_HUMAN	z18b09.s1 Soares fetal liver spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:431129 3'
1953	14973		4.69	3.0E-50	MT8048.1	NT	Human endogenous retrovirus RTVL-H2
2544	15544	28542	1.08	3.0E-50	BE259196.1	EST_HUMAN	601109717F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3350309 5'
3342	16388	29288	1.01	3.0E-50	AA746142.1	EST_HUMAN	6503f06.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
6973	20000	33230	0.53	3.0E-50	11419317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6973	20000	33231	0.53	3.0E-50	11419317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
7070	20276	33531	1.46	3.0E-50	11421514	NT	Homo sapiens similar to sema domain, Immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
8093	21005	34328	4.33	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8093	21005	34329	4.33	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
9145	22073	35435	0.65	3.0E-50	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10333	23222	36638	0.82	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
10342	23231	36649	1.09	3.0E-50	11418514	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA
10998	23862	37313	0.77	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0298 gene, partial cds
11546	24455	37917	1.86	3.0E-50	11436995	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
11996	23996	37434	7.68	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
804	13959		4.48	2.0E-50	AF055086.1	NT	Homo sapiens MHC class 1 region
1107	14149	27089	5.31	2.0E-50	4567752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1461	14492	27454	4.01	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4380	17374	30237	0.71	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
7183	20183	33437	0.58	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001609 5'
8891	21821	35172	1.01	2.0E-50	AB038182.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8891	21821	36173	1.01	2.0E-50	AB038182.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
9024	21953	35310	5.27	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
9024	21953	35311	5.27	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10396	23265	36706	1.64	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
10396	23265	36707	1.64	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12087	24928		1.59	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
484	13555	26471	1.52	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2388	15393		13.03	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8161	21068		1.07	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10690	23576	37006	1.34	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6212	19267	32418	1.16	9.0E-51	AW511225.1	EST_HUMAN	h444d02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2812378 3' similar to TR:O56536
6469	19514	32689	0.93	9.0E-51	AA744837.1	EST_HUMAN	O98686 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II. ;
							ny67h03.s1 NCI_CGAP_G0581 Homo sapiens cDNA clone IMAGE:1283391 3'
9230	22158	35512	0.65	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#537210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
9864	22779	36168	1.19	9.0E-51	AA043738.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
							zk51c09.r1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486362 5'
10032	22892	36318	0.6	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#537210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
							SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
10032	22932	36319	0.6	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#537210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
11907	24007	37448	2.9	9.0E-51	H89078.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
11907	24007	37449	2.9	9.0E-51	H89078.1	EST_HUMAN	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
4545	17554	30415	2.45	8.0E-51		NT	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
4545	17554	30416	2.45	8.0E-51		NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4684	17689	30556	1.86	8.0E-51	AA610842.1	EST_HUMAN	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
7534	20473	33761	0.49	8.0E-51	AF064254.1	NT	np08e09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:U12671_mn1
8101	21013	34339	1.85	8.0E-51		NT	HETEROGEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
9997	22814		1.01	8.0E-51	AU138590.1	EST_HUMAN	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
							Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-36), mRNA
							AU138590 PLACET Homo sapiens cDNA clone PLACE100887 5'
3062	16114	29017	1.14	7.0E-51	AW274720.1	EST_HUMAN	xr34e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q92340
							Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3326	16372	29273	1.53	7.0E-51	AW889219.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3418	16460	29366	0.66	7.0E-51	AW274720.1	EST_HUMAN	xn34a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q92340
4264	17280	30149	1.50	7.0E-51	AL078628.1	EST_HUMAN	Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
4264	17280	30150	1.56	7.0E-51	AL078628.1	EST_HUMAN	DKFZp43B2229_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp43B2229 5'
4359	17373	30236	2.19	7.0E-51	11421595	NT	DKFZp43B2229_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp43B2229 5'
4461	17472	30328	1.22	7.0E-51	AW285603.1	EST_HUMAN	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
1550	14581	27541	0.92	6.0E-51	6678763	NT	U1H-BW0-ai-p-05-0-U1.61 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2728817 3'
1995	15013	28003	5.46	6.0E-51	7657266	NT	Homo sapiens putative DNA binding protein (M86), mRNA
3333	16571	29475	15.72	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4413	17424	30286	1.06	6.0E-51	6910563	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4413	17424	30286	1.06	6.0E-51	9910563	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6222	19277	32431	122.6	6.0E-51	X01788.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6233	19287	32445	9.71	6.0E-51	AF070083.1	NT	Human lactoglobulin related (Hlr) gene exon 3
6233	19287	32446	9.71	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
7066	20272	33528	1.03	6.0E-51	4506736	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
7219	20219	33466	0.72	6.0E-51	11416761	NT	Homo sapiens ribosomal protein S8 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7301	18470	31292	1.92	6.0E-51	11429665	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
9880	22605	35978	0.73	6.0E-51	11428525	NT	Homo sapiens cerebral cell adhesion molecule (LOC61148), mRNA
9880	22605	35979	0.73	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
10208	23099	36499	1.66	6.0E-51	7661535	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
10282	23172	36594	0.78	6.0E-51	U50093.1	NT	Homo sapiens B9 protein (B9), mRNA
11703	24605	38080	1.67	6.0E-51	11526289	NT	Human ankyrin (ANK1) gene, exon 2
11960	24803	38301	1.4	6.0E-51	5453949	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
11960	24803	38302	1.4	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
818	13873	26810	7.71	5.0E-51	AL163203.2	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
829	13884	26822	1.66	5.0E-51	4507500	NT	Homo sapiens chromosome 21 segment HS21C003
1018	15890	27010	1	5.0E-51	AL133204.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1630	14660	27623	1.08	5.0E-51	5031980	NT	Novel human gene mapping to chromosome X
2634	15632	28628	11.15	5.0E-51	AJ007558.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
							Homo sapiens mRNA for nucleoporin 156

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4022	17049	26938	1.37	5.0E-51	M80938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4022	17049	26938	1.37	5.0E-51	M80938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5208	18197	31040	1.46	5.0E-51	AB037832.1	NT	Human sapiens mRNA for KIAA1411 protein, partial cds
11726	24628	38108	4.77	5.0E-51	5803136	NT	Human sapiens RNA binding motif protein 3 (RBM3), mRNA
139	13241	26160	13.51	3.0E-51	AI587348.1	EST_HUMAN	trb1c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326
1204	14243	27184	39.82	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4434	17445	30305	2.75	3.0E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
8014	20831	34249	1.88	3.0E-51	R15914.1	EST_HUMAN	ya47c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4
8988	22326		3.71	3.0E-51	M29063.1	NT	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
12851	25462		2.17	3.0E-51	AF003528.1	NT	Human hnRNP C3 protein mRNA
387	13471	26389	1.68	2.0E-51	4507798	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
712	13771	26687	1.61	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
712	13771	26688	1.61	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1714	14742	27711	9.09	2.0E-51	AA233392.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
3795	16826	29713	3.81	2.0E-51	AI492415.1	EST_HUMAN	zr30a05.r1 Stratagene NT2 neuronal precursor 987230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233228 G233228 RTV-L-H PROTEIN. ; contains LTR7.3 LTR7 repetitive element;
4610	17618	30480	0.74	2.0E-51	AW137826.1	EST_HUMAN	tr27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
5388	18370	31209	0.68	2.0E-51	AI381520.1	EST_HUMAN	U1H-B11-adj-d02-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5824	18700	31598	0.48	2.0E-51	AI732851.1	EST_HUMAN	tr76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092622 3' similar to TR:P93107
5824	18700	31599	0.48	2.0E-51	AI732851.1	EST_HUMAN	P83107 PF20. ;
5824	18700	31599	0.48	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
6246	18301	32461	3.15	2.0E-51	BE782016.1	EST_HUMAN	P35436 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
7693	20625		0.76	2.0E-51	AF219927.1	NT	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
7693	20625		0.76	2.0E-51	AF219927.1	NT	P35436 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
7693	20625		0.76	2.0E-51	AF219927.1	NT	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7693	20625		0.76	2.0E-51	AF219927.1	NT	Homo sapiens diacylglycerol kinase iota (DGKI) gene, exon 23
7693	20625		0.76	2.0E-51	AF219927.1	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
9256	22184	35539	2.11	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9256	22184	35539	2.11	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9596	22512	35875	0.97	2.0E-51	11037064	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
10043	22959	36347	2.08	2.0E-51	A917078.1	EST_HUMAN	ts74e07.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
10130	23021	36416	7.06	2.0E-51	BE165980.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
10145	23036	36434	0.65	2.0E-51	AB007926.1	NT	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10914	23799	37228	1.86	2.0E-51	AV682474.1	EST_HUMAN	Homo sapiens mRNA for KIAA0457 protein, partial cds
10951	23835	37262	1.14	2.0E-51	AA378559.1	EST_HUMAN	AV682474.GKB Homo sapiens cDNA clone GKBAGF05 5'
11770	18700	31598	7.84	2.0E-51	AF732851.1	EST_HUMAN	EST191298 Synovial sarcoma Homo sapiens cDNA 5' end
11770	18700	31599	7.84	2.0E-51	AF732851.1	EST_HUMAN	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
12843	25455	31779	1.81	2.0E-51	11419159	NT	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
118	13226	26138	14.5	1.0E-51	4503528	NT	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
1511	14542	30389	15.85	1.0E-51	AV742248.1	EST_HUMAN	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
4515	17524	30390	1.8	1.0E-51	4759071	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4
4515	17524	30390	1.8	1.0E-51	4759071	NT	(MLLT4), mRNA
5574	18652	31530	3.19	1.0E-51	T18862.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
8098	21010	34336	0.91	1.0E-51	AE572332.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBC12 5'
8482	21413	34750	0.94	1.0E-51	BF434359.1	EST_HUMAN	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
12191	26995		2.17	1.0E-51	AV760590.1	EST_HUMAN	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
11130	24050	37508	1.71	9.0E-52	R91638.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b12056
11130	24050	37507	1.71	9.0E-52	R91638.1	EST_HUMAN	ts39g02.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
12643	25319		7.46	9.0E-52	AA777621.1	EST_HUMAN	7086b02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644091 3' similar to TR:P87892 P87892
162	13263	26161	0.39	8.0E-52	AA720574.1	EST_HUMAN	PROTEASE ;
1515	14546	27508	1.32	8.0E-52	X84900.1	NT	AV760590 MDJ5 Homo sapiens cDNA clone MDSCEB02 5'
1681	14711	27673	2.22	8.0E-52	11988028	NT	y410h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196567 5' similar to
							SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3 REGION ;
							y410h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196567 5' similar to
							SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3 REGION ;
							z195a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to
							contains THR13 THR repetitive element ;
							tm21g02.s1 NCI_CGAP_G060 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
							THR repetitive element ;
							H.sapiens mRNA for laminin-5, alpha3b chain
							Homo sapiens hypothetical protein FLJ13556 similar to N-mye downstream regulated 3 (FLJ13556), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1681	14711	27674	2.22	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4080	14711	27673	8.4	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4080	14711	27674	8.4	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7940	20862	34170	1.36	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7940	20862	34171	1.36	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9665	22492	35854	1.91	7.0E-52	W56471.1	EST_HUMAN	z659e06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:328578 5' similar to contains Alu repetitive element;
1215	14253		0.82	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271299-049-d07 BT0537 Homo sapiens cDNA
1720	14748	27716	6.03	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5929	18936	32115	2.45	6.0E-52	AL208794.1	EST_HUMAN	qg44f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11657	24563	38035	1.97	6.0E-52	BE048172.1	EST_HUMAN	tz48f04.y1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE Q05763 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR;
1688	14719	27680	1.1	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1811	14836	27807	1.09	4.0E-52	4758843	NT	Homo sapiens nucleoporin 168kD (NUP165) mRNA
4001	17028	29917	0.65	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4863	17855	30720	0.86	4.0E-52	AJ766814.1	EST_HUMAN	w189b02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
5469	18550	31391	1.26	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5469	18550	31392	1.26	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
8616	21547	34898	2.19	4.0E-52	BE622032.1	EST_HUMAN	601440887F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
9098	22027	35383	4.17	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12485	25228		3.77	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12950	25513		8.17	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM1, complete cds
4181	17201		13.74	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
584	13652	26557	1.34	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
584	13652	26558	1.34	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2027	15044	28039	1.17	2.0E-52	AB033075.1	NT	Homo sapiens mRNA for KIAA1249 protein, partial cds
2522	15523	28527	1.47	2.0E-52	BE207576.1	EST_HUMAN	b568b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2785	15775		11.64	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6098	18095	30942	4.53	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5138	18133	30975	1.63	2.0E-52	A1141802.1	EST_HUMAN	q45605.s1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5138	18133	30976	1.63	2.0E-52	A1141802.1	EST_HUMAN	q45605.s1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5902	18971	32089	3.3	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231289-059-E12 CT0214 Homo sapiens cDNA
6927	19667	32852	1.71	2.0E-52	11141868	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
7011	20038	33271	0.95	2.0E-52	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7273	20226	33474	0.76	2.0E-52	A1792146.1	EST_HUMAN	os43d12.y6 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
8339	21244	34577	0.64	2.0E-52	5032168	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8339	21244	34578	0.64	2.0E-52	5032168	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
9212	22140		7.92	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
9491	22419	35781	0.82	2.0E-52	AA778785.1	EST_HUMAN	z145g05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
10012	22829		1.26	2.0E-52	4788788	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (16kD) (NADH-coenzyme Q reductase) (NDUFB5) mRNA
10816	23502	36935	5.77	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10816	23502	36936	5.77	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11653	24559	38029	3.32	2.0E-52	A1831462.1	EST_HUMAN	w149c04.x1 NCL_CGAP_Lu10 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2
11653	24559	38030	3.32	2.0E-52	A1831462.1	EST_HUMAN	THR repetitive element ;
11684	24570	38046	3.19	2.0E-52	AV715377	EST_HUMAN	AV715377 DGB Homo sapiens cDNA clone DGBAIE03 6'
11791	24713		1.44	2.0E-52	W70260.1	EST_HUMAN	z048g12.r1 Soares_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:344038 5'
12043	24884		2.92	2.0E-52	11417890	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
12317	25052	31359	14.39	2.0E-52	AW236297.1	EST_HUMAN	xt72e07.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element ;
12684	26343		5.81	2.0E-52	A1808985.1	EST_HUMAN	w167d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859
556	13625	26534	1.62	1.0E-52	AA634445.1	EST_HUMAN	Q16859 CARBOXYLESTERASE ;
1398	14428	27383	6.3	1.0E-52	4504026	NT	z175h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
2564	15563		2.01	1.0E-52	4502238	NT	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA
3107	16168	28053	1.42	1.0E-52	S61070.1	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
5516	18596	31443	4.46	1.0E-52	M29426.1	NT	pol-reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 680 nt]
6857	18696	32892	2.18	1.0E-52	U98984.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
7834	20762	34065	2.57	1.0E-52	X07282.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
						NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8384	21288	34620	0.45	1.0E-52	U60017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
9034	21953		1.2	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9730	22655	36038	1.06	1.0E-52	AF078770.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11049	23833		0.89	1.0E-52	AW020370.1	EST_HUMAN	cd08g05.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
11059	23943		1.24	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11204	24130	37578	1.87	1.0E-52	U48288.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
3858	18885	29769	0.82	9.0E-53	4608084	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4499	17509	30375	1.65	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12532	25255		3.76	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4132793 5'
12925	25942		9.63	7.0E-53	AM421782.1	EST_HUMAN	64407.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098077 3' similar to contains THR.11 THR repetitive element;
4189	17209	30075	1.78	5.0E-53	4788543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
12574	25278		2.36	5.0E-53	AW813563.1	EST_HUMAN	RG3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
52	13169	26068	1.39	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
52	13169	26067	1.39	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9950	22855		0.89	4.0E-53	AF13037.1	EST_HUMAN	ly06h04.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2278327 3'
10278	23168		0.9	4.0E-53	F13080.1	EST_HUMAN	HSC3ID041 normalized infant brain cDNA Homo sapiens cDNA clone c-3id04
11662	24568	38042	2.92	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4053977 5'
11662	24568	38043	2.92	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4053977 5'
2709	15703	28699	2.4	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3794	18825	29712	1.06	3.0E-53	AW050838.1	EST_HUMAN	w22c07.x1 Soares Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2558798 3'
5810	18686	31565	1.08	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5820	18892	32005	1.19	3.0E-53	11526297	NT	Homo sapiens MIL-1 protein (MIL-1), mRNA
6435	19482	32657	0.8	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
7457	20397	33669	0.86	3.0E-53	Y10388.3	NT	H. sapiens graf gene
7457	20397	33670	0.86	3.0E-53	Y10388.3	NT	H. sapiens graf gene
8879	21809	35182	11.67	3.0E-53	SF2043.1	NT	GLF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
9418	22346	35710	0.54	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9809	22535		10.63	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
12858	25466	31782	4.13	3.0E-53	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
480	13551		5.6	2.0E-53	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2349	15357	28359	3.57	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2565	16564		10.24	2.0E-53	4502316	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP9E), mRNA
2773	15765	28757	1.03	2.0E-53	4757916	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), mRNA
2773	15765	28758	1.03	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), mRNA
3265	16313	29216	0.79	2.0E-53	7705987	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
4144	17165	30039	2.54	2.0E-53	M61873.1	NT	Human Kruppel-related DNA-binding protein (TF34) gene, partial cds
4608	17616	30477	0.92	2.0E-53	4506062	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5611	18687	31566	2.35	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
5611	18687	31567	2.35	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0398 Homo sapiens cDNA
8452	21384	34725	1.02	2.0E-53	AW975598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
9942	22847		5.93	2.0E-53	AW245678.1	EST_HUMAN	2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'
1465	14493	27457	1.4	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3470	16510	29411	1.49	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5078	18075	30924	1.17	1.0E-53	BE296388.1	EST_HUMAN	601176725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631919 5'
6989	20016	33248	1.17	1.0E-53	BF384201.1	EST_HUMAN	GM4-BN1028-150800-543-e02 NN1029 Homo sapiens cDNA
7018	20553	33846	0.7	1.0E-53	BE012071.1	EST_HUMAN	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
8314	21445	34787	0.71	1.0E-53	AA249072.1	EST_HUMAN	109571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9634	22560	35929	6.44	1.0E-53	X79536.1	NT	H. sapiens mRNA for hnRNP core protein A1
12311	25117	38156	2.34	1.0E-53	AW245422.1	EST_HUMAN	2822943.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822943 3'
5485	25627	31410	5.61	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
220	13319	26235	4.27	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1959	14981	27861	1.92	8.0E-54	4504810	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA
5235	17850	30717	0.85	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
5235	17850	30718	0.85	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
6160	19218	32369	21.39	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
405	13518	26439	1.25	7.0E-54	AA812537.1	EST_HUMAN	af9c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element
1854	14876	27856	1.68	7.0E-54	Y16945.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2220	15230	28238	6.73	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_B5c6weeks_2NbHP8c9W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element ;
10827	23513	36946	2.38	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
11736	24638		3.8	7.0E-54	AH60189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
12203	25038	38540	1.44	7.0E-54	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
12203	25038	38541	1.44	7.0E-54	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
24	13140	26028	1.73	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MIOB, exon 4, 5 and partial cds
406	13519	26440	1.04	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
408	13519	26441	1.04	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3327	16373	29274	1.02	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3597	16634	26539	0.94	6.0E-54	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4090	17115	29583	3.1	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (GLCN6) mRNA
4573	17881	30443	1.05	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4893	17892	30758	0.97	6.0E-54	AV724885.1	EST_HUMAN	AV724885 HTB Homo sapiens cDNA clone HTBACE02 5'
5121	17980		1.98	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p86 isoform
5353	18338		1.24	6.0E-54	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2165	15177	28183	1.2	5.0E-54	P51623	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
194	13292		47.94	4.0E-54	AF110103.1	NT	Tupaia belangeri beta-actin mRNA, partial cds
982	14033	26976	46.51	4.0E-54	AA306764.1	EST_HUMAN	EST177686 Jurkat T-cells VI Homo sapiens cDNA 5' and similar to glyceraldehyde-3-phosphate dehydrogenase
1827	14850	27827	2.37	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1827	14850	27828	2.37	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3248	16298		2.63	4.0E-54	A935086.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711
7686	20619		0.53	4.0E-54	BE544889.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPYRROLINE ;
96	13209	26121	8.58	3.0E-54	AA373487.1	EST_HUMAN	601075004F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461017 5'
1563	14624		0.97	3.0E-54	AW515742.1	EST_HUMAN	EST165371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2604	15602	28596	1.4	3.0E-54	AL110383.1	EST_HUMAN	hdb7g08.x1 NCJ_CGAP_G06 Homo sapiens cDNA clone IMAGE:2816542 3'
2670	15666		1.49	3.0E-54	A908757.1	EST_HUMAN	DKFZp434E0731.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731 5'
8122	19181	32316	1.4	3.0E-54	4502434	NT	IL-BT189-190389-007 BT189 Homo sapiens cDNA Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7766	20716	34017	1.44	3.0E-54	AA844061.1	EST_HUMAN	af92c08.s1 Soares_paritydd_tumor_Nb-IPA Homo sapiens cDNA clone IMAGE:1388270 3'
7768	20716	34018	1.44	3.0E-54	AA844061.1	EST_HUMAN	af92c08.s1 Soares_paritydd_tumor_Nb-IPA Homo sapiens cDNA clone IMAGE:1388270 3'
8280	21165	34523	0.41	3.0E-54	AI742922.1	EST_HUMAN	wg4b1.1.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367833 3'
11464	24378		1.59	3.0E-54		NT	Homo sapiens gldg autoantigen, golgin subfamily 4, 5 (GOLGA5), mRNA
11527	24437	37895	4.36	3.0E-54	BF345600.1	EST_HUMAN	602019408F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121 5'
11807	24728	38220	2.78	3.0E-54	AA393382.1	EST_HUMAN	z70f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
12408	25177	31876	2.17	3.0E-54	AW954559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
12445	25922		2.84	3.0E-54	AW748965.1	EST_HUMAN	EST366629 MAGE resequencas, MAGC Homo sapiens cDNA
665	13727	26637	21.66	2.0E-54	5031900	NT	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA
1392	14423	27377	1.23	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1569	14600	27559	1.14	2.0E-54	AA655008.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2569	15567	28587	1.04	2.0E-54	AW163175.1	EST_HUMAN	nt78a06.s1 NCL_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element ;
2642	15638	28637	3.64	2.0E-54	AL163210.2	NT	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2937	15990	28892	1.86	2.0E-54	AW067524.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3607	16644		1.79	2.0E-54	AA532925.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2652927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
4300	17314		1.6	2.0E-54	4502642	NT	nt45g08.s1 NCL_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S
4560	17559		1.6	2.0E-54	AF208161.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
5662	18736	31644	7.2	2.0E-54	4750069	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
5797	18869	31978	1.22	2.0E-54	BE047894.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
5970	19036	32157	3.72	2.0E-54	11426657	NT	Homo sapiens small inducible cytokine subfamily A (Oys-Oys), member 14 (SCYA14) mRNA
6076	19137	32271	15.01	2.0E-54	AB046811.1	NT	tz43c11.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
6076	19137	32272	15.01	2.0E-54	AB046811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6951	19890	33204	0.78	2.0E-54	AF008915.1	NT	Homo sapiens KIAA0100 protein, partial cds
7122	20326	33590	0.67	2.0E-54	AB028212.1	NT	Homo sapiens mRNA for KIAA1691 protein, partial cds
7122	20326	33591	0.67	2.0E-54	AB028212.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
7483	20423	33703	9.24	2.0E-54	11426544	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
10165	23046	36445	3.96	2.0E-54	AB001025.1	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
10514	23401	36812	1.18	2.0E-54	11426127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10621	23507	36941	0.99	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10621	23507	36942	0.99	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
11463	19980	33204	1.41	2.0E-54	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
12148	21988		2.35	2.0E-54	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
12866	25498	31761	1.91	2.0E-54	8567387	NT	Homo sapiens perid (Drosophila) homolog 3 (PER3), mRNA
4577	17585		1.48	1.0E-54	BF315418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
-13021	25564		2.58	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human
10845	23731	37154	1.03	9.0E-55	BE081493.1	EST_HUMAN	gamma-glutamyl transpeptidase mRNA, 5 end
1342	14375		0.7	8.0E-55	Y07829.2	NT	QV2-BT0635-180400-143-1712 BT0635 Homo sapiens cDNA
1346	14378		3.23	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11641	24547		1.85	8.0E-55	AW409714.1	EST_HUMAN	Homo sapiens RFB30 gene for RING finger protein
9362	22260		0.81	7.0E-55	AW103839.1	EST_HUMAN	h02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'
9724	22849	36031	1.59	7.0E-55	AA89581.1	EST_HUMAN	xd76c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603522 3' similar to TR:O60365
9756	22680	36065	1.74	7.0E-55	AU139809.1	EST_HUMAN	O60365 FOS39554.1
11658	24564	38036	10.05	7.0E-55	A1561056.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
11658	24564	38037	10.06	7.0E-55	A1561056.1	EST_HUMAN	AU139809 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'
12749	25732	31669	1.52	7.0E-55	BE670608.1	EST_HUMAN	iq28f08.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2210249 3'
12999	25868		5.96	7.0E-55	H23396.1	EST_HUMAN	iq28f09.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2210249 3'
11946	24760	38288	1.84	6.0E-55	AB040934.1	NT	7e37c01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284640 3'
1795	14821	27768	1.49	5.0E-55	AA704971.1	EST_HUMAN	ym57g07.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:52444 5'
1795	14821	27789	1.49	5.0E-55	AA704971.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
4854	17883	30749	0.95	5.0E-55	AW206021.1	EST_HUMAN	z155b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6819	19852	33063	3.38	5.0E-55	4502240	NT	z155b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6819	19852	33064	3.38	5.0E-55	4502240	NT	UI-H-B1-afy-g-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
6961	25659	33214	1.92	5.0E-55	4505952	NT	Homo sapiens ariylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6961	25659	33215	1.92	5.0E-55	4505952	NT	Homo sapiens ariylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
7388	20381	33680	0.61	5.0E-55	7382477	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7675	20809	33908	0.68	5.0E-55	11434422	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
8596	22522	35886	2.83	6.0E-55	4506302	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA
9859	22774		1.69	5.0E-55	BE064396.1	EST_HUMAN	Homo sapiens speckle-type POZ protein (SPOP), mRNA
10540	23426	36844	1.58	5.0E-55	AB014511.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
10540	23426	36845	1.58	5.0E-55	AB014511.1	NT	RC4-BT0310-110300-0715-F10 BT0310 Homo sapiens cDNA
							Homo sapiens mRNA for KIAA0611 protein, partial cds
							Homo sapiens mRNA for KIAA0611 protein, partial cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10718	23604	37033	1.26	5.0E-55	5453765	NT	Homo sapiens nei (chicken)-like 2 (NELL2), mRNA
12479	25223		3.46	5.0E-55	114717972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
58	15865	26075	1.22	4.0E-55	AW957994.1	EST_HUMAN	EST370064 IMAGE resequences, MAGE Homo sapiens cDNA
695	13765	26672	37.86	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1535	14565		1.88	4.0E-55	BF061411.1	EST_HUMAN	7182b10.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element;
2038	15055	28054	1.13	4.0E-55	4508180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2038	15055	28055	1.13	4.0E-55	4508180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2098	16112	28115	6.85	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2098	16112	28116	6.85	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2331	15339	28344	2.26	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
2629	15627		1.39	4.0E-55	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8918	21848		11.14	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11878	24582		2.36	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12407	25178		6.99	4.0E-55	BF303941.1	EST_HUMAN	601886575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6883	19913	33129	0.79	3.0E-55	AA077156.1	EST_HUMAN	7809A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B09A09
12352	25143		2.13	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-p08 HT0603 Homo sapiens cDNA
13035	25573		5.4	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
398	13480	26400	1.76	2.0E-55	X57147.1	NT	Human endogenous retrovirus p1E.1 (ERV9)
573	13641		1.09	2.0E-55	M10976.1	NT	Human endogenous retrovirus DNA (4-1), complete retroviral segment
872	13734	26846	2.14	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products
2989	16051	28955	0.86	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4888	17887	30752	1.77	2.0E-55	BE119886.1	EST_HUMAN	GM1-HT0876-150800-357-p03 HT0876 Homo sapiens cDNA
7928	26890	34154	0.76	2.0E-55	AW501989.1	EST_HUMAN	UI-HF-BN0-ake-f-06-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
9617	22543	35913	0.52	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCL_CGAP_Kjd11 Homo sapiens cDNA clone IMAGE:3134463 3'
9617	22543	35914	0.52	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCL_CGAP_Kjd11 Homo sapiens cDNA clone IMAGE:3134463 3'
9703	22628		5.6	2.0E-55	AJ002836.1	EST_HUMAN	am88405.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
9783	22707		0.71	2.0E-55	BE007959.1	EST_HUMAN	QY0-BN0147-280400-213-p08 BN0147 Homo sapiens cDNA
11389	24305	37752	1.77	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005563 5'
99	13212	26124	1.25	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphatase receptor (cation dependent) (M6PR) mRNA
202	13301	26216	29.8	1.0E-55	U06823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefia2) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
596	13663	26565	0.66	1.0E-55	AI026718.1	EST_HUMAN	ov85g09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644160 3'
1177	14217	27158	3.79	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1965	14983	27866	2.32	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987027 5'
1965	14983	27867	2.32	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987027 5'
2347	15356		7.77	1.0E-55	5903174	NT	Homo sapiens SMA3 (SMA3), mRNA
2361	15858	28372	1.04	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y.1 (TTY1) mRNA, partial cds
2843	15943	28541	26.29	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2888	15886	28580	5.22	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2898	15896	28581	5.22	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2854	15649	28648	2.35	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
3469	16509	29410	1.29	1.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
3942	16678	29576	1.03	1.0E-55	7691675	NT	Homo sapiens DKFZP686G1219 protein (DKFZP686G1219), mRNA
4075	17101	29880	4.49	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4397	17410	30276	0.98	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4843	17844		1.14	1.0E-55	N77261.1	EST_HUMAN	y44g03.t1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:245620 5'
4942	17941	30798	1.42	1.0E-55	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
4942	17941	30799	1.42	1.0E-55	AB037163.1	NT	Homo sapiens DSCR6b mRNA, complete cds
5357	18340	31185	0.91	1.0E-55	BE077198.1	EST_HUMAN	RC6-BT0605-160200-031-B11 BT0605 Homo sapiens cDNA
5687	18760	31684	30.3	1.0E-55	AF119896.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6523	19567	32750	6.54	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6523	19567	32751	6.54	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7435	20132		0.56	1.0E-55	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
8013	20530	34248	0.46	1.0E-55	4503242	NT	Homo sapiens cytochrome P450, 5f (lancetol 14-alpha-demethylase) (CYP51) mRNA
8568	21499	34842	1.32	1.0E-55	11432984	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8568	21499	34843	1.32	1.0E-55	11432984	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8660	21891	34929	1.16	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8660	21891	34930	1.16	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
11349	24267	37708	1.48	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11349	24267	37708	1.48	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11881	23961	37419	1.8	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11899	23969	37497	1.68	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA Cct8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft01 5' similar to similar to Chinese Hamster DHFR-coamplified protein mRNA
12008	24850	38349	1.41	1.0E-55	10587821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
7757	20887	33987	1.99	9.0E-56	BE379074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609562 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2782	15773	28768	8.27	7.0E-56	H19834.1	EST_HUMAN	Yn62g03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element;
8089	21001	34323	2.29	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
8089	21001	34324	2.29	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1718	14746	27714	3.14	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
9704	22629	36007	0.71	5.0E-56	AW015507.1	EST_HUMAN	UJH-B10p-eau-a-05-0-U1s1 NCL_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10876	23762		1.63	5.0E-56	W28180.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12564	25911	31368	3.32	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
29	13145	26032	7.23	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
29	13145	26033	7.23	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2758	15749	28744	4.1	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2758	15749	28745	4.1	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2859	13618	26526	2.73	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2878	15653	28662	1.16	4.0E-56	AI632488.1	EST_HUMAN	W50908.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE;
2879	15653	28663	1.16	4.0E-56	AI632488.1	EST_HUMAN	W50908.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE;
6507	19551	32731	5.84	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6507	19551	32732	5.84	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10984	23668	37296	1.4	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
11360	24278	37719	8.51	4.0E-56	AI498066.1	EST_HUMAN	tm55g12.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'
11360	24278	37720	8.51	4.0E-56	AI498066.1	EST_HUMAN	tm55g12.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163046 3'
1370	14402	27356	2.44	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1789	14815	27784	1.15	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
2164	15176	28182	0.93	3.0E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3170	16220	29110	1.93	3.0E-56	AA325826.1	EST_HUMAN	EST128889 Cerebellum II Homo sapiens cDNA 5' end
3170	16220	29111	1.93	3.0E-56	AA325826.1	EST_HUMAN	EST128889 Cerebellum II Homo sapiens cDNA 5' end
3008	16837	29909	1.44	3.0E-56	AF055066.1	NT	Homo sapiens MHC class 1 region
3982	17016	29909	0.79	3.0E-56	BE393512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4495	17605	30371	0.67	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4531	17540	30402	5.37	3.0E-56	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4688	17693	30560	2.3	3.0E-56	5902085	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKIVL2), mRNA
5257	18243	31094	0.67	3.0E-56	6912553	NT	Homo sapiens phosphotyrosine transfer protein, beta (PTPNB), mRNA

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5881	18950	32065	1.66	3.0E-56	4759163	NT	Homo sapiens sparco/osteonectin, cwev and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5881	18950	32066	1.66	3.0E-56	4759163	NT	Homo sapiens sparco/osteonectin, cwev and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
7200	20200	33446	7.84	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7707	20639	33936	0.86	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
7707	20639	33937	0.86	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
9375	22303	35664	6.27	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10329	23218	36632	0.89	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10959	23843	37269	1.58	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
11759	24660	38144	1.77	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIC), mRNA
11759	24660	38145	1.77	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIC), mRNA
12443	25198	31847	1.64	3.0E-56	11434876	NT	Homo sapiens cavedin 3 (CAV3), mRNA
12443	25198	31848	1.64	3.0E-56	11434876	NT	Homo sapiens cavedin 3 (CAV3), mRNA
547	13616		1.44	2.0E-56	AA199818.1	EST_HUMAN	z552a08.a1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645206 3'
758	15883	26740	2.26	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
758	15883	26741	2.26	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
3030	16082	28983	1.12	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3361	16405		1.13	2.0E-56	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3595	16632	29537	1.75	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
7449	20390	33660	3.5	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1007	14056		5.82	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3742	16774	29660	1.66	1.0E-56	AW689833.1	EST_HUMAN	hg23c11.x1 NCJ CGAP GC6 Homo sapiens cDNA clone IMAGE:2948452 3'
3742	16774	29661	1.66	1.0E-56	AW689833.1	EST_HUMAN	hg23c11.x1 NCJ CGAP GC6 Homo sapiens cDNA clone IMAGE:2948452 3'
5355	18338	31183	0.94	1.0E-56	6681002	NT	Mus musculus cytoplasmic polyadenylation element binding protein (Opeb), mRNA
7134	20242	33493	0.5	1.0E-56	AW609520.1	EST_HUMAN	MR3-ST0203-180100-208-f02 ST0203 Homo sapiens cDNA
10482	23350		0.76	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10551	23437	36858	1.79	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220999-001-E502 CT0163 Homo sapiens cDNA
849	13710		1.44	9.0E-57	AW808885.1	EST_HUMAN	QV0-OT0033-070300-152-f03 OT0033 Homo sapiens cDNA
11689	24573	38049	1.83	9.0E-57	AF229497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11689	24573	38050	1.93	9.0E-57	AF229497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
14	13129	26015	1.51	8.0E-57	8923349	NT	Homo sapiens hypodermal protein FLJ20371 (FLJ20371), mRNA
317	13409	26327	2.22	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
909	13961	26908	5.82	8.0E-57	AW264599.1	EST_HUMAN	xt05d10.x1 NCL CGAP_Bm63 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1838	14861	27843	2.95	8.0E-57	AA496108.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3439	16480	29386	1.07	8.0E-57	4758279	NT	z151b12.1 Sceres_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
3439	16480	29387	1.07	8.0E-57	4758279	NT	Homo sapiens Epha4 (EPHA4) mRNA
5016	18014	30873	1.05	8.0E-57	4557630	NT	Homo sapiens Epha4 (EPHA4) mRNA
5421	25834	31491	1.63	8.0E-57	11418185	NT	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4) mRNA
6864	19702	32897	0.62	8.0E-57	AB020705.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6737	19771	32981	10.9	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0888 protein, partial cds
6737	19771	32982	10.9	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7853	20780	34082	0.68	8.0E-57	7882263	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
8215	21120	34453	3.92	8.0E-57	AB020644.1	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8215	21120	34454	3.92	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11910	13129	26015	3	8.0E-57	8923349	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
12165	25001	38502	3	8.0E-57	11433356	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
1247	14283	27226	1.83	7.0E-57	AJ003100.1	NT	Homo sapiens nilein (LOC61189), mRNA
3295	16342	29244	1.16	7.0E-57	7242158	NT	Homo sapiens GYS2 gene, exon 14
3295	16342	29245	1.16	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3315	16362	29263	0.8	7.0E-57	6005979	NT	Homo sapiens NME7 (NME7), mRNA
3947	16975	29898	1.84	7.0E-57	AF012872.1	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3947	16975	29859	1.84	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p44K230) mRNA, complete cds
13084	25864		4.99	5.0E-57	AJ271735.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p44K230) mRNA, complete cds
							Homo sapiens Xq pseudautosomal region; segment 1/2
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3817	18847	29732	4.21	4.0E-57	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
830	13885	26823	0.97	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1359	14390		20.84	3.0E-57	AA230279.1	EST_HUMAN	nc1307.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2414	15418	28419	1.07	3.0E-57	AA248335.1	EST_HUMAN	P40783 40S RIBOSOMAL PROTEIN S10.1
3782	16794		86.65	3.0E-57	AW853964.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
4148	17169	30042	1.36	3.0E-57	P08547	SWISSPROT	RC3-GT0254-110300-027-010 GT0254 Homo sapiens cDNA
6252	19313	32478	1.17	3.0E-57	11225608	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6393	19412	32577	3.44	3.0E-57	BE786537.1	EST_HUMAN	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
8723	21653	35000	3.38	3.0E-57	W28130.1	EST_HUMAN	601598988F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
							4278 Human retina cDNA randomly primed sublibrary/Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8748	21678	35020	1.77	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8748	21678	35021	1.77	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8858	21789	35138	0.74	3.0E-57	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
9417	22345	35709	0.28	3.0E-57	AL117659.1	EST_HUMAN	AL117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9792	22756	36140	0.81	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9792	22756	36141	0.81	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
11346	24265	37705	2.78	3.0E-57	AW248374.1	EST_HUMAN	2820473.Sprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2820473 5'
12450	26927	31371	4.65	3.0E-57	W28871.1	EST_HUMAN	zb45d11.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12780	25837		1.84	3.0E-57	AW178575.1	EST_HUMAN	RCO-HT0112-080998-001-C06 HT0112 Homo sapiens cDNA
1453	14485	27449	1.28	2.0E-57	AA845418.1	EST_HUMAN	hm26c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157618 3' similar to contains Alu repetitive element;
1518	14549	27509	1.34	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1518	14549	27510	1.34	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2778	15769	28764	3.93	2.0E-57	AA845418.1	EST_HUMAN	ak02b02.s1 Soares_parenchyma_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
3500	16398		1.85	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3610	16847	29547	0.67	2.0E-57	R07702.1	EST_HUMAN	ye98h01.1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3610	16847	29548	0.67	2.0E-57	R07702.1	EST_HUMAN	ye98h01.1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4006	17033	29923	0.95	2.0E-57	BE073264.1	EST_HUMAN	MR0-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA
4284	17298	30164	0.73	2.0E-57	AA018298.1	EST_HUMAN	ze94c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4284	17298	30165	0.73	2.0E-57	AA018298.1	EST_HUMAN	ze94c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4632	17638	30501	11.45	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5865	18936		1.51	2.0E-57	AA018131.1	EST_HUMAN	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element;
6287	19318		30.03	2.0E-57	BF115286.1	EST_HUMAN	7n80104.x1 NCI_OGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570866 3' similar to contains TAR1.1
6400	19448	32619	0.73	2.0E-57	11431281	NT	MER22 repetitive element;
9190	22118	35474	0.93	2.0E-57	AF045452.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
10360	23249	36869	2.16	2.0E-57	AF057722.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
11717	24619	38036	2.27	2.0E-57	11424084	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
11717	24619	38037	2.27	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11757	24658	38141	1.63	2.0E-57	AJ245503.1	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11757	24658	38142	1.63	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
1653	14653	27646	1.32	1.0E-57	BE173102.1	EST_HUMAN	MR0-H10559-240400-014-h12 HT0559 Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2245	15255	28281	3.88	1.0E-57	AW503208.1	EST_HUMAN	UI-HF-BNO-ekt-g-07-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
8416	21319	34651	0.46	1.0E-57	H55076.1	EST_HUMAN	CHR220015 Chromosome 22 exon Homo sapiens cDNA clone C22_25 5'
9261	22170		2.52	1.0E-57	BE043031.1	EST_HUMAN	h032a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN;
12589	25286		8.43	1.0E-57	AW470791.1	EST_HUMAN	h033d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
5874	18944	32060	0.87	9.0E-58	AA297847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
12838	25451	31777	2.89	9.0E-58	BE395081.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
610	13675		4.49	8.0E-58	BE868715.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
677	13739	26652	3.76	8.0E-58	AI798376.1	EST_HUMAN	h34b07.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN;
677	13739	26653	3.76	8.0E-58	AI798376.1	EST_HUMAN	h34b07.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN;
1881	14902	27885	2.05	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1881	14902	27886	2.05	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
3016	16068		3.15	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
7808	20543	33834	0.54	7.0E-58	BE561971.1	EST_HUMAN	601346704F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687577 5'
11280	24210		5.09	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
11367	24285	37729	3.15	7.0E-58	AW504709.1	EST_HUMAN	UI-HF-BNO-ekt-g-10-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
11367	24285	37730	3.15	7.0E-58	AW504709.1	EST_HUMAN	UI-HF-BNO-ekt-g-10-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2270	15260	28287	1.48	6.0E-58	BE395081.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2398	15403	28407	5.2	6.0E-58	AI130688.1	EST_HUMAN	AU130688 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2845	15997	28998	1.28	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2945	15997	28999	1.28	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
8411	19459	32633	1.61	6.0E-58	AF106911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10789	23985	37115	1.2	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
320	13412	26329	3.29	5.0E-58	4507334	NT	Homo sapiens synapobelin 1 (SYNJ1), mRNA
733	13791	26715	4.74	5.0E-58	BE763984.1	EST_HUMAN	RC-HNT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1222	14260	27201	2.33	5.0E-58	AW797948.1	EST_HUMAN	CMS-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1222	14260	27202	2.33	5.0E-58	AW797948.1	EST_HUMAN	CMS-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1223	14260	27201	1.83	5.0E-58	AW797948.1	EST_HUMAN	CMS-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1223	14260	27202	1.93	5.0E-58	AW797948.1	EST_HUMAN	OM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3368	16412	29313	5.27	5.0E-58	AA988183.1	EST_HUMAN	α98e07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4357	17371	30235	0.74	6.0E-58	AI636745.1	EST_HUMAN	ts89e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2236468 3' similar to SW:PRO2_ACACA
5090	18087		0.98	5.0E-58	AW848834.1	EST_HUMAN	P19984 PROFILIN II:
5823	18894		1.9	5.0E-58	11496282	NT	IL3-CT0214-090300-081-F06 CT0214 Homo sapiens cDNA
6419	19466	32640	6.15	5.0E-58	H23072.1	EST_HUMAN	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6658	19687	32893	1.1	5.0E-58	AL163285.2	NT	ym51h07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:62071 5'
6744	19778	32991	0.94	5.0E-58	11421330	NT	Homo sapiens chromosome 21 segment HS21C085
7085	20291	33550	1.03	5.0E-58	AF051334.1	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
7085	20291	33551	1.03	5.0E-58	AF051334.1	NT	Homo sapiens ribirin (NBS) mRNA, complete cds
7465	20405	33681	0.73	5.0E-58	4885400	NT	Homo sapiens holochochrome c synthase (cytochrome c heme-lyase) (HCCS) mRNA
8547	21478	34820	8.34	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10828 (FLJ10828), mRNA
8928	21856	36212	0.76	5.0E-58	AB046887.1	NT	Homo sapiens mRNA for KIAA1817 protein, partial cds
10371	23260	36661	0.83	5.0E-58	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10823	23509	36943	2	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10886	23771	37196	0.64	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10886	23771	37197	0.64	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
12419	25860		2.26	5.0E-58	11526233	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
394	13478	26397	4.5	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
823	13878	26815	1.54	4.0E-58	4504034	NT	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA
1487	14518	27479	3.55	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2613	15811	28606	1.27	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2878	15874	28672	2	4.0E-58	U96251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3370	16414	29316	1.81	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3803	16834	29720	1.11	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discolin-like domains 3 (EDIL3), mRNA
5123	18119	30961	1.08	4.0E-58	S75264.1	NT	WT1-wfms' tumor suppressor protein [human, fetal kidney, mRNA, 521 nt]
8338	21243	34576	0.67	4.0E-58	BE463857.1	EST_HUMAN	hy18a02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3187642 3'
11783	24682	38172	5.37	4.0E-58	11424069	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
355	13442		1.61	3.0E-58	R17879.1	EST_HUMAN	yg10a02.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
1416	14447	27401	1.73	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3071	16123		0.85	3.0E-58	R17879.1	EST_HUMAN	yg10a02.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3221	16269	29167	2.98	3.0E-58	BF59848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3221	16269	29168	2.98	3.0E-58	BF59848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6511	19555	32735	0.69	3.0E-58	BE089509.1	EST_HUMAN	QVQ-BT0702-170400-194-009 BT0702 Homo sapiens cDNA
6714	19750	32954	2.78	3.0E-58	F07056.1	EST_HUMAN	HSC1TG081 normalized infant brain cDNA Homo sapiens cDNA clone c-1q08
6932	19961	33182	1.8	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 5'
968	14019	26963	8.48	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
							ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391.60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
1316	14349		13.31	2.0E-58	BE208532.1	EST_HUMAN	xa08a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567704 3'
5518	18598	31447	0.81	2.0E-58	AW074831.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5542	25629	31471	3.35	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5542	25629	31495	3.35	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6292	18943	32511	1.36	2.0E-58	BF513488.1	EST_HUMAN	UH-BW1-ams-g-11-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
							am57602.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP_ZK328.1 CEG5065 UBQUITIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6361	19410	32575	2	2.0E-58	AI24874.1	EST_HUMAN	YQ08h08.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:186379 5'
6395	19443	32612	0.89	2.0E-58	RQ2567.1	EST_HUMAN	qm84601.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895424 3'
7256	20165	33404	0.89	2.0E-58	AI291407.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7618	20457	33742	2.69	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7518	20457	33743	2.69	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
11182	24108	37555	14.38	2.0E-58	BF307745.1	EST_HUMAN	601890312F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
11402	24318	37765	1.95	2.0E-58	AW872641.1	EST_HUMAN	hm26f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
745	13803	26727	6.68	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
							Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1095	14138	27075	4.52	1.0E-58	6274549	NT	EST1369252 MAGE resequences, MAGD Homo sapiens cDNA
1355	14387	27340	1.25	1.0E-58	AW957182.1	EST_HUMAN	EST1369252 MAGE resequences, MAGD Homo sapiens cDNA
1355	14387	27341	1.25	1.0E-58	AW957182.1	EST_HUMAN	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1423	14454	27408	1.29	1.0E-58	AJ238093.1	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
2849	15838	28836	0.95	1.0E-58	4759189	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNPT1) mRNA
3784	16816	29702	0.66	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNPT1) mRNA
4846	17847	30715	0.95	1.0E-58	M66903.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 4
5091	18088	30938	9.03	1.0E-58	AI141063.1	EST_HUMAN	q243h01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678128 3'
6055	19117	32246	1.2	1.0E-58	BE061860.1	EST_HUMAN	RC1-BT0254-290100-015-e01 BT0254 Homo sapiens cDNA
7187	20187	33430	1.04	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8991	21822		0.81	1.0E-58	AW973537.1	EST_HUMAN	EST385637 MAGC resequences, MAGM Homo sapiens cDNA
9427	22355	35720	0.69	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA
9533	22450	35822	1.23	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09 5'
9927	22553	35922	0.62	1.0E-58	AA412397.1	EST_HUMAN	Z69105.11 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:730487 5'
9927	22553	35923	0.62	1.0E-58	AA412397.1	EST_HUMAN	Z69105.11 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:730487 5'
10883	23559	36998	0.69	1.0E-58	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
12188	25024		1.99	1.0E-58	X63392.1	NT	H. sapiens Immunoglobulin kappa light chain variable region L14
2243	15253	28259	20.74	8.0E-69	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
7154	20262	33516	0.53	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis I Homo sapiens cDNA 5' end
7154	20262	33517	0.53	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis I Homo sapiens cDNA 5' end
8758	21688	35031	2.87	8.0E-59	A1761963.1	EST_HUMAN	WH50406.x1 NCL CGAP_K1411 Homo sapiens cDNA clone IMAGE:2384171 3'
8337	21242	34574	0.43	7.0E-59	BE149117.1	EST_HUMAN	RC4-HT0251-140100-013-h01 HT0251 Homo sapiens cDNA
8337	21242	34575	0.43	7.0E-59	BE149117.1	EST_HUMAN	RC4-HT0251-140100-013-h01 HT0251 Homo sapiens cDNA
189	15668		1.82	6.0E-59	BF035327.1	EST_HUMAN	601456531F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3862086 5'
8386	21290	34623	0.55	6.0E-59	AA962431.1	EST_HUMAN	om81a04.s1 NCL CGAP_K143 Homo sapiens cDNA clone IMAGE:1553550 3' similar to TR:Q13732 Q13732 SA GENE PRODUCT PRECURSOR.;
8821	21751	35097	0.85	6.0E-59	A1750970.1	EST_HUMAN	cn06h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 random
1779	14805	27773	0.95	5.0E-59	AW157281.1	EST_HUMAN	au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
1779	14805	27774	0.96	6.0E-59	AW157281.1	EST_HUMAN	au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR:O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
3172	16222	29113	8.44	5.0E-59	A1807484.1	EST_HUMAN	Wf48c11.x1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2356836 3'
4768	17773	30640	4.66	5.0E-59	X63497.1	NT	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
7330	18498	31274	8.72	5.0E-59	AW162304.1	EST_HUMAN	au88c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element;
9364	22282	35657	0.87	5.0E-59	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39KD) (RPC39), mRNA
10227	23118	36520	1.09	5.0E-59	AV762869.1	EST_HUMAN	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
11349	24264	37704	3.44	5.0E-59	11424908	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
820	13875	26813	2.59	4.0E-59	D60006.1	NT	Human mRNA for KIAA0184 gene, partial cds
4907	17906	30776	1.03	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4907	17906	30777	1.03	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5727	18900	31893	1.08	4.0E-59	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12549	25799		6.79	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	13125		4.23	3.0E-59	AW965524.1	EST_HUMAN	EST377682 IMAGE resequences, MAGI Homo sapiens cDNA
244	13341	26253	3.83	3.0E-59	7662247	NT	Homo sapiens KIAA0660 gene product (KIAA0660), mRNA
1739	14768	27736	8.88	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1739	14768	27737	8.88	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2143	15168	28157	5.78	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2143	15168	28158	5.78	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3086	18137	29033	1.21	3.0E-59	T18865.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3086	18137	29034	1.21	3.0E-59	T18865.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3174	16224	29117	4.6	3.0E-59	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3174	16224	29118	4.6	3.0E-59	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3888	16927	29805	1.35	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (perm receptor) (ZP2) mRNA
4798	17607	30668	2.2	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4955	17953	30812	1.45	3.0E-59	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
6465	19510	32685	1.91	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7751	20881	33981	1.99	3.0E-59	5464137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
8510	21441	34782	1.31	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
8510	21441	34783	1.31	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
10547	23433	36852	0.75	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
10547	23433	36853	0.75	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12527	25251		1.82	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12655	25336		10.58	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6100	18161	32294	0.53	2.0E-59	BF509383.1	EST_HUMAN	U1-H-B14-ay-b-02-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
6100	19161	32295	0.53	2.0E-59	BF509383.1	EST_HUMAN	U1-H-B14-ay-b-02-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
7118	20322		0.49	2.0E-59	AA470073.1	EST_HUMAN	z58d05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730377 3'
7424	20123	33360	0.59	2.0E-59	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
8281	21186		0.41	2.0E-59	BF373328.1	EST_HUMAN	MRO-FT0144-260700-002-at0 FT0144 Homo sapiens cDNA
10163	23054		5.72	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
11006	23950		1.53	2.0E-59	BF366554.1	EST_HUMAN	RCO-NT0036-100700-032-at07 NT0036 Homo sapiens cDNA
11270	24192	37642	1.77	2.0E-59	AW410698.1	EST_HUMAN	rh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
11270	24192	37643	1.77	2.0E-59	AW410698.1	EST_HUMAN	rh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
12439	25196	31881	7.18	2.0E-59	A1631809.1	EST_HUMAN	w536c12.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542 Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12930	26820	31482	1.83	2.0E-59	L11945.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
173	13274		5.53	1.0E-59	BE296411.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631927 5'
2436	15440	28441	1.71	1.0E-59	D11456.2	NT	Homo sapiens Xdh mRNA for xanthine dehydrogenase, complete cds
2436	16440	28442	1.71	1.0E-59	D11456.2	NT	Homo sapiens Xdh mRNA for xanthine dehydrogenase, complete cds
2662	15628		3.67	1.0E-59	AA748488.1	EST_HUMAN	oa56h11.e1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1308029 3' similar to TR:Q13537
6678	19715	32811	0.43	1.0E-59	11426724	NT	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
6678	19715	32912	0.43	1.0E-59	11426724	NT	Homo sapiens phosphatidylinositol transfer protein (PITPN), mRNA
7995	20913	34229	1.92	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
8178	21085	34418	0.89	1.0E-59	BE256814.1	EST_HUMAN	60111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
8178	21085	34419	0.89	1.0E-59	BE256814.1	EST_HUMAN	60111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'
9922	22910	36298	0.83	1.0E-59	11419630	NT	Homo sapiens zinc finger protein 276 (ZNF276), mRNA
10131	23022	36417	2.01	1.0E-59	11428849	NT	Homo sapiens 3-hydroxyisobutyl-Coenzyme A hydrolase (HIBCH), mRNA
10131	23022	36418	2.01	1.0E-59	11428849	NT	Homo sapiens 3-hydroxyisobutyl-Coenzyme A hydrolase (HIBCH), mRNA
11289	20913	34229	6.87	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4424	17435	30295	0.65	9.0E-60	AF084630.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
789	13845	26779	1.88	8.0E-60	AW877945.1	EST_HUMAN	EST368849 MAGE resequences, MAGE Homo sapiens cDNA
1490	14821	27482	1.62	8.0E-60	4769169	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2185	15196	28201	2.12	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2185	15196	28202	2.12	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6211	18266	32417	1.12	8.0E-60	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6781	19814	33026	2.92	8.0E-60	SE3182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8151	21060	34391	0.88	8.0E-60	11420841	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCTT1B), mRNA
8543	21474	34816	3.95	8.0E-60	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9495	22423	35786	3.17	8.0E-60	11428949	NT	Homo sapiens S-enigen, retina and pineal gland (arrestin) (SAG), mRNA
10004	22821	36208	0.85	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10004	22821	36209	0.85	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11046	23930	37370	0.76	8.0E-60	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11272	24184	37645	5.04	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
11272	24184	37646	5.04	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
778	13635	26769	8.58	7.0E-60	AF055086.1	NT	Homo sapiens MHC class 1 region
779	13835	26769	26.62	7.0E-60	AF055086.1	NT	Homo sapiens MHC class 1 region
840	13995	26832	1.36	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2142	15155	28156	1.23	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4275	17289	30196	2.35	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
5304	18288		0.99	7.0E-60	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21O008
9941	22846	36237	4.67	7.0E-60	H58041.1	EST_HUMAN	Y12104.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
11803	24724	38216	2.15	7.0E-60	H58041.1	EST_HUMAN	Y12104.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
2192	15203	28208	1.07	6.0E-60	BE964974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
8394	21297	34628	0.49	6.0E-60	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
9006	21835		11.73	6.0E-60	H52456.1	EST_HUMAN	Y478109.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element ;
86	13199	26111	1.61	5.0E-60	AI807917.1	EST_HUMAN	Wf52c07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
86	13199	26112	1.61	5.0E-60	AI807917.1	EST_HUMAN	Wf52c07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2250	15260	28268	3.93	4.0E-60	AW503208.1	EST_HUMAN	U1-HF-BNO-akt-g-07-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2250	15260	28269	3.93	4.0E-60	AW503208.1	EST_HUMAN	U1-HF-BNO-akt-g-07-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
3013	16065		1.52	4.0E-60	AA298037.1	EST_HUMAN	EST11498 Ulenus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7741	20672	33970	0.89	4.0E-60	BF196088.1	EST_HUMAN	hr8105.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
8671	22567		0.67	4.0E-60	AL163278.2	NT	Q61085 GTP-RHO BINDING PROTEIN 1 ;
1884	14905	27889	4.2	3.0E-60	BE562611.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1884	14905	27890	4.2	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1892	14913		2.02	3.0E-60	6031190	NT	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
4588	17576	30438	3.09	3.0E-60	AJ271735.1	NT	Homo sapiens prohibitin (PHB) mRNA
5563	18841	31519	0.4	3.0E-60	BF365143.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
5837	18908	32023	1.93	3.0E-60	AW836196.1	EST_HUMAN	QV44-N1149-250900-423-011 NN1149 Homo sapiens cDNA
7287	18456	31326	1.28	3.0E-60	AI792814.1	EST_HUMAN	RC3-LT0023-200100-012-a01 LT0023 Homo sapiens cDNA
8973	21903	35258	4.65	3.0E-60	5174644	NT	cl60h11.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE
8973	21903	35259	4.65	3.0E-60	5174644	NT	P52624 URIDINE PHOSPHORYLASE ;
9146	22074	35436	0.63	3.0E-60	AI040235.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9301	22229	35599	0.71	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
32	13148	26037	5.75	2.0E-60	AY008285.1	NT	α5δ409.x1 Soares NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE Q05890 FORMIN ;
							Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
							Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1446	14477	27436	2.16	2.0E-60	Z11694.1	NT	H sapiens 41kDa protein kinase related to rat ERK2
1750	14777	27745	1.18	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 6' end
1760	14787	27767	0.94	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2649	15844	28644	0.91	2.0E-60	7657229	NT	Homo sapiens Interleukin 17 receptor (IL17R), mRNA
3639	16875	29573	0.67	2.0E-60	4757867	NT	Homo sapiens v-ref murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3988	17015	28904	0.72	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4221	17237		0.66	2.0E-60	BF513458.1	EST_HUMAN	U1-H-BW1-ams-e-05-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070952 3'
6555	19597	32785	0.9	2.0E-60	AT91952.1	EST_HUMAN	nc01112.y5 NCI_CGAP_C06 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR repetitive element;
6768	19802	33013	1.43	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
7013	20040	33274	1.09	2.0E-60	AF167476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
7168	18440	31342	2.11	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7168	18440	31343	2.11	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7469	20409	33686	5.72	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7469	20409	33687	5.72	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7593	20529	33820	0.44	2.0E-60	A1308124.1	EST_HUMAN	tb23d09.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055185 3' similar to SW:GALR_RAT
8080	20962		1.19	2.0E-60	BF512808.1	EST_HUMAN	Q62805 GALANIN RECEPTOR;
8584	21515	34859	1.07	2.0E-60	X85597.1	EST_HUMAN	UI-H-BW1-ams-e-02-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
8425	22353	36719	4.02	2.0E-60	L36033.1	NT	HS15BEST human adult testis Homo sapiens cDNA clone CAM_IEST15
10484	23372	36786	2.47	2.0E-60		NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
10484	23372	36786	2.47	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
10484	23372	36787	2.47	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
12697	25353		2.08	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12821	25440		1.58	2.0E-60	11418088	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC883504), mRNA
12835	25450		1.78	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
545	13614	26522	1.03	1.0E-60	BE178586.1	EST_HUMAN	PM8-H10605-270200-001-e06-H10605 Homo sapiens cDNA
3974	17002	29889	1.55	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
5071	18068	30918	1.75	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8527	21458	34801	0.86	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141199-0711-H08 BT0311 Homo sapiens cDNA
8315	22243		3.32	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9341	22269	35631	1.3	1.0E-60	AV764081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1126	14168	27105	2.8	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
9270	22198	35555	0.58	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9270	22108	35556	0.58	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2719	15712	28710	1.59	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2508555 3'
2719	15712	28711	1.58	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2508555 3'
2892	16044		4.8	8.0E-61	X67147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
8475	21406	34745	1.5	8.0E-61	AA583988.1	EST_HUMAN	m59g08.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
132	13235	28152	0.91	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
132	13235	28153	0.91	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
5229	13235	28152	1.94	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
5229	13235	28153	1.94	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
285	13379	26283	1.99	6.0E-61	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
837	13892	26829	1.86	6.0E-61	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1349	14381	27333	10.83	6.0E-61	AF119880.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1654	14684	27647	1.09	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1674	14704	27666	2.39	6.0E-61	AA596033.1	EST_HUMAN	m66h109.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
2141	15154	28155	1.13	6.0E-61	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3352	16398	29298	7.97	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
6264	19315	32480	3.16	6.0E-61	S79249.1	NT	Ig-beta/B29-CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7728	20860	33958	1.61	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
8064	20977	34292	1.82	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 24 (GTF2) mRNA, complete cds
235	13333	26247	1.15	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
235	13333	26248	1.15	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
380	13485	26382	0.67	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1706	14734	27700	2.45	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3083	16134	28030	2.75	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3198	16244	29139	1.42	5.0E-61	AB020632.1	NT	Homo sapiens mRNA for KIAA0825 protein, partial cds
4066	17082		1.77	5.0E-61	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBRT on chromosome 21q22; segment 1/3
1784	14810	27778	0.95	4.0E-61	AU140307.1	EST_HUMAN	AU140307 PLACE2 Homo sapiens cDNA clone PLACE200302 5'
6028	19088	32214	0.51	4.0E-61	7681637	NT	Homo sapiens DKFZP566B023 protein (DKFZP566B023), mRNA
12418	25185		5.43	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
8992	21921	35277	0.83	3.0E-61	AF150180.1	EST_HUMAN	AF150180 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDA9B04

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
521	13591	26503	1.23	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1240	14276	27219	2.07	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1240	14276	27220	2.07	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1692	14722	27666	1.6	2.0E-61	NS3039.1	EST_HUMAN	y53d11.s1 Scars fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gbL25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
2689	15683		1.08	2.0E-61	N38397.1	EST_HUMAN	y03f11.1 Scars melanocyte 2NfHM Homo sapiens cDNA clone IMAGE:270189 5'
6894	19730	32930	0.97	2.0E-61	11426166	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110116kD) (ATP6N1A), mRNA
9567	22494	35867	1.74	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKG Homo sapiens cDNA clone GKCELG06 5'
10091	22884		0.89	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
10433	23322	36740	2.01	2.0E-61	AW500258.1	EST_HUMAN	U1HF-BNO-ekd-f-12-0-U1.1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076774 5'
10744	23630	37062	2.81	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
11321	24240		3.43	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
13062	25568	31741	1.99	2.0E-61	AW96326.1	EST_HUMAN	QV0-BN0042-170300-162-f10 BN0042 Homo sapiens cDNA
458	13530		0.74	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
799	13854	26790	1.26	1.0E-61	5433829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1794	14920		1.07	1.0E-61	U32657.1	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1883	14904	27888	3.39	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2212	15223	28226	1.35	1.0E-61	AW827281.1	EST_HUMAN	zn11b09.y1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element MSR1 repetitive element;
4849	17558	30418	0.87	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4549	17558	30419	0.87	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4967	17965	30823	10.94	1.0E-61	AW298181.1	EST_HUMAN	U1H-BW0-elt-b-08-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
4967	17965	30824	10.94	1.0E-61	AW298181.1	EST_HUMAN	U1H-BW0-elt-b-08-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732871 3'
5578	18656	31533	0.87	1.0E-61	M76423.1	NT	H. sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5887	18956	32073	0.87	1.0E-61	7662303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6099	19160	32293	1.52	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
7229	20138	33377	12.66	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
7450	20391	33661	0.71	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP128), mRNA
7665	20492	33781	1.37	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7555	20492	33782	1.37	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8710	21641	34988	3.04	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8888	21618	35169	3.49	1.0E-61	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9822	22728		3.19	1.0E-61	AW689726.1	EST_HUMAN	MRO-BN070-04040-010-h01 BN0070 Homo sapiens cDNA
9895	22810	36189	0.87	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
10532	23418	36833	5.12	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
11080	24012	37463	1.88	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11509	24419	37874	1.72	1.0E-61	AB007830.1	NT	Homo sapiens mRNA for CSR2, complete cds
12362	25831	31489	3.87	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12362	25831	31490	3.87	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12705	25950	31797	2.7	1.0E-61	M20809.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
12982	25641	31751	10.22	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10843	23729	37152	1.94	9.0E-62	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
4687	17672	30543	1.24	8.0E-62	AA830420.1	EST_HUMAN	cc68h11.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK
13102	25617		2.23	8.0E-62	AA768881.1	EST_HUMAN	P31795 POL POLYPROTEIN;
1134	14176	27113	2.72	7.0E-62	AV714334.1	EST_HUMAN	AV714334 DGB Homo sapiens cDNA clone DCBAMA08 5'
3563	16600	29504	1.02	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
6138	19197	32335	1.04	7.0E-62	11427965	NT	(AUTOANTIGEN NOR-90)
11789	24711	38202	1.81	7.0E-62	AI208681.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20261), mRNA
3042	16094		1.66	6.0E-62	U09410.1	NT	q956a04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1839160 3' similar to TR:O15103
3443	16484		5.38	6.0E-62	11418255	NT	O15103 HYPOTHETICAL 27.3 KD PROTEIN ;
8073	20966	34302	3.69	6.0E-62	AI762801.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
8073	20966	34303	3.68	6.0E-62	AI762801.1	EST_HUMAN	Homo sapiens CGI-56 protein (CGI-56), mRNA
8664	21655		0.64	6.0E-62	AW501124.1	EST_HUMAN	wf04d02.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8833	21763	35110	1.82	6.0E-62	11431139	NT	wf04d02.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
9892	22807	36195	3.49	6.0E-62	AW614393.1	EST_HUMAN	U1-HF-BP0p-alt-d-08-Q-U1r1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3072833 5'
439	13510	26434	1.44	5.0E-62	AI950528.1	EST_HUMAN	Homo sapiens CGI-18 protein (LOC31008), mRNA
2430	15434	28434	6.38	5.0E-62	AJ271735.1	NT	MR3-ST0203-130100-025-q09 ST0203 Homo sapiens cDNA
2430	15434	28435	6.38	5.0E-62	AJ271735.1	NT	wf51e07.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
2631	15829	28622	1.75	5.0E-62	U39487.1	NT	Q08379 GOLGIN-95 ; contains element MER22 repetitive element ;
2631	15829	28623	1.75	5.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3480	16520	29419	2.41	5.0E-62	4506788	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
							Human xanthine dehydrogenase/oxidase mRNA, complete cds
							Human xanthine dehydrogenase/oxidase mRNA, complete cds
							Homo sapiens ryanodine receptor 3 (RYR3) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4435	17446	30306	2.23	5.0E-62	AA431093.1	EST_HUMAN	z078009.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
4674	17679		1.18	5.0E-62	AW905887.1	EST_HUMAN	P47245 NARDILYSIN ;
9113	22041	35308	0.72	5.0E-62	4505758	NT	RC6-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
10048	22964	36353	6.75	5.0E-62	AW410687.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
865	13919	26863	3.34	4.0E-62	AW161479.1	EST_HUMAN	h07g09.x1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:2861618 5'
865	13919	26894	3.34	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
866	13919	26863	3.58	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
866	13919	26864	3.58	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2482	15484	28486	1.74	4.0E-62	A827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2482	15484	28486	1.74	4.0E-62	A827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3459	16500		8.31	4.0E-62	4557887	NT	Wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
6147	19206	32344	1.64	4.0E-62	4508978	NT	gb:X57138.maf1 HISTONE H2B.2 (HUMAN);
6551	19663	32781	3.62	4.0E-62	11420654	NT	Wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
7535	20474	33782	1.76	4.0E-62	11421041	NT	gb:X57138.maf1 HISTONE H2B.2 (HUMAN);
8082	20994	34312	2.41	4.0E-62	7657057	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
8082	20994	34313	2.41	4.0E-62	7657057	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
8749	21679	35022	1.06	4.0E-62	11428973	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
9406	22333	35697	7.46	4.0E-62	A8033089.1	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11450	24366	37815	3.37	4.0E-62	Z78766.1	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11450	24366	37816	3.37	4.0E-62	Z78766.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
12548	25793	31747	1.52	4.0E-62	11418192	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
12916	25527	31747	1.49	4.0E-62	11418322	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
12965	25523	31744	8.56	4.0E-62	11417862	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
12965	25523	31745	8.56	4.0E-62	11417862	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
13004	25555	31758	1.67	4.0E-62	11430460	NT	Homo sapiens cadherin EGF LA G seven-pass G-type receptor 1 (CELSR1), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
77	13191	26102	1.03	3.0E-62	4567794	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3093	16144	29040	0.74	3.0E-62	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3093	16144	29041	0.74	3.0E-62	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3763	16795	29684	2.2	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
5082	18079	30928	1.22	3.0E-62	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
9104	22032	35387	0.84	3.0E-62	A1632733.1	EST_HUMAN	was3304.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2289903 3' similar to contains THR.12
1269	14294	27240	1.74	2.0E-62	AL163284.2	NT	T-IR repetitive element:
8365	21268	34603	0.42	2.0E-62	AA307480.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
9334	22262	35625	5.06	2.0E-62	BF328911.1	EST_HUMAN	EST178374 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9334	22262	35626	5.06	2.0E-62	BF328911.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10669	23555		4.56	2.0E-62	AF224688.1	NT	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
12113	24954		8.4	2.0E-62	BF330876.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
1070	14114	27054	1.2	1.0E-62	AF248540.1	NT	(UBE2D3) genes, complete cds
1668	14567	27557	16.22	1.0E-62	L78810.1	NT	QV4-BT0257-081109-017-e03 BT0257 Homo sapiens cDNA
2857	16009	28909	1.24	1.0E-62	AL039044.1	EST_HUMAN	Homo sapiens interectin 2 (SH3D18) mRNA, complete cds
4460	17471		0.66	1.0E-62	BE168413.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4844	17650	30515	1.47	1.0E-62	8923201	NT	DKFZp566F104.1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566F104.5'
							QV0-HT0493-280200-135-h12 HT0493 Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), GDM protein (CDM), adrenoleukodystrophy protein >
6542	19585	32770	1.01	1.0E-62	U52111.2	NT	ab05c02.s1 Stralagene fetal retina S37202 Homo sapiens cDNA clone IMAGE:839906 3'
7494	20434	33713	0.95	1.0E-62	AA490060.1	EST_HUMAN	z689f10.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7505	20444	33727	2.54	1.0E-62	AA722878.1	EST_HUMAN	z689f10.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7505	20444	33728	2.54	1.0E-62	AA722878.1	EST_HUMAN	z689f10.s1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:409771 3'
9610	22538	35906	1.79	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9610	22538	35907	1.79	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9646	22572	35942	2.32	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9646	22572	35943	2.32	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
10086	22879	36286	3.44	1.0E-62	AA468170.1	EST_HUMAN	aa33408.s1 NCL CGAP GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
11805	24726	38218	2.2	1.0E-62	Z78698.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA14D8
12229	25063	38561	1.41	1.0E-62	11424055	NT	Homo sapiens exosome component Rrp46 (LOC56815), mRNA
12802	25427		3.45	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12993	25648	31754	2.78	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
358	13445	26357	2.34	9.0E-63	AW819405.1	EST_HUMAN	QV4-ST0234-181189-037-405 ST0234 Homo sapiens cDNA
2368	16374		1.56	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFUJ1wara) Homo sapiens cDNA clone GEN-558C10 5'
4125	17148	30022	11.76	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4125	17148	30023	11.76	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5424	18421	38565	4.19	9.0E-63	11448185	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), mRNA
5652	18726	31631	1.49	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for Pkfb kinase
7546	20484	33773	3.99	9.0E-63	11426385	NT	Homo sapiens nucleoporin 89kD (NUP88), mRNA
8562	21268	34601	0.56	9.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8901	21831	35185	1.63	9.0E-63	11421160	NT	Homo sapiens Ras association (RafGDS/AF-6) domain family 2 (RASSF2), mRNA
2367	15373	28376	1.68	8.0E-63	4557734	NT	Homo sapiens monamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2397	15402	28408	1.63	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3522	16560	29462	3.97	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3522	16560	29463	3.97	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4365	17379	30243	3.79	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
957	14007		2.12	7.0E-63	A1872197.1	EST_HUMAN	wn55g11.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439908 3'
5523	18602		94.77	6.0E-63	AA420803.1	EST_HUMAN	nc83f02.r1 NCL_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S RIBOSOMAL PROTEIN (HUMAN);
9432	22360	35723	0.7	5.0E-63	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3366	16410	29312	0.85	4.0E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3876	16806	29786	1.66	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3876	16905	29786	1.66	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6715	19751	32955	2.22	4.0E-63	AW150372.1	EST_HUMAN	CM3-BT0595-190100-072-e09 BT0595 Homo sapiens cDNA
6715	19751	32956	2.22	4.0E-63	AW150372.1	EST_HUMAN	CM3-BT0595-190100-072-e09 BT0595 Homo sapiens cDNA
11572	24481	37948	1.75	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-e-02-UJ.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
11572	24481	37949	1.75	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-e-02-UJ.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1950	14970	27951	1.24	3.0E-63	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2830	15819	28614	1.43	3.0E-63	J00310.1	NT	Homo Mat-tRNA-I gene 1
2869	14301	27249	8.92	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
6748	19782	32984	30.52	3.0E-63	11548910	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC693928), mRNA
10228	23119	36521	0.92	3.0E-63	BE876158.1	EST_HUMAN	60148566F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889253 5'
10228	23119	36522	0.92	3.0E-63	BE876158.1	EST_HUMAN	60148566F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889253 5'
204	13303	26219	1.22	2.0E-63	U07804.1	NT	Homo DNA topoisomerase I mRNA, partial cds
211	13310	26227	1.47	2.0E-63	4885226	NT	Homo sapiens eves absent (Drosophila) homolog 2 (EYA2), mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
520	13590		2.42	2.0E-63	4557824	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC)
851	13906	26848	8.15	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
1586	14617	27590	1.53	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1586	14617	27581	1.53	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1791	14817	27786	1.64	2.0E-63	BE410735.1	EST_HUMAN	601301827F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
3329	16375	29278	2.29	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3978	17007	29895	2.87	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4974	17872	30833	1.47	2.0E-63	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5443	25628	31250	3.83	2.0E-63	11419428	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
6101	19162	32296	2.9	2.0E-63	BF373541.1	EST_HUMAN	QV4-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6101	19162	32297	2.9	2.0E-63	BF373541.1	EST_HUMAN	QV4-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6427	19474	32648	0.91	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6427	19474	32649	0.91	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6999	20026	33259	1.09	2.0E-63	U66059.1	NT	Homo sapiens MIST mRNA, partial cds
7062	20078	33311	0.68	2.0E-63	AB032365.1	NT	Homo sapiens MIST mRNA, partial cds
7062	20078	33312	0.68	2.0E-63	AB032366.1	NT	Homo sapiens MIST mRNA, partial cds
7430	20128	33368	1.37	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56834), mRNA
7430	20128	33369	1.37	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56834), mRNA
8252	21157	34490	0.84	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8331	21236	34569	0.46	2.0E-63	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
9097	22026	35382	4.21	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9606	22532	35900	1.34	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9606	22532	35901	1.34	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
10448	23337	36754	1.32	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11187	24113	37581	7.04	2.0E-63	N78945.1	EST_HUMAN	zb18b05.s1 Soares fetal_lung_NH-L19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gbX17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);
11212	24138	37588	3.23	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11212	24138	37589	3.23	2.0E-63	AF09810.1	NT	Homo sapiens neuritin III-alpha gene, partial cds
12446	25745	31569	5.21	2.0E-63	114718185	NT	Homo sapiens acornase 2, mitochondrial (ACO2), mRNA
13077	25569	31730	2.16	2.0E-63	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
4451	17461	30318	3.64	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zid11
4451	17461	30319	3.64	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zid11
5537	18616	31466	0.87	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
5978	18043	32166	1.23	1.0E-63	AW582266.1	EST_HUMAN	QV6-ST0215-060100-083-b09 ST0215 Homo sapiens cDNA
6855	19694	32889	0.68	1.0E-63	AW451950.1	EST_HUMAN	UI-H-B18-alt-h-02-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
6855	19694	32889	0.68	1.0E-63	AW451950.1	EST_HUMAN	UI-H-B18-alt-h-02-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
9042	21971		3.2	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
13046	25843		12.74	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6165	19251	32366	0.52	9.0E-64	AW401433.1	EST_HUMAN	UI-HF-BKO-ead-b-09-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3053153 5'
8448	21380	34721	5.81	9.0E-64	AI478186.1	EST_HUMAN	tm50607.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2181625 3'
1072	14116		9.22	8.0E-64	BE280706.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6380	19429	32597	3.97	8.0E-64	BE885756.1	EST_HUMAN	601508968F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910338 5'
12274	25090		3.73	8.0E-64		NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12325	25125		3.1	8.0E-64	T60651.1	EST_HUMAN	y698502.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79179 5'
3591	16628		0.99	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4844	17845	30712	2.34	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOPT1) mRNA
4844	17845	30713	2.34	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOPT1) mRNA
8303	21207	34542	0.52	7.0E-64	4505788	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
10536	23422	36837	2.77	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gcr22, rrp22 and bam22 genes
1751	14778	27746	2.63	6.0E-64	A1651892.1	EST_HUMAN	wb51e07.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1751	14778	27747	2.63	6.0E-64	A1651892.1	EST_HUMAN	wb51e07.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3167	18217	29106	9.85	6.0E-64	AW028446.1	EST_HUMAN	wv13e03.x1 NCL_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2529436 3'
3167	18217	29107	9.86	6.0E-64	AW028446.1	EST_HUMAN	wv13e03.x1 NCL_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2529436 3'
5816	18868	31999	2.49	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5816	18868	32000	2.49	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5838	18908	32024	4.1	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5847	18918	32032	0.47	6.0E-64	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
6042	19104	32233	0.75	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6042	19104	32234	0.75	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALOR), mRNA
7605	20540	33829	2.54	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7605	20540	33830	2.54	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9897	22762	36171	8.48	6.0E-64	11420655	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
10037	22937	36326	1.7	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK), mRNA, complete cds
10240	23131	36534	2.23	6.0E-64	S76475.1	NT	ttkc [human, brain, mRNA, 2715 nt]
11208	24134	37582	4.89	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11208	24134	37583	4.89	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11456	16217	29106	1.77	6.0E-64	AW026445.1	EST_HUMAN	wy13e03.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2629436 3'
11456	16217	29107	1.77	6.0E-64	AW026445.1	EST_HUMAN	wy13e03.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
12482	25209	31853	3.51	6.0E-64	11526198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
845	13900	26839	2.66	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
845	13900	26840	2.66	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1366	14398	27352	2.65	5.0E-64	AB020710.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP), gene, complete cds
1444	14475	27433	1.71	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP), gene, complete cds
1444	14475	27434	1.71	5.0E-64	L40933.1	NT	Human I(3)mbt protein homolog mRNA, complete cds
1740	14767	27738	1.36	5.0E-64	U89358.1	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2874	14530	27493	3.68	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2874	14530	27494	3.68	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4043	17070	29956	9.61	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53), mRNA, partial cds
4197	17216	30082	1.09	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0603 protein, partial cds
8344	21249	34584	0.55	4.0E-64	BE794607.1	EST_HUMAN	601590382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:39444397 5'
11252	24176	37624	2.14	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
11252	24176	37625	2.14	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2213	15224	28227	10.14	3.0E-64	C18896.1	EST_HUMAN	C18895 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-669E02 5'
3299	16346	29260	0.83	3.0E-64	BE794381.1	EST_HUMAN	601590565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3504	16542	29441	1.54	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3504	16542	29442	1.54	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6318	19368	32537	1.42	3.0E-64	Z26273.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 28
6596	18639	32819	0.59	3.0E-64	AW600861.1	EST_HUMAN	UHF-EP0p-ax-c-05-QJL71 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3073161 5'
6769	19803	33014	3.06	3.0E-64	BF370000.1	EST_HUMAN	RC8-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
9035	21964	35323	1.88	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2), mRNA, complete cds
9035	21964	35324	1.88	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2), mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9082	21991	35343	2.84	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
9062	21991	35344	2.84	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
9961	22866	36253	1.78	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9961	22866	36254	1.78	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10046	22961	36349	0.75	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe resequences, MAGO Homo sapiens cDNA
10046	22961	36350	0.75	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe resequences, MAGO Homo sapiens cDNA
12115	24956	38459	2.03	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1116	14157	27096	0.86	2.0E-64	AA609940.1	EST_HUMAN	af09cd08.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1424	14455	27409	1.98	2.0E-64	4767701	NT	Homo sapiens alF4E-like cap-binding protein (4EHP) mRNA wc87501.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2552	15952		2.34	2.0E-64	AI927030.1	EST_HUMAN	L1 repetitive element;
2558	15557	28556	4.95	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2558	15557	28557	4.95	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6238	19292	32432	2.09	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2D02113 5'
6490	19634	32712	1.08	2.0E-64	AF113708.1	NT	Homo sapiens angiopeptin 4 (ANG4) mRNA, partial cds
6760	19794	33008	5.25	2.0E-64	BF686537.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
6877	19808	33123	1.35	2.0E-64	AI078387.1	EST_HUMAN	alpha29b03.x1 Soares fetal N52HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
6998	20026	33258	3.9	2.0E-64	MT77185.1	NT	H sapiens dopamine receptor D5 pseudogene 1, partial cds
8320	21225	34559	0.48	2.0E-64	11431054	NT	Homo sapiens ataxin 2-binding protein 1 (A2BP1), mRNA
8406	21309	34641	0.53	2.0E-64	AW606785.1	EST_HUMAN	QV1-H-T0413-010200-059-h12 HT0413 Homo sapiens cDNA
9226	22154	35505	0.86	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9226	22154	35506	0.86	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9772	22696	36082	1.29	2.0E-64	AU132570.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'
10485	23373	36788	0.55	2.0E-64	T06397.1	EST_HUMAN	EST042868 Fetal brain, Stragagene (cat#936206) Homo sapiens cDNA clone HFBDS88
10485	23373	36789	0.55	2.0E-64	T06397.1	EST_HUMAN	EST042868 Fetal brain, Stragagene (cat#936206) Homo sapiens cDNA clone HFBDS88
11201	24127	37574	2.3	2.0E-64	BF528114.1	EST_HUMAN	602042862F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4180556 5'
11489	24401	37851	4.81	2.0E-64	AI922911.1	EST_HUMAN	wn81506.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11489	24401	37852	4.81	2.0E-64	AI922911.1	EST_HUMAN	wn81506.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
11692	24586	38063	1.71	2.0E-64	AW864773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
12391	25187	31873	2	2.0E-64	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12798	25424		1.86	2.0E-64	H55192.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132.5'
277	13372	26286	1.52	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1803	14823	27798	10.08	1.0E-64	AI928419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2516136 3' similar to gb:L21696 cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element;
3570	16607	29511	6.12	1.0E-64	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α)
3646	16682	29579	1.12	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3646	16682	29580	1.12	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3972	17000	29887	0.67	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
10566	23452	36873	1.34	1.0E-64	AA042975.1	EST_HUMAN	zk63f08.s1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486567 3'
12397	25153		1.98	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2295	15303	28309	1.89	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2295	15303	28310	1.89	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
11966	24809		16.21	9.0E-65	BF330876.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
11941	24785	38281	3.88	8.0E-65	AI929244.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21.;
10652	23638	36972	2.26	7.0E-65	BE081663.1	EST_HUMAN	QV2-BT0636-240400-182-e02 BT0636 Homo sapiens cDNA
1083	14127	27085	0.89	6.0E-65	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC08 5'
1937	14958		7.75	8.0E-65	AA550926.1	EST_HUMAN	rl66d10.s1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:998379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
6951	19883	33097	0.7	6.0E-65	AA503892.1	EST_HUMAN	rh37607.s1 NCI_CGAP_P15 Homo sapiens cDNA clone IMAGE:954517
9305	22233	35593	1.27	8.0E-65	AW083252.1	EST_HUMAN	xe07609.x1 NCI_CGAP_Oc21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFS.; contains L1 b2 L1 repetitive element;
9563	22490	35851	4.74	6.0E-65	AA427878.1	EST_HUMAN	zx53b06.s1 Soares total_fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:773747 3'
9563	22490	35852	4.74	6.0E-65	AA427878.1	EST_HUMAN	zx53b06.s1 Soares total_fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:773747 3'
9623	22549	36920	0.76	6.0E-65	AI085314.1	EST_HUMAN	qf18h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750425 3'
9623	22549	35921	0.75	6.0E-65	AI085314.1	EST_HUMAN	qf18h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750425 3'
11308	24227	37873	2.94	6.0E-65	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
11928	24773	38271	2.05	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1382	14414	27368	1.25	5.0E-65	7681931	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1382	14414	27369	1.25	5.0E-65	7681951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2169	15161	28187	0.97	5.0E-65	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3300	16347	29251	1.98	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3300	16347	29252	1.98	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7194	20194	33438	0.63	5.0E-65	4504606	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
10945	23830	37256	1.2	5.0E-65	AF009698.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
206	13305	26222	1.36	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108.5
769	13826	26756	1.18	4.0E-65	AI268488.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
769	13826	26757	1.18	4.0E-65	AI268488.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
1108	14148	27088	0.96	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1504	14535	27498	11.58	4.0E-65	4506636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2359	15368	28369	1.1	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2359	15368	28370	1.1	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
4028	17056	28945	1.09	4.0E-65	AW993185.1	EST_HUMAN	RC2-BN0033-160200-073-a03 BN0033 Homo sapiens cDNA
6396	19444	32613	4.32	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6396	19444	32614	4.32	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7443	20364	33653	0.59	4.0E-65	A7008372.1	NT	Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds
7478	20416	33694	0.98	4.0E-65	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and A1 repeats
7588	20524	33813	2.01	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7980	20901	34216	0.67	4.0E-65	U40372.1	NT	Human 3' 5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7980	20901	34217	0.67	4.0E-65	U40372.1	NT	Human 3' 5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
8335	21240	34572	0.56	4.0E-65	U39656.1	NT	Human MAP kinase kinase 5 (MKK5) mRNA, complete cds
8424	21356	34693	0.74	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
8424	21356	34694	0.74	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
9688	22814	35987	0.77	4.0E-65	11429127	NT	Homo sapiens Janus Kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
11053	23937		1.62	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11542	24452	37915	1.63	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
100	13214	26127	2.79	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
101	13214	26127	2.07	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1260	15850		4.62	3.0E-65	X78932.1	NT	H.sapiens HZF9 mRNA for zinc finger protein
1845	14868	27850	1.53	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
3321	16367	29269	1.13	3.0E-65	4504950	NT	MSR1 repetitive element;
						NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3785	16816	29703	1.54	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4760	17765	30628	1.22	3.0E-65	6912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
10571	23457	36877	1.63	3.0E-65	BE787366.1	EST_HUMAN	601479685F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3892405 5'
11827	23962	37398	10.67	3.0E-65	AA430006.1	EST_HUMAN	2W65a06.r1 Soares_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3464	16504	29408	6.88	2.0E-65	BF680294.1	EST_HUMAN	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5'
4035	17062	29951	0.75	2.0E-65	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
6815	19848		5.77	2.0E-65	BE263373.1	EST_HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
7492	20432	33711	22.59	2.0E-65	BF576922.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
9404	22332	35695	1.17	2.0E-65	AK024483.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
9404	22332	35698	1.17	2.0E-65	AK024483.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
12324	25124		5.37	2.0E-65	AA307904.1	EST_HUMAN	EST178755 Colon carcinoma (H-CC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
12764	25728		2.46	2.0E-65	BF246096.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
93	13206		0.86	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
562	13631	26540	1.49	1.0E-65	7657496	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
1866	14888	27869	1.11	1.0E-65	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2054	15071	28072	0.97	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3430	16471	29379	0.77	1.0E-65	BE466681.1	EST_HUMAN	1224a09.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208888 3'
4084	17109	29987	1.76	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4084	17109	29988	1.76	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4302	17316	30182	2.3	1.0E-65	AW029340.1	EST_HUMAN	W009a09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4302	17316	30183	2.3	1.0E-65	AW029340.1	EST_HUMAN	W009c09.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5468	18549	31389	0.58	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-009 BT0702 Homo sapiens cDNA
5468	18549	31390	0.58	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-194-009 BT0702 Homo sapiens cDNA
5665	18739	31648	0.83	1.0E-65	AI243738.1	EST_HUMAN	qH88h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR:Q07823
8829	21759	35104	1.86	1.0E-65	AW820481.1	EST_HUMAN	Q07823 MAC30 PROTEIN
8829	21759	35105	1.86	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA
8857	21767	35136	0.67	1.0E-65	BE732118.1	EST_HUMAN	QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA
8857	21767	35137	0.67	1.0E-65	BE732118.1	EST_HUMAN	601356124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8894	21824	35175	2.44	1.0E-65	AU141295.1	EST_HUMAN	601568124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8894	21824	35176	2.44	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYROT1 Homo sapiens cDNA clone THYRO1000358 5'
8899	22327	35889	0.93	1.0E-65	BF698707.1	EST_HUMAN	AU141295 THYROT1 Homo sapiens cDNA clone THYRO1000358 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9571	22498	35861	2.05	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9571	22498	35862	2.05	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9582	22509		3.43	1.0E-65	11431984	NT	Homo sapiens Inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
10010	22827	36214	6.56	1.0E-65	AI191716.1	EST_HUMAN	q55a02.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC
10397	23286	36708	1.5	1.0E-65	AU153793.1	EST_HUMAN	FINGER PROTEIN 8 (HUMAN); contains MER19.1 MER19 repetitive element
10791	23677	37107	0.72	1.0E-65	AA06959.1	EST_HUMAN	AU153793 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
11043	23927	37368	1.14	1.0E-65	AB037832.1	NT	z75a04.r1 Soares, pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'
11094	24025	37468	2.2	1.0E-65	M26187.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11216	24142	37594	2.92	1.0E-65		NT	Human platelet factor 4 variant 1 (PF4var1) gene, complete cds
11570	24479	37945	2.68	1.0E-65	BF698707.1	EST_HUMAN	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11659	24585	38038	2.62	1.0E-65	AI621017.1	EST_HUMAN	602126239F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4283313 5'
12368	25154		1.93	1.0E-65	11418041	NT	is76a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L16533_ma1
12458	26205	31850	5.41	1.0E-65	11418322	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
74	13189	26098	2.8	9.0E-68	AL160311.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
74	13189	26099	2.8	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
1502	14533	29885	5.81	9.0E-66	M87239.1	NT	Novel human gene mapping to chromosome 22
3971	16959	29886	0.8	9.0E-66	M72393.1	NT	Human transposon-like element, partial
						NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
						NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4472	17483	30341	1.35	6.0E-66	AI924653.1	EST_HUMAN	wn57n07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
						EST_HUMAN	CE18595;
4472	17483	30342	1.35	6.0E-66	AI924653.1	EST_HUMAN	wn57n07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
						EST_HUMAN	CE18595;
4472	17483	30343	1.35	6.0E-66	AI924653.1	EST_HUMAN	wn57n07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
9003	21932		0.53	6.0E-66	BE179563.1	EST_HUMAN	PM2-HT0604-030300-001-b06 HT0604 Homo sapiens cDNA
11599	24508	37975	3.24	6.0E-68	X69181.1	NT	H. sapiens mRNA for ribosomal protein L31
1394	14425	27379	1.81	5.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141169-011-h06 BT0311 Homo sapiens cDNA
5254	18240	31091	0.98	5.0E-66	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
5254	18240	31092	0.98	5.0E-66	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
9834	22740	36121	13.19	5.0E-66	11420667	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
817	13872	26809	1.31	4.0E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1765	14791	27761	0.92	4.0E-66	AW897768.1	EST_HUMAN	RC1-NN0063-100500-022-402 NN0063 Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2300	16308	28314	4.89	4.0E-66	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2495	15497		5.65	4.0E-66	AJ223384.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4896	17895		2.61	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
5742	18815	31911	3.4	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5948	19015	32135	0.77	4.0E-66	AW939119.1	EST_HUMAN	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA
7177	18449	31318	5.28	4.0E-66	AW965473.1	EST_HUMAN	EST377549 MAGE resequences, MAGI Homo sapiens cDNA
7491	20431	33710	7.63	4.0E-66	U78198.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
8077	18815	31911	0.9	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
8655	21566	34922	7.27	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
8711	21642	34989	1.52	4.0E-66	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV6)
11817	24738	38229	1.53	4.0E-66	AB023215.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1448	14479	27438	6.99	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1448	14479	27439	6.99	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1999	15017	28007	1.08	3.0E-66	N55323.1	EST_HUMAN	y27g12.1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35058 HISTONE H2B.1/H2B.2. [2] PIR:B568612;
1999	15017	28008	1.08	3.0E-66	N55323.1	EST_HUMAN	y27g12.1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35058 HISTONE H2B.1/H2B.2. [2] PIR:B568612;
1999	15017	28009	1.08	3.0E-66	N55323.1	EST_HUMAN	y27g12.1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35058 HISTONE H2B.1/H2B.2. [2] PIR:B568612;
2757	15748	28743	2.88	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3182	16212	29102	6.3	3.0E-66	7682223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5653	18727	31632	0.79	3.0E-66	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5768	18842	31944	0.77	3.0E-66	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5981	19046	32169	2.58	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5981	19046	32170	2.58	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
7830	20759	34063	0.92	3.0E-66	X92211.1	NT	H.sapiens germline immunoglobulin heavy chain, variable region, (15-1)
10055	22871	36360	0.62	3.0E-66	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
10241	23132	36535	0.73	3.0E-66	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10575	23481	36893	0.8	3.0E-66	7019480	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11003	23987	37320	1.3	3.0E-66	AF156593.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein E (MCBPE) mRNA, complete cds
11942	24786	38282	5.48	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
54	13171	26089	1.25	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
54	13171	26070	1.25	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
445	13112	25998	1.05	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
445	13112	25999	1.05	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1849	14871	27853	1.82	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2246	15256	28262	1.05	2.0E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3015	16067	28909	1.08	2.0E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3581	16618	29521	0.71	2.0E-66	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3629	16859	29741	0.75	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4766	17771	30637	8.52	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4766	17771	30638	8.52	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
6027	18089	32215	0.76	2.0E-66	AW698854.1	EST_HUMAN	EST380930 MAGe resequences, MAGJ Homo sapiens cDNA
6027	18089	32216	0.76	2.0E-66	AW698854.1	EST_HUMAN	EST380930 MAGe resequences, MAGJ Homo sapiens cDNA
9406	22334	35698	2.82	2.0E-66	N45480.1	EST_HUMAN	Y959c02.r1 Soares multiple sclerosis 2/NBHMSP Homo sapiens cDNA clone IMAGE:277826 5'
12667	25920		1.87	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
2836	15959	28890	1.62	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2836	15959	28891	1.62	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4492	15989	28890	3.9	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4492	15989	28891	3.9	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5566	18844	31522	5.43	1.0E-66	BF673098.1	EST_HUMAN	602152995F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
5989	18054	32180	0.6	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NTO101 Homo sapiens cDNA
5989	18054	32181	0.6	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NTO101 Homo sapiens cDNA
7269	20177	33420	1.07	1.0E-66	BF328623.1	EST_HUMAN	RC5-EN0193-010900-034-G06 EN0193 Homo sapiens cDNA
9026	21955	35313	0.87	1.0E-66	AA668896.1	EST_HUMAN	ae80e04.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:327262 3'
9950	22855	36252	0.57	1.0E-66	AA018828.1	EST_HUMAN	ze57e12.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:363118 5'
10859	23745	37169	0.93	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10859	23745	37170	0.93	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
11381	24297	37743	1.86	1.0E-66	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12480	26207		1.65	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
401	13514	26435	3.05	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1408	14440	27394	1.18	7.0E-67	AA388416.1	EST_HUMAN	EST186812 Testis 1 Homo sapiens cDNA 5' and similar to C. elegans hypothetical protein, cosmid
1577	14607	27566	1.45	7.0E-67	W85947.1	EST_HUMAN	ZK353
1577	14607	27567	1.45	7.0E-67	W85947.1	EST_HUMAN	zh58b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2048	15063	28063	1.08	7.0E-67	7657243	NT	zh58b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2048	15063	28064	1.08	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2857	13514	26435	4.15	7.0E-67	AW162232.1	EST_HUMAN	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
6317	19307	32536	0.93	7.0E-67	10190695	NT	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6522	19566	32748	1.83	7.0E-67	11425572	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6522	19566	32749	1.83	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
7024	20050	33283	0.95	7.0E-67	4885084	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8079	20991	34309	1.06	7.0E-67	11419212	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
8079	20991	34310	1.08	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8845	21576	34913	0.56	7.0E-67	4826895	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8898	21828	35180	0.72	7.0E-67	4557732	NT	Homo sapiens phosphodiesterase 1/nucleotide pyrophosphatase 3 (PDNFP3) mRNA
9487	22415	35778	0.96	7.0E-67	10835044	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
12101	24942	36445	5.09	7.0E-67	U92486.1	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
12255	25075	38569	3.03	7.0E-67	11430480	NT	Human cytochrome oxidase subunit Via (COX6A1P) pseudogene, complete cds
12255	25075	38570	3.03	7.0E-67	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12688	25346	31827	2	7.0E-67	AB011399.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
581	13848	26556	1.2	6.0E-67	X68668.1	NT	Homo sapiens gene for AF-3, complete cds
822	13877	26814	2.05	6.0E-67	Z17227.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
1300	14533	27279	1	6.0E-67	Y14320.1	NT	Homo sapiens mRNA for transmembrane receptor protein
3210	16258	29157	0.97	6.0E-67	4505434	NT	Homo sapiens PMP68 gene, exons 3,4,5,6 & 7
3499	16537	29435	1.43	6.0E-67	4507332	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3499	16537	29436	1.43	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4223	17239	30105	1.33	6.0E-67	AL163201.2	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4223	17239	30106	1.33	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4818	17816	30687	1.89	6.0E-67	7657020	NT	Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4818	17819	30688	1.89	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3288	16316	28219	2.04	5.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11422	24338		2.53	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1356	14388	27342	1.34	4.0E-67	R00819.1	EST_HUMAN	yn02d11.1 Scores adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'
8953	21883		1.37	4.0E-67	BF357321.1	EST_HUMAN	RCO-HT0934-150900-028-c03 HT0934 Homo sapiens cDNA
2850	13717	26628	1.86	3.0E-67	AA333768.1	EST_HUMAN	EST137903 Embryo, 9 week Homo sapiens cDNA 5' end
4807	17808	30674	3.31	3.0E-67	AW869159.1	EST_HUMAN	MR3-SN0065-040900-008-701 SN0066 Homo sapiens cDNA
4835	17838		1.06	3.0E-67	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
8759	21699	35032	2.81	3.0E-67	BF198088.1	EST_HUMAN	h81f05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
11706	24608		17.59	3.0E-67	AA927874.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1;
200	13299	26214	1.31	2.0E-67	BE348354.1	EST_HUMAN	om18b07.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
870	13923	26870	4.73	2.0E-67	AW816405.1	EST_HUMAN	hmf8g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
1132	14174		1.27	2.0E-67	AF167460.1	NT	CE09617;
1904	14925	27803	1.18	2.0E-67	BE303037.1	EST_HUMAN	QV4-S10234-181189-037-f05 S10234 Homo sapiens cDNA
1904	14925	27804	1.18	2.0E-67	BE303037.1	EST_HUMAN	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
2456	15460	28457	1.39	2.0E-67	4788796	NT	bar2g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892
3528	16566	29470	4.49	2.0E-67	AA625755.1	EST_HUMAN	KIAA0798 PROTEIN.;
4088	17113	28991	2.87	2.0E-67	AL163300.2	NT	KIAA0798 PROTEIN.;
6307	19357	32528	0.82	2.0E-67	AL049784.1	NT	Homo sapiens chromosome 21 segment HS21C100
6364	19413	32578	5	2.0E-67	BF240758.1	EST_HUMAN	Naval human gene mapping to chromosome 13
6550	19582	32779	1.95	2.0E-67	AB051763.1	NT	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
6550	19582	32780	1.95	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6933	19982	33183	0.65	2.0E-67	AL120642.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
9121	22049	35408	1.36	2.0E-67	AA334609.1	EST_HUMAN	DKFZp761A229.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
9121	22049	35408	1.36	2.0E-67	AA334609.1	EST_HUMAN	EST138850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
9548	22475	35832	1.14	2.0E-67	AW602835.1	EST_HUMAN	EST138850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
6548	22476	35833	1.14	2.0E-67	AW602835.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
10095	22946	36332	0.69	2.0E-67	AV731333.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
10231	23122	36524	1.06	2.0E-67	AW293024.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
11495	25954		3.06	2.0E-67	11436448	NT	UI-H-B12-ahn-e-10-01.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
							Homo sapiens KIAA0985 protein (KIAA0985), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11677	24581	38059	2.05	2.0E-67	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:35531038 5'
11889	23989	37428	2.36	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-002 TN0103 Homo sapiens cDNA
12573	25782	31579	1.64	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G2P1), mRNA
12850	25461	31780	1.45	2.0E-67	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
272	13387	26283	2.72	1.0E-67	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
731	13789	26713	1.71	1.0E-67	AA702794.1	EST_HUMAN	z50004.s1 Soares fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:448015 3'
2189	15200	28205	1.3	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3862264 5'
3938	16966	29848	6.65	8.0E-68	AA209456.1	EST_HUMAN	z182h10.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07890 SAV PROTEIN ;
3938	16966	29849	6.65	8.0E-68	AA209456.1	EST_HUMAN	z182h10.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07890 SAV PROTEIN ;
8680	21611	34952	0.86	7.0E-68	AI810505.1	EST_HUMAN	w68603.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2312860 3'
7975	20896	34208	0.47	6.0E-68	AW953543.1	EST_HUMAN	EST366913 MAGC resequences, MAGC Homo sapiens cDNA
7975	20896	34209	0.47	6.0E-68	AW953543.1	EST_HUMAN	EST366913 MAGC resequences, MAGC Homo sapiens cDNA
10930	23815	37244	2.47	6.0E-68	11422068	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
11589	24458	37966	1.96	6.0E-68	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
12852	25463		2.04	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865761 5'
844	13869	26837	3.89	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
844	13869	26838	3.89	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2831	15820	28815	0.93	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3190	16239	29134	3.96	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4277	17291		1.37	5.0E-68	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
7028	20054	33286	0.77	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3i)-like 1 (RAB3IL1), mRNA
7028	20054	33287	0.77	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3i)-like 1 (RAB3IL1), mRNA
2554	15554	28551	1.31	4.0E-68	11421398	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2554	15554	28552	1.31	4.0E-68	11421398	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5096	18093		2.68	4.0E-68	P04406	SWISSPROT	GLYERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6191	19248	32394	0.61	4.0E-68	AF157063.1	NT	Homo sapiens sedlin (SEDL) gene, exon 4
7080	20288	33544	6.72	4.0E-68	11055901	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7080	20288	33545	6.72	4.0E-68	11055901	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
8135	21044	34374	0.78	4.0E-68	7661683	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA
9592	22518	35880	6.07	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9592	22518	35881	6.07	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9721	22646	36028	2.82	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
11441	24357	37805	2.32	4.0E-68	4505282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11441	24357	37806	2.32	4.0E-68	4505282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11603	24512	37980	1.4	4.0E-68	AB040946.1	NT	Homo sapiens mRNA for KIAA1515 protein, partial cds
12750	25388	31804	4.73	4.0E-68	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3729	16761	29648	2.71	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9899	21347		4.86	3.0E-68	AI342323.1	EST_HUMAN	q38h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950281 3' similar to contains THR12 THR repetitive element ;
10990	23894	37291	1.12	3.0E-68	F28794.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
2904	18408		6.96	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4109	17133	30008	0.73	2.0E-68	BE575766.1	EST_HUMAN	715f02.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828
4793	17797	30665	2.81	2.0E-68	AB008681.1	NT	HYPOTHETICAL 88.8 KD PROTEIN ;
7201	20201		9.51	2.0E-68	R46098.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
7417	20116	33352	4.34	2.0E-68	BF036316.1	EST_HUMAN	Yg38g04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34896 3'
7584	20520		0.51	2.0E-68	11525737	NT	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
7762	20692	33991	0.71	2.0E-68	BF336745.1	EST_HUMAN	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GlcNAc-T8) (GALNT8), mRNA
8504	22431	35794	0.63	2.0E-68	Q05859	SWISSPROT	IL3-CT0534-180900-273-A01 CT0534 Homo sapiens cDNA
11691	24553	38071	1.53	2.0E-68	BF330594.1	EST_HUMAN	FORMIN 4 (LIMB DEFORMITY PROTEIN)
12361	25938		2.83	2.0E-68	BE597376.1	EST_HUMAN	QV0-BT0074-130999-014-g04 BT0074 Homo sapiens cDNA
13090	25607		1.53	2.0E-68	AW016803.1	EST_HUMAN	601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922182 5'
82	13185	26108	0.78	1.0E-68	4505222	NT	UI-H-B10-eam-b-05-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709824 3'
316	13408	26326	8.85	1.0E-68	AW816405.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
2268	16278	28284	1.1	1.0E-68	AB011149.1	NT	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2268	15278	28285	1.1	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2806	15795	28795	1.15	1.0E-68	AW451832.1	EST_HUMAN	Homo sapiens mRNA for KIAA0577 protein, complete cds
4096	17121	29998	1.03	1.0E-68	BE290032.1	EST_HUMAN	UHH-B13-alk-5-01-Q-U1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
5159	18152	30998	0.81	1.0E-68	AA897343.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
5503	18584	31433	1.55	1.0E-68	7662349	NT	al47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460519 3'
8129	21039	34368	0.65	1.0E-68	11436716	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
10679	23565	36995	0.53	1.0E-68	11419429	NT	Homo sapiens sentrin/SUMO-specific protease (SENP1), mRNA
							Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11287	24208	37688	1.54	1.0E-68	11418889	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11287	24208	37689	1.54	1.0E-68	11418889	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11341	24260	37700	1.54	1.0E-68	L78416.1	NT	Homo sapiens MIF2 suppressor (HSMF2), complete cds
11638	24544	38018	2.03	1.0E-68	11493277	NT	Homo sapiens myosin IC (MYO1C), mRNA
11748	24647	38127	1.72	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11748	24647	38128	1.72	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
12091	24932	38438	1.45	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12091	24932	38439	1.45	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12836	13185	26108	1.88	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
13033	25878	31476	1.75	1.0E-68	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13072	25986		1.74	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
21	13137	26023	11.09	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
21	13137	26024	11.09	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
1054	14088	27036	1.58	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
1054	14088	27037	1.58	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
11327	24246		4.82	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000988 5'
3445	16486		1.67	8.0E-69	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
6610	19851	32836	4.03	7.0E-69	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
8444	21376	34716	4.78	6.0E-69	A192764.1	EST_HUMAN	q62h01.x1 Scores_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743801 3' similar to gclL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8444	21376	34717	4.78	6.0E-69	A192764.1	EST_HUMAN	q62h01.x1 Scores_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743801 3' similar to gclL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
9525	22452	35815	1.17	5.0E-69	AA826039.1	EST_HUMAN	cd60a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1372300 3'
543	13612		1.32	4.0E-69	A1873630.1	EST_HUMAN	wm28h11.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437125 3'
5986	25636	32156	1.55	4.0E-69	BE561063.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677641 5'
6057	19119	32248	5.86	4.0E-69	A1764973.1	EST_HUMAN	wh57606.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137
6918	18948	33168	2.5	4.0E-69	4557732	NT	O55137 ACYL-COA THIOESTERASE...
6918	18948	33168	2.5	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
9471	22399	35782	0.62	4.0E-69	AU116634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
407	13520	26442	3	3.0E-69	BE258012.1	EST_HUMAN	AU116634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
635	13688	26601	1.39	3.0E-69	AF221712.1	NT	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
2399	15404		1.11	3.0E-69	5726970	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
4189	17190	30062	1.05	3.0E-69	A1765888.1	EST_HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1), mRNA
							wh66g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385788 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5423	18420	38564	1.92	3.0E-69	11418186	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
5825	18698	32009	0.51	3.0E-69	U14178.1	NT	Human type II IL-1 receptor gene, exon 1B
7113	20317		0.85	3.0E-69	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
7179	18451	31320	0.59	3.0E-69	11428786	NT	Homo sapiens sperm surface protein (HSS), mRNA
7764	20694	33993	0.8	3.0E-69	AF098703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
7821	20750	34055	1.39	3.0E-69	U52351.1	NT	encoding mitochondrial protein, complete cds
7983	20904	34220	8.3	3.0E-69	AF268075.1	NT	Homo sapiens arm-repeat protein NPRAP/neuriligin (CTNND2) mRNA, partial cds
8944	21874	35235	0.8	3.0E-69	AW138648.1	EST_HUMAN	Homo sapiens TRAF6-binding protein TBBP mRNA, complete cds
9327	22255		0.82	3.0E-69	AA376395.1	EST_HUMAN	U1-HBI-aw-g-01-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
9528	22455	35817	0.54	3.0E-69	8923248	NT	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
9947	22852	38240	1.49	3.0E-69	X13223.1	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
10062	22978	36369	3.86	3.0E-69	X06233.1	NT	H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
10344	23233	36651	0.63	3.0E-69	5730036	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
11088	24018	37459	2.12	3.0E-69	11432120	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
11278	24201		14.26	3.0E-69	AA376399.1	EST_HUMAN	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
12378	25159		6.23	3.0E-69	11419197	NT	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
133	13498	26421	1.03	2.0E-69	AF160252.1	NT	Homo sapiens HGC6.2 protein (HGC6.2), mRNA
133	13498	26422	1.03	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
427	13498	26421	3.54	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
427	13498	26422	3.54	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1905	14926	27905	1.23	2.0E-69	BE257857.1	EST_HUMAN	Homo sapiens 601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2889	15943		3.17	2.0E-69	AA431157.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:781882 5'
9117	22045	35402	0.94	2.0E-69	AA114270.1	EST_HUMAN	zw71g02.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:527088 5'
1730	14757	27727	1.92	1.0E-69	AF053788.1	NT	ztn28g01.11 Strategene pancreas (#937208) Homo sapiens cDNA clone IMAGE:527088 5'
5151	18144		0.82	1.0E-69	BE400094.1	EST_HUMAN	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
6285	19336	32502	0.64	1.0E-69	BE602501.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
6285	19336	32503	0.64	1.0E-69	BE602501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
6800	19920	33135	3.67	1.0E-69	AW393369.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958532 5'
7131	20335	33599	1.37	1.0E-69	7662283	NT	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
7131	20335	33600	1.37	1.0E-69	7662283	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7150	20258	33511	3.87	1.0E-69	AB032973.1	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
							Homo sapiens mRNA for KIAA1147 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7150	20258	33512	3.87	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7208	20208	33454	0.44	1.0E-69	BE631007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
7208	20208	33455	0.44	1.0E-69	BE631007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
10670	23556	36987	4.25	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10670	23556	36988	4.25	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10761	23847	37080	1.26	1.0E-69	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10898	23783	37209	0.62	1.0E-69	BF528429.1	EST_HUMAN	602043782F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181325 5'
11307	24226		3.18	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
12320	25121	38161	1.52	1.0E-69	BF125987.1	EST_HUMAN	601782902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12899	25355		5.43	1.0E-69	AI809994.1	EST_HUMAN	wf64c08.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2354	15921	26364	1.51	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4480	17491	30351	1.88	8.0E-70	L77566.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1835	14858	27839	2.36	7.0E-70	AI497807.1	EST_HUMAN	tr8970.1.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1835	14858	27840	2.36	7.0E-70	AI497807.1	EST_HUMAN	tr8970.1.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1945	14956	27945	1.13	7.0E-70	AA282956.1	EST_HUMAN	zf15h04.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2077	15091		3.09	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4324	17338	30203	4.6	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5071	18745	31655	5.41	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5071	18745	31656	5.41	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7254	20163	33402	1.79	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
8237	21142	34475	0.5	7.0E-70	11417306	NT	Homo sapiens titin immunoglobulin domain protein (myotilin) (TTID), mRNA
8321	21228	34560	0.41	7.0E-70	11419404	NT	Homo sapiens cerebral cavernous malformations 1 (CCM1), mRNA
9000	21929	35284	2.39	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
9000	21929	35285	2.39	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
9281	22209	35567	5.31	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9281	22209	35568	5.31	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9700	22626	36003	4.08	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9700	22625	36004	4.08	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9899	21327	34680	5.5	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9993	21350	34686	1.93	7.0E-70	11525984	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9993	21350	34687	1.93	7.0E-70	11525984	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10181	23072	36472	0.57	7.0E-70	4557824	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLG) mRNA
10787	23673	37101	0.92	7.0E-70	AB036428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10787	23673	37102	0.92	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11513	24423	37880	1.64	7.0E-70	11429885	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
11513	24423	37881	1.64	7.0E-70	11429885	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
12027	24869	38371	1.6	7.0E-70	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
12027	24869	38372	1.6	7.0E-70	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
13080	25002	31731	2.17	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa 1)
896	13949	26896	2.07	6.0E-70	4502168	NT	Homo sapiens amyloid beta (A β) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2151	15163	28165	1.59	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2534	15535	28535	1.01	6.0E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
4629	17635	30499	0.87	6.0E-70	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
2585	15927	28576	2.07	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2585	15927	28577	2.07	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12330	25128	33317	0.82	5.0E-70	BE168034.1	EST_HUMAN	MR3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
7059	20084	33568	1.44	4.0E-70	T06037.1	EST_HUMAN	EST03928 Fetal brain, Stratiogene (cat#836206) Homo sapiens cDNA clone HFBDN25
7102	20308	33568	3.67	4.0E-70	AW793226.1	EST_HUMAN	GM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
7102	20308	33569	3.67	4.0E-70	AW793226.1	EST_HUMAN	GM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
1612	14642	27602	1.64	3.0E-70	BE071798.1	EST_HUMAN	RCO-BT0522-071299-011-a12 B10522 Homo sapiens cDNA
1612	14642	27603	1.64	3.0E-70	BE071798.1	EST_HUMAN	RCO-BT0522-071299-011-a12 B10522 Homo sapiens cDNA
5312	18236	31149	1.3	3.0E-70	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
5814	18836	31998	0.57	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5814	18836	31997	0.57	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6170	19227	32372	0.89	3.0E-70	AJ831975.1	EST_HUMAN	wh90d03.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2388005 3'
6633	19673	32859	3.05	3.0E-70	BF085233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
6633	19673	32860	3.05	3.0E-70	BF085233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
10609	23495	36925	0.67	3.0E-70	BE502973.1	EST_HUMAN	h281h02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
40	13156	28047	1.17	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
713	13772	26689	11.81	2.0E-70	N42161.1	EST_HUMAN	y07a10.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
713	13772	26690	11.81	2.0E-70	N42161.1	EST_HUMAN	y07a10.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
728	13786	26712	3.34	2.0E-70	A1246989.1	EST_HUMAN	qx51h01.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1048	14032	27031	1.7	2.0E-70	8923689	NT	Homo sapiens hypothetical protein FLJ20768 (FLJ20768), mRNA
1212	14250	27191	2.33	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1212	14250	27192	2.33	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1770	14756	27766	4.33	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2341	15349		7.86	2.0E-70	AA054010.1	EST_HUMAN	Z48g04.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3691	16920	29797	0.9	2.0E-70	AL133207.2	NT	PC3345 GAG POLYPROTEIN ;
4133	17155	30032	6.28	2.0E-70	M69181.1	NT	Novel human gene mapping to chromosome X
5410	18391		0.65	2.0E-70	BE394321.1	EST_HUMAN	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5705	18778	31707	8.09	2.0E-70	X72662.1	NT	y07g02.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:3633204 5'
5705	18778	31708	8.09	2.0E-70	X72662.1	NT	H. sapiens gene for schwannomin (CS8)
6445	19491	32668	1.57	2.0E-70	AF310105.1	NT	H. sapiens gene for schwannomin (CS8)
6925	19984	33174	1.91	2.0E-70	D12825.1	NT	Homo sapiens NALP1 mRNA, complete cds
6963	19991	33217	9.46	2.0E-70	AF123074.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
6963	19991	33218	9.46	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7338	18506	31282	1.76	2.0E-70		NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7802	20731	34033	0.91	2.0E-70	AF288207.1	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA
8497	21428	34768	4.41	2.0E-70	M21741.1	NT	Homo sapiens cysteine-RNA synthetase mRNA, complete cds, alternatively spliced
8800	21730	35079	0.61	2.0E-70		NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-e-alpha), exons 4 and 5
9218	22146		0.78	2.0E-70	H47859.1	EST_HUMAN	Homo sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA
9711	22636	36017	1.29	2.0E-70	11526355	NT	storage disease type III (AGL), mRNA
10637	23523	36958	1.56	2.0E-70	AF123303.1	NT	y07g02.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:193882 5'
11508	24418	37872	2.96	2.0E-70	8923420	NT	Homo sapiens dynactin p82 subunit (LOC51184), mRNA
11508	24418	37873	2.96	2.0E-70	8923420	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
12066	24907	38409	10.99	2.0E-70	4503520	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
12687	25344	31824	2.1	2.0E-70	11430460	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
12687	25344	31825	2.1	2.0E-70	11430460	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (48KD) (EIF3S6) mRNA
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3452	16493		2.92	1.0E-70	4507478	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9820	22726		0.94	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416024 5'
10315	23204		0.61	1.0E-70	AA442302.1	EST_HUMAN	zv64c03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
11373	24289	37733	2.86	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLGB10 5'
6169	19226	32370	7.7	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6169	19226	32371	7.7	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
7381	20375	33644	2.07	9.0E-71	AI654903.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE. ;
11955	20375	33644	3.96	9.0E-71	AI654903.1	EST_HUMAN	wb52e05.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
9821	22547		2.73	8.0E-71	AA171451.1	EST_HUMAN	wb52e05.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
11069	23953	37388	0.57	8.0E-71	AW273820.1	EST_HUMAN	zp21d11.r1 Strategene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:310101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL. ;
7768	20698	33998	8.09	7.0E-71	AA44230.1	EST_HUMAN	TR:G1143061 G1143061 STRAIN XA34 POL. ;
9236	22184	35517	1.26	7.0E-71	AA706457.1	EST_HUMAN	XG24d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR:O54730
11774	24673	38162	1.93	7.0E-71	AL163210.2	NT	O64730 TRANSPLANTABILITY ASSOCIATED PROTEIN 1 ;
2225	15235	28242	5.03	5.0E-71	AF096322.1	NT	zv60f08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
4216	17232	30101	1.16	5.0E-71	AW818405.1	EST_HUMAN	zv91a06.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
6096	19157	32290	1.82	5.0E-71	4602740	NT	Homo sapiens chromosome 21 segment HS21C010
6956	19885	33209	1.56	5.0E-71	11641408	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
7249	20158	33397	0.95	5.0E-71	7662209	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
7314	18482	31305	0.42	5.0E-71	AB033106.1	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
7314	18482	31306	0.42	5.0E-71	AB033106.1	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7506	20445	33729	0.82	5.0E-71	11431580	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7533	20855	34163	1.7	5.0E-71	M38106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
8166	21073	34403	0.89	5.0E-71	11526445	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
8198	21104	34436	22.82	5.0E-71	AF072810.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
9087	22016	35371	0.85	5.0E-71	5453777	NT	Homo sapiens MAGUK protein p57, Protein Associated with Lins 2 (LOC51678), mRNA
9087	22016	35372	0.85	5.0E-71	5453777	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
10422	23311		2.54	5.0E-71	X13467.1	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
							Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
							Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11418	24334	37783	5.21	5.0E-71	11438514	NT	Homo sapiens pro-platelet basic protein (Includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11637	24543	38017	2.73	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC63325), mRNA
12284	25098	38574	1.49	5.0E-71	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0930), mRNA
107	13220	26133	1.14	4.0E-71	4607592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
370	13457	26371	80.47	4.0E-71	AF157826.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
370	13457	26372	90.47	4.0E-71	AF157826.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2928	15981	28878	2.47	4.0E-71	4605880	NT	Homo sapiens plasminogen (PLG) mRNA
4535	17544	30405	2.84	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5708	18705	30952	7.02	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
8612	21543		1.3	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element;
11134	24063	37909	4	3.0E-71	AA557683.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
1258	14293	27239	3.15	2.0E-71	AL163206.2	NT	Human mRNA for KIAA0272 gene, partial cds
5503	18582	31431	6.55	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5503	18582	31432	6.55	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
7305	18474	31295	0.64	2.0E-71	ALD42439.1	EST_HUMAN	DKFZp434D1721 J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1721 5'
8286	21190	34527	0.43	2.0E-71	AW601779.1	EST_HUMAN	QV4-BT0407-190100-082-g11 BT0407 Homo sapiens cDNA
8557	22484	35844	0.62	2.0E-71	BF195585.1	EST_HUMAN	7n85c11.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571221 3' similar to TR:Q9Z165 Q9Z165 PUTATIVE FOUR REPEAT ION CHANNEL. ;
11058	23942	37378	3.02	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
11058	23942	37378	3.02	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
11136	24065	37510	1.64	2.0E-71	BE018477.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW_R23B_HUMAN P64727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B ;
12014	24856	38356	2.43	2.0E-71	R55826.1	EST_HUMAN	y77c11.r1 Soares breast 2NbIBst Homo sapiens cDNA clone IMAGE:164772 5'
12390	25168		3.46	2.0E-71	T95489.1	EST_HUMAN	ye43a09.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120520 5'
							cy15d03.a1 Soares senescent fibroblasts 1NbHSP Homo sapiens cDNA clone IMAGE:1685916 3' similar to contains LORI b2 LORI repetitive element ;
661	13723	26634	1.42	1.0E-71	A1077927.1	EST_HUMAN	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
969	14020	26954	1.43	1.0E-71	7708281	NT	Homo sapiens disabled-2 gene, exons 2 through 16 and complete cds
1127	14169	27106	4.66	1.0E-71	AF205890.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
1368	14400	27354	9.53	1.0E-71	AF012872.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2095	15108	28112	1.73	1.0E-71	AB017007.1	NT	

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2095	15109	28113	1.73	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2743	15736	28730	3.8	1.0E-71	7697153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3658	16893	29588	8.66	1.0E-71	AF246210.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3658	16893	29589	8.66	1.0E-71	AF246210.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3717	16749	29636	0.9	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3717	16749	29637	0.9	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3804	16835	29721	2.12	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4582	17590	30451	2.75	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
7046	20072	33306	1.39	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GON5L2), mRNA
7445	20386	33655	1.35	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7695	20827	33926	11.37	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8725	21655	35001	0.76	1.0E-71	AF105287.1	NT	Homo sapiens glycyl-3 (GPC3) mRNA, complete cds
8747	21677	35019	2.11	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
9014	21943	35298	5.05	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
9014	21943	35298	5.05	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
9770	22694	36080	0.91	1.0E-71	S72393.1	NT	GSNK2A1=casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
10512	23399	36811	7.78	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
10370	23456		3.88	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
11017	23901	37339	1.18	1.0E-71	11433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
11223	24149		3.17	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
11319	24238	37682	4.22	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
12734	25375		11.87	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-9, complete cds
430	13501	26424	1.25	9.0E-72	AB57635.1	EST_HUMAN	wk95g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN; contains Alu repetitive element
430	13501	26425	1.25	9.0E-72	AB57635.1	EST_HUMAN	wk95g03.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN; contains Alu repetitive element
12202	25037	38538	1.6	9.0E-72	BF573955.1	EST_HUMAN	602131973F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271155 5'
12202	25037	38539	1.6	9.0E-72	BF573955.1	EST_HUMAN	602131973F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271155 5'
6349	18398	32566	0.94	8.0E-72	BF035762.1	EST_HUMAN	601458747F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862451 5'
4206	17223	30088	1.38	7.0E-72	4501896	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4206	17223	30089	1.38	7.0E-72	4501866	NT	Homo sapiens acylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4206	17223	30090	1.38	7.0E-72	4501866	NT	Homo sapiens acylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7484	20424	33704	2.67	7.0E-72	G41694.1	NT	{pseudogene} PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
12840	25453		2.12	7.0E-72	F26259.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s4000051G02
8955	21885		5.71	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21G046
68	13182	26089	0.9	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	13182	26090	0.9	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
67	13182	26089	4.78	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
67	13182	26090	4.78	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1166	14207		1.98	5.0E-72	L11045.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7282	20235	33485	1.42	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP203761 5'
9336	22264	35628	4.11	5.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to
10467	23355	36770	0.68	5.0E-72	AV724632.1	EST_HUMAN	TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ; contains element MSR1 repetitive element ;
11689	24591	38088	2.84	5.0E-72	BF331571.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAK801 5'
11689	24591	38089	2.84	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
12070	24911	38413	1.82	5.0E-72	BE208545.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
12070	24911	38414	1.82	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
12455	25910		3.12	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
4936	17934		1.57	4.0E-72	11034844	NT	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
5651	18725	31630	0.66	4.0E-72	AF170025.1	NT	Homo sapiens hypothetical protein dJ1057B20.2 (DJ1057B20.2), mRNA
6898	19870	33085	0.86	4.0E-72	T87947.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
7808	20737	34040	6.48	4.0E-72	5729867	NT	y83a07.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
10303	23193	36604	1.17	4.0E-72	8923669	NT	SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
							Homo sapiens hec domain and RLD 2 (HERC2), mRNA
							Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10903	23788	37216	0.99	4.0E-72	A1248796.1	EST_HUMAN	ql67c02.x1 Soares fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to
11731	24633	38114	1.52	4.0E-72	AA465388.1	EST_HUMAN	TR:Q14498 Q14498 SPlicing factor, [1]; contains Alu repetitive element; contains element L1 repetitive element;
							aa23f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:914121 3' similar to SW:CPTR_FLAPR
							P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11731	24633	38115	1.52	4.0E-72	AA465386.1	EST_HUMAN	aa23f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR
11959	24802	38300	7.7	4.0E-72	H79421.1	EST_HUMAN	P49731 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
12105	24946	38449	2.25	4.0E-72	T81910.1	EST_HUMAN	y428a03.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:236084 5'
							y429d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
12788	25415	31788	6.47	4.0E-72	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
20	13136	26022	3.4	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
928	13980		1.46	3.0E-72	AA723823.1	EST_HUMAN	af03a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1310290 3'
1182	14222	27169	4.37	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1182	14222	27160	4.37	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1221	14259	27199	3.81	3.0E-72	U80228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1221	14259	27200	3.81	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1541	14571	27530	0.98	3.0E-72	BE242161.1	EST_HUMAN	TCAAPE1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP1252
3124	16175	28070	15.69	3.0E-72	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3323	16369	29270	2.74	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3866	16925	29802	2.48	3.0E-72	S77569.1	NT	TCR V delta 2-C alpha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4661	17666	30634	3.32	3.0E-72	11416196	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
5710	18763		1.15	3.0E-72	4760093	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
6209	19264	32414	1.98	3.0E-72	AF073367.1	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6209	19264	32415	1.98	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6407	19455	32628	4.54	3.0E-72	AB028004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6407	19455	32629	4.54	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6868	19928	33146	3.61	3.0E-72	4826987	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
8022	20638	34253	2.47	3.0E-72	U80017.1	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
8754	21684	35027	1.39	3.0E-72	5031892	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nap) and survival motor neuron protein (smn) genes, complete cds
10913	23798	37227	1.23	3.0E-72	X08289.1	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
12706	25361	31798	2.29	3.0E-72	AB011399.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
						NT	Homo sapiens gene for AF-6, complete cds
6184	19241	32388	1.3	2.0E-72	11426671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9841	22587	35937	1.01	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9841	22587	35938	1.01	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
11181	24107	37554	2.45	2.0E-72	AA789277.1	EST_HUMAN	q28b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb.X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
12782	25411	31786	3.84	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphatidylphosphorylase translocator mRNA, complete cds
2089	15103	28103	1.04	1.0E-72	AA848225.1	EST_HUMAN	g183402.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387385 3'
6975	19040	32162	3.82	1.0E-72		NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS44), mRNA
6840	19872	33086	1.11	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6840	19872	33087	1.11	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6923	25658	33172	1.19	1.0E-72	AV751818.1	EST_HUMAN	AV751818 NPd Homo sapiens cDNA clone NPDAIE11 5'
7732	20684	33862	0.43	1.0E-72	BE701978.1	EST_HUMAN	601585888F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940460 5'
8086	20898	34318	3.7	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
8086	20898	34319	3.7	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
10119	23010	36406	9.3	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
10119	23010	36407	9.3	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1480	14511	27471	0.91	9.0E-73	AW374968.1	EST_HUMAN	MR0-C10063-071099-002-h11 C10063 Homo sapiens cDNA
6273	19324	32490	0.89	9.0E-73	11625883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
11380	24306		13.13	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1084	14107	27045	2.01	8.0E-73	AW071755.1	EST_HUMAN	ws53c08.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q69050
3336	16382	29281	0.74	8.0E-73	11436180	NT	Q59050 HYPOTHETICAL PROTEIN MJ1658 ;
5772	18845	31948	0.94	8.0E-73	4505798	NT	Homo sapiens gephyrin (GPH), mRNA
6854	19886	33100	4.57	8.0E-73	11426469	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
8674	21605	34947	2.13	8.0E-73	AF113129.1	NT	Homo sapiens lysocyme homolog (LOC57161), mRNA
						NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9891	22808	36184	4.46	8.0E-73	BE019900.1	EST_HUMAN	bb52a06.v1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb.X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb.M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
10260	23150	36557	1.54	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10260	23150	36558	1.54	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
12830	25447	31775	4.36	8.0E-73	11418189	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
1161	14202	27140	0.94	7.0E-73	8923260	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
3344	16390	29290	0.91	7.0E-73	AL183206.2	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
						NT	Homo sapiens chromosome 21 segment HS21C008

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4314	17328	30193	2.32	7.0E-73	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes >
5058	18055		1.6	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
168	13269		2.12	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7338	20475	33763	3.31	6.0E-73	BE166574.1	EST_HUMAN	QV6-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA
5435	18517	31242	1.85	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM/4A1), mRNA
1369	14401	27355	0.98	3.0E-73	AW943789.1	EST_HUMAN	CM0-CN0044-260100-164-f08 CN0044 Homo sapiens cDNA
1887	14908	27893	1.08	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1887	14908	27894	1.08	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
6995	20022	33254	0.98	3.0E-73	AA139403.1	EST_HUMAN	zn95d4.s1 Stratagene fetal retina 037202 Homo sapiens cDNA clone IMAGE:565950 3' similar to gb:223064 cd61 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
6317	22245	35606	0.87	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071 5'
6317	22245	35607	0.87	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAAF071 5'
12038	24980		1.57	3.0E-73	AI004040.1	EST_HUMAN	cu11d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625955 3'
13047	25580		2.1	3.0E-73	AW698081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
876	13929	26876	2.1	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1981	14980		3.01	2.0E-73	AW698081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2317	15325		1.83	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3224	16272	28172	2.63	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3609	16646	29345	0.73	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3609	16646	29546	0.73	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
6705	19741	32942	0.72	2.0E-73	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6705	19741	32943	0.72	2.0E-73	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Crik) mRNA, complete cds
6755	19786	33003	7.13	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6997	20024	33256	1.49	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6997	20024	33257	1.49	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
8299	21203	34539	0.6	2.0E-73	M94048.1	NT	Human peripheral myosin protein 22 mRNA, complete cds
8307	21211	34548	0.54	2.0E-73	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
10905	23790	37219	1.25	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10975	23859	37287	1.59	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10975	23859	37288	1.59	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11494	24408	37858	3.28	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11494	24408	37859	3.28	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11622	24432	37880	1.83	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12636	14980		2.74	2.0E-73	AW98081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1807	14833	27803	4.82	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2507	15508	28510	1.09	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
6819	19659	32843	1.1	1.0E-73	BE151283.1	EST_HUMAN	CM1-HT0282-111199-042-h10 HT0282 Homo sapiens cDNA
10031	22831	36317	1.58	1.0E-73	AI147427.1	EST_HUMAN	qg61b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element
11884	23984	37422	1.65	1.0E-73	BE385477.1	EST_HUMAN	MER22 repetitive element
764	13821	26760	2.58	8.0E-74	4557428	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6136	19195	32332	1.96	8.0E-74	S93194.1	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6136	19195	32333	1.96	8.0E-74	S93194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
11315	24234		1.47	8.0E-74	N52339.1	EST_HUMAN	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
1964	14982	27965	8.12	7.0E-74	AJ001689.1	NT	y44g10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246826 3'
3375	18419	28321	2.2	7.0E-74	AL163246.2	NT	Homo sapiens NK2D gene, exon 10
9785	22749	36131	2.77	7.0E-74	BE967432.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
12829	25446	31774	6.5	7.0E-74	BE268305.1	EST_HUMAN	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5'
1149	14191	27130	4.16	6.0E-74	AF109807.1	NT	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533855 5'
1650	14881	27643	0.98	6.0E-74	AW263177.1	EST_HUMAN	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
2337	15345	28348	8.31	6.0E-74	BE388280.1	EST_HUMAN	xt78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3'
2337	15345	28349	8.31	6.0E-74	BE388280.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2906	15959	28880	1.13	6.0E-74	AW014039.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2906	15959	28881	1.13	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-seah-h-03-o-UJ.st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3776	16807	28684	1.43	6.0E-74	BE048846.1	EST_HUMAN	UI-H-B10-seah-h-03-o-UJ.st NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3776	16807	29695	1.43	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5550	18828	31505	3.1	6.0E-74	11056013	NT	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
930	13982	26927	1.86	5.0E-74	AW020986.1	EST_HUMAN	Homo sapiens actin filament associated protein (AFAP), mRNA
2753	15744		2.92	5.0E-74	AW362756.1	EST_HUMAN	df17c09.y1 Morton_Fetal_Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
5592	18668	31546	2.06	5.0E-74	11425417	NT	PMO-GT0289-271089-001-h07 CT0289 Homo sapiens cDNA
6000	18065	32182	11.56	5.0E-74	X89670.1	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
6052	19114	32243	10.24	5.0E-74	4507896	NT	H.sapiens mRNA for TPCP16 protein
							Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6128	19187	32322	2.34	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6128	19187	32323	2.34	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7223	20222	33470	3.39	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8121	20222	33470	0.88	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8614	21545	34886	1.82	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
11176	24103	37549	2.08	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
11176	24103	37550	2.06	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
289	13392	26311	1.99	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
877	13930	26877	2.7	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1976	14994	27977	1.97	4.0E-74	AB028988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1976	14994	27978	1.97	4.0E-74	AB028988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2086	15100	28099	3.61	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA
2086	15100	28100	3.61	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA
2146	15159	28181	1.35	4.0E-74	AB032694.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2451	15455	28452	0.91	4.0E-74	AJ008976.1	NT	Homo sapiens PLP gene
3140	16190	29063	4.65	4.0E-74	AJ008976.1	NT	Homo sapiens PLP gene
3588	16628	29529	0.87	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4150	17171	30043	0.93	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4198	17217	30083	1.02	4.0E-74	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCLAT displacement protein) (CUTL1), mRNA
4672	17671	30546	1.08	4.0E-74	7662163	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4727	17732	30594	1.13	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor, protein
9114	22042		5.63	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
9138	22066	36427	0.61	3.0E-74	9668912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
9911	22899	36286	2.27	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Stratagene (cat. #836205) Homo sapiens cDNA clone HHCPF91
10828	23712	37139	2.9	3.0E-74	AA001493.1	EST_HUMAN	nc17g05.st NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
984	14035	26978	107.11	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
984	14035	26979	107.11	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1203	14242	27183	0.96	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1272	14306	27257	1.38	2.0E-74	AI960528.1	EST_HUMAN	wx51e07.x1 NC1_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95, contains element MER22 repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1618	14648	27610	2.74	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1618	14648	27611	2.74	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2644	15640	28639	2.02	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.r tumor2 Homo sapiens cDNA 3'
5127	18123	30984	3.33	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5127	18123	30985	3.33	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5133	18128	30971	4.76	2.0E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' and
5393	18375	31216	0.98	2.0E-74	BE409484.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
5393	18375	31217	0.98	2.0E-74	BE409484.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
6009	25637	32198	1.75	2.0E-74	BE711134.1	EST_HUMAN	RC8-H10878-220500-011-C03 HT0678 Homo sapiens cDNA
6114	25640	32306	1.97	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6114	25640	32307	1.97	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6193	25640	32308	2.87	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6193	25640	32307	2.87	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7462	20402	33677	1.22	2.0E-74	BF030788.1	EST_HUMAN	601557624F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
8519	21450	34782	1.83	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
9920	22908	36297	6.09	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12572	25277		2.33	2.0E-74	AA198181.1	EST_HUMAN	z986a06.s1 Stretagen muscle 937209 Homo sapiens cDNA clone IMAGE:928018 3'
13065	25591	31742	2.38	2.0E-74	BF666588.1	EST_HUMAN	602121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278569 5'
13075	25944		1.5	2.0E-74	BF002855.1	EST_HUMAN	7950a08.x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309878 3'
56	13173	26073	1.27	1.0E-74	7657334	NT	Homo sapiens Mieshaen/NIK-related kinase (MINK), mRNA
357	13444	26356	3.35	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
522	13592	26504	0.91	1.0E-74	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
529	13598	26509	6.61	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
622	13687	26590	2.31	1.0E-74		NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1027	14076	27016	1.47	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2239	15249	28256	4.43	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3184	16233	29128	2.62	1.0E-74	4758687	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
4051	17078	29983	5.43	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4151	17172	30044	0.68	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0842-270300-019-06 BT0842 Homo sapiens cDNA
7002	20029	33260	3.95	1.0E-74	M89914.1	NT	Human neurofilament (NF1) gene, complete cds
8074	20987	34304	1.3	1.0E-74	11417977	NT	Homo sapiens KIAA0862 protein (KIAA0862), mRNA
8323	21228	34562	0.45	1.0E-74	9508868	NT	Homo sapiens hypothetical protein similar to tumor suppressor p33ING1 (FLJ20089), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar: (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8634	21565	34902	1.33	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8634	21565	34903	1.33	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9363	22291	35656	4.87	1.0E-74	AF214502.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9392	22320	35683	0.84	1.0E-74	BF351951.1	EST_HUMAN	MRO-HT0599-230500-021-a03 HT0599 Homo sapiens cDNA
10734	23620	37049	0.62	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10734	23620	37050	0.62	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10960	23844	37270	1.81	1.0E-74	11420549	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
12245	25089	38567	1.63	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12321	25122		4.66	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12451	15249	28256	1.9	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2692	16686		5.41	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12596	25292		4.03	8.0E-75	AL169202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2342	15350	28353	2.84	6.0E-75	AB17415.1	EST_HUMAN	wk38a08.x1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL. POLYPEPTIDE (HUMAN);
6959	19988	33212	0.48	5.0E-75	BF211517.1	EST_HUMAN	601812201F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048497 5'
8274	21178	34516	0.41	5.0E-75	AA573446.1	EST_HUMAN	nk99d03.st NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:1028933 3'
8274	21178	34517	0.41	5.0E-75	AA573446.1	EST_HUMAN	nk99d03.st NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:1028933 3'
9485	22393	35754	2.98	5.0E-75	BE272325.1	EST_HUMAN	601126088F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2889865 5'
9661	22587	35958	0.63	5.0E-75	AA132611.1	EST_HUMAN	zot17e08.r1 Stratiogene colon (#837204) Homo sapiens cDNA clone IMAGE:587174 5'
9736	22661	36044	0.53	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9736	22661	36045	0.53	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9912	22900	36287	1.18	6.0E-75	BF690264.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
10729	23615	37042	2.99	5.0E-75	AB386623.1	EST_HUMAN	tt31c12.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 HYPOPHYSICAL 20.1 KD PROTEIN ;
116	13224	28136	1.89	4.0E-75	BE081333.1	EST_HUMAN	QV1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
481	13552		1.19	4.0E-75	N36757.1	EST_HUMAN	yedh08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:269055 5'
1790	14816	27785	1.28	4.0E-75	AW897230.1	EST_HUMAN	CMD-NN0057-150400-335-at1 NN0057 Homo sapiens cDNA
2893	15947	28847	5.51	4.0E-75	BE409484.1	EST_HUMAN	601303888F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
3359	16596	28500	1.23	4.0E-75	8922637	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
5719	18792	31883	0.58	4.0E-75	11417949	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5719	18792	31884	0.58	4.0E-75	11417949	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6521	18565	32747	5.28	4.0E-75	5579457	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (EIF3S8), mRNA
7064	20088	33322	3.83	4.0E-75	11417949	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
7064	20088	33323	3.83	4.0E-75	11417949	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1127	24057	37503	16.27	4.0E-75	7669805	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1030	14079	27019	3.17	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1031	14079	27019	2.28	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1860	14882	27862	2.12	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2124	15137	28143	1.01	3.0E-75	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2448	15450	28446	2.67	3.0E-75	4759153	NT	Homo sapiens synaptonemal-associated protein, 28kD (SNAP28) mRNA
3067	16119	29020	0.86	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3232	16280	29180	1.16	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3398	16441	29346	0.84	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3399	16441	29347	0.84	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4543	17552	30412	0.74	3.0E-75	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
9432	18514	31237	0.82	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
9432	18514	31238	0.82	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
8786	18819	33031	0.71	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
8788	18819	33032	0.71	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7078	20282	33538	1.67	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7076	20282	33539	1.67	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7495	20435	33714	4.51	3.0E-75	7662209	NT	Homo sapiens KIAA0823 gene product (KIAA0823), mRNA
7495	20435	33716	4.51	3.0E-75	7662209	NT	Homo sapiens KIAA0823 gene product (KIAA0823), mRNA
8070	20963	34297	3.06	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
8070	20963	34298	3.06	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
9536	22463	35825	1.39	3.0E-75	11420804	NT	Homo sapiens snail 1 (Drosophila homolog), zinc finger protein (SNAIL), mRNA
10203	23094	36494	0.62	3.0E-75	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
12200	26035	38635	1.91	3.0E-75	6715588	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12200	25035	38536	1.91	3.0E-75	6715588	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
5870	18541		1.48	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone cdaBED02 5'
9310	22238	35569	2.53	2.0E-75	AB11783.1	EST_HUMAN	q91e02.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to TR:Q69386 Q69386 POL/ENV GENE;
2322	16330	28333	13.14	1.0E-75	AW168135.1	EST_HUMAN	Xg60d02.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains P TR7.1
2988	16040	28945	2.2	1.0E-75	X62221.1	NT	PTR7 repetitive element;
8027	20543	34258	0.64	1.0E-75	BE082528.1	EST_HUMAN	H. sapiens ERCC2 gene, exons 1 & 2 (partial)
							RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8027	20943	34259	0.64	1.0E-75	BE082528.1	EST_HUMAN	RC5-B1064D-020300-031-H03 BT0640 Homo sapiens cDNA
8086	21014		6.94	1.0E-75	AA390270.1	EST_HUMAN	z57H03.31 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:M13932 40S
9962	22867	36266	3.62	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
9962	22867	36266	3.92	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
11320	24239		5.75	1.0E-75	AA664377.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
11535	24445	37906	2.88	1.0E-75	AF223391.1	NT	ac77b08.s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
12495	18435	31357	2.2	1.0E-75	BE894192.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
47	13164	26057	1.62	9.0E-76	A1652648.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
47	13164	26058	1.62	9.0E-76	A1652648.1	EST_HUMAN	w630b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O76235 O75235
10413	23302	36719	13.15	9.0E-76	M12937.1	NT	TRAP1;
153	13263	26171	9.17	8.0E-76	AF154830.1	NT	Human ferritin Heavy subunit mRNA, complete cds
968	14017	26960	15.99	8.0E-76	4504374	NT	Homo sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
966	14017	26981	15.99	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2668	15566	28666	1.48	8.0E-76	AF228180.1	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2953	16005	28907	0.99	8.0E-76	7706724	NT	Homo sapiens alpha-antitrypsin semialdehyde synthase mRNA, complete cds
6412	19460	32634	5.93	8.0E-76	11421442	NT	Homo sapiens mediator (Sur2), mRNA
7910	20834	34136	1.96	8.0E-76	11436216	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7999	20917	34233	1.07	8.0E-76	11419212	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
8872	21802	35156	0.73	8.0E-76	11418961	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
10866	23752	37177	1.15	8.0E-76	M13792.1	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
11110	24041	37486	5.26	8.0E-76	10442821	NT	Human adenosine deaminase (ADA) gene, complete cds
12816	25437		2.4	8.0E-76	11417862	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
802	13857	26793	3.07	7.0E-76	5016092	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3337	16383	29282	4.12	7.0E-76	AF056490.1	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3943	16389	29289	11.03	7.0E-76	4505052	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3384	16427	29332	1.09	7.0E-76	4757915	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4478	17489	30348	6.17	7.0E-76	4507184	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2, translocated to, 1; cyclin D-related (CBFA2T1) mRNA
							Homo sapiens espiaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4478	17489	30349	6.17	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1282	14288		6.16	6.0E-76	BE396283.1	EST_HUMAN	601312018F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
11897	23987	37435	2.86	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508029 5'
1958	14977	27959	4.81	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1958	14977	27960	4.81	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1958	14977	27961	4.81	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3252	16300	29205	0.85	4.0E-76	BE814088.1	EST_HUMAN	QV3-BN0047-270700-283-g06 BN0047 Homo sapiens cDNA
5452	18533	31259	1.36	4.0E-76	BE783412.1	EST_HUMAN	801471725F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3874470 5'
10527	23413	36826	5.86	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiiwara) Homo sapiens cDNA clone GEN-178G01 5'
10527	23413	36827	5.86	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiiwara) Homo sapiens cDNA clone GEN-178G01 5'
653	13714	26823	2.1	3.0E-76	BF516262.1	EST_HUMAN	U1-H-BW1-enz-b-04-0-U1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
653	13714	26824	2.1	3.0E-76	BF516262.1	EST_HUMAN	U1-H-BW1-enz-b-04-0-U1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1622	14652	27815	4	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1622	14652	27816	4	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3490	16529	29428	6.96	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3490	16529	29429	6.96	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
4165	17188	30059	1.14	3.0E-76	BE348893.1	EST_HUMAN	h87f12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151823 3' similar to TR:O94886 O94886
5418	18417	38563	2.05	3.0E-76	Z41314.1	EST_HUMAN	KIAA0792 PROTEIN ;
5936	19002	32121	1.04	3.0E-76	AA160611.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
6219	19274	32428	0.6	3.0E-76	AW027705.1	EST_HUMAN	z073c07.r1 Strategene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592524 5' similar to gb:L32976 MIXED LINEAGE KINASE 1 (HUMAN);
6628	19668	32853	9.03	3.0E-76	AF286588.1	NT	ww7605.x1 Soares_thymus_NHFT Homo sapiens cDNA clone IMAGE:2535368 3'
8728	21659	35006	1	3.0E-76	N42671.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
10238	23129	36532	3.26	3.0E-76	AW289353.1	EST_HUMAN	y20g10.r1 Soares_melanocyte_2N8HM Homo sapiens cDNA clone IMAGE:271842 5'
10261	23151	36559	0.81	3.0E-76	AA442308.1	EST_HUMAN	xa49h01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
10261	23151	36560	0.81	3.0E-76	AA442309.1	EST_HUMAN	z064d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
12237	25757	31573	2.3	3.0E-76	AW967884.1	EST_HUMAN	z054d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
12333	25953	31360	2.7	3.0E-76	AW956465.1	EST_HUMAN	EST1380059 MAGe resequences, MAGJ Homo sapiens cDNA
301	13394	26313	1.03	2.0E-76	D64295.1	NT	EST1388525 MAGe resequences, MAGD Homo sapiens cDNA
362	13449	26360	2.95	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
362	13449	26361	2.95	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
483	13554		1.24	2.0E-76	4557662	NT	Human mRNA for possible protein TPRDII, complete cds
611	13676	26579	0.95	2.0E-76	4503944	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
							Homo sapiens glucagon (GCG) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1559	14500	27550	1.5	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1559	14500	27551	1.5	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1943	14864	27943	1.08	2.0E-76	AA253954.1	EST_HUMAN	zs60h11.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:701025 3'
2887	15941	28943	4.42	2.0E-76	P23288	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3340	16386	29286	2.19	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
3340	16386	29287	2.19	2.0E-76	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3535	16573	29477	1.03	2.0E-76	AI821149.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
4612	17620	30483	0.9	2.0E-76	11545921	NT	ec83b02.y6 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:O14591
4647	17653	30519	1.03	2.0E-76	AL163283.2	NT	O14591 SIMILARITY TO P22059 ;
5062	18059	30911	8.04	2.0E-76	AW879818.1	EST_HUMAN	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
5492	18572	31624	1.54	2.0E-76	AF127845.1	NT	Homo sapiens chromosome 21 segment HS21C083
5646	18720	31624	0.49	2.0E-76	9968846	NT	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5813	18865	31995	4.95	2.0E-76	AB029004.1	NT	Gorilla gorilla olfactory receptor (GGO18) gene, partial cds
7812	20741	34045	0.82	2.0E-76	11421326	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7838	20766	34069	0.64	2.0E-76	11426908	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
8112	21024	34350	1.77	2.0E-76	11427410	NT	Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA
10774	23660	37089	2.86	2.0E-76	11437211	NT	Homo sapiens TPCR96 protein (HSTPCR96P), mRNA
11355	24276	37718	3	2.0E-76	7549807	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63150), mRNA
4400	17413	30279	2.02	1.0E-76	D63874.1	NT	Homo sapiens HIRA interacting protein 4 (dnaj-like) (HIRIP4), mRNA
4400	17413	30280	2.02	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5633	18708	31609	5.05	1.0E-76	BE795537.1	EST_HUMAN	Human mRNA for HMG-1, complete cds
6492	19536		0.82	1.0E-76	AA333207.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
7302	18471		0.46	1.0E-76	7706540	NT	EST37301 Embryo, 8 week I Homo sapiens cDNA 5' end
7253	20162	33401	5.09	9.0E-77	BE889525.1	EST_HUMAN	Homo sapiens helicase-like protein NHL (LOC51750), mRNA
199	13297	26212	1.05	8.0E-77	R83144.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
4642	17648	30513	1.67	8.0E-77	BF205181.1	EST_HUMAN	yp11h02.r1 Soares breast 3NhbBst Homo sapiens cDNA clone IMAGE:187155 5' similar to SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
5638	18714	31615	2.98	8.0E-77		NT	601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
11824	24744	38235	1.9	8.0E-77	AA019770.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mox34 homolog) (PSMD7) mRNA
11824	24744	38236	1.9	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11824	24744	38236	1.9	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12943	25509	31772	25.24	8.0E-77	R00245.1	EST_HUMAN	y68904.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element;
1944	14965	27944	2.21	7.0E-77	AA825755.1	EST_HUMAN	Zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2435	15439	28439	3.76	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2435	15439	28440	3.78	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
282	13376	28291	4.07	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1169	14210	27148	1.12	6.0E-77	AW957753.1	EST_HUMAN	EST359823 IMAGE resequences, MAGE Homo sapiens cDNA
1585	14598	27558	1.4	6.0E-77	A1204066.1	EST_HUMAN	qe77h12.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
165	13255	28173	3.56	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
155	13255	28174	3.56	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
1284	14288	27244	1.77	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1387	14418	27373	1.19	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2734	15727	28724	1.16	5.0E-77	AF162886.1	NT	Homo sapiens tousel-like kinase 1 (TLK1) mRNA, complete cds
2814	15803	28801	0.94	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3583	16620	28524	1.08	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
5050	18047	30801	2.53	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
7091	20297	33557	0.67	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7711	20643	33940	0.44	5.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8033	20643	33940	0.49	5.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8940	21870	35228	1.98	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8940	21870	35229	1.98	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
10095	22847	36335	3.66	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10098	22847	36336	3.66	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10869	23853	37279	0.7	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10969	23853	37280	0.7	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
12212	25046	38549	1.83	5.0E-77	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
1988	15006	27894	1.5	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1988	15006	27895	1.5	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10780	23666	37094	0.6	3.0E-77	H65187.1	EST_HUMAN	y64901.r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY295 - ;
10780	23666	37095	0.8	3.0E-77	H65187.1	EST_HUMAN	y64901.r1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to
11310	24229	37675	3.65	3.0E-77	BF359917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA clone IMAGE:238608 5' similar to
1381	14413	27367	1.2	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBT10 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1462	14484	27445	5.01	2.0E-77	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-101 BN0053 Homo sapiens cDNA
2103	15117	28121	2.01	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2115	15128	28133	2.84	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51034), mRNA
2635	15928	28627	2.42	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2635	15928	28628	2.42	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4116	17139	30012	1.51	2.0E-77	BE044316.1	EST_HUMAN	h04305.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4881	17880	30745	1.13	2.0E-77	AA653025.1	EST_HUMAN	ns58g12.s1 NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L28 [1]; contains element MSR1 repetitive element ;
6180	19237	32384	1.91	2.0E-77	BE288940.1	EST_HUMAN	601119862F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
6413	19461	32635	1.7	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
7538	20477	33765	14.83	2.0E-77	AI833003.1	EST_HUMAN	at74e09.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151 [1] ;
9093	22022	35379	0.87	2.0E-77	AI362707.1	EST_HUMAN	qy70c09.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F28D11.1 CE05765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN ;
10058	22874	36365	5.95	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10058	22874	36368	5.95	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10500	23388	36788	0.53	2.0E-77	BF310349.1	EST_HUMAN	607895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
10500	23388	36789	0.53	2.0E-77	BF310349.1	EST_HUMAN	607895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
46	13162	26053	1.92	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
46	13162	26054	1.92	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
292	13386	26302	2.43	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
292	13386	26303	2.43	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
900	15887	26801	3.14	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
900	15887	26902	3.14	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2468	15471	28471	1.88	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3092	16143	29039	3.16	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4463	17474	30331	4.05	1.0E-77	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4618	17626	30490	0.7	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4643	17649	30514	24.64	1.0E-77	AJ228041.1	NT	Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4761	17766	30629	1.74	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4989	17897	30844	1.11	1.0E-77	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
6153	19211	32350	1.26	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6153	19211	32351	1.26	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6282	19333	32499	1.64	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6718	19754	32960	1.18	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7406	20105	33339	16.49	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
8117	21026	34355	1.17	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
8232	21137	34469	0.62	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
11004	23898	37321	1.15	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
11004	23898	37322	1.15	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
11517	24427	37895	1.59	1.0E-77	11433426	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
11026	23912	37354	3.18	9.0E-78	AW769302.1	EST_HUMAN	RC3-CT0254-280998-011-005 CT0254 Homo sapiens cDNA
6716	19752	32957	2.04	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-005 ET0023 Homo sapiens cDNA
6716	19752	32958	2.04	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-005 ET0023 Homo sapiens cDNA
88	13201	26114	1.79	8.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
88	13201	26115	1.79	8.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
6841	19873		2.66	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
233	13331	26245	1.91	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2597	15595	28590	4.66	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE2900405 5' similar to WP.Y4856A.6
3444	16485	26393	4.49	5.0E-78	M55586.1	NT	GE22121 :
5597	18673	31551	2.28	5.0E-78	AF038536.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5707	18840	31941	12.03	5.0E-78	11416885	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
7515	20454	33740	2.46	5.0E-78	AW953120.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9029	22555	35925	7.07	5.0E-78	U60889.1	NT	EST365160 MAGE resequences, MAGEB Homo sapiens cDNA
9630	22556	35926	3.47	5.0E-78	BE960836.1	EST_HUMAN	Human lysosomal alpha-mannosidase (manB) gene, exon 7
1184	14206	27143	1.57	4.0E-78	AL043314.2	EST_HUMAN	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE3031887 5'
1539	14569	27528	2	4.0E-78	AL355841.1	NT	DKFZP434N0323 J1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZP434N0323 5'
1676	14705	27687	1.06	4.0E-78	AI985094.1	EST_HUMAN	Novel human gene mapping to chromosome 22
2338	15347	28351	2.49	4.0E-78	AF107405.1	NT	wf97b12.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE2495615 3' similar to SW.WAP_PIG
4428	17439	30298	2.2	4.0E-78	7656876	NT	O46855 WHEY ACIDIC PROTEIN PRECURSOR :
							Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
							Homo sapiens synectin (LOC30816), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5978	19041	32163	1.03	4.0E-78	11420732	NT	Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA
6414	19462	32636	0.57	4.0E-78	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
6414	19462	32637	0.57	4.0E-78	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
6855	19887	33101	0.74	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7912	20836	34139	0.59	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9412	22340	35704	1.32	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9412	22340	35705	1.32	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9907	22895	36282	0.74	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XROCC4), mRNA
10925	23810	37237	1.74	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H-2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10925	23810	37238	1.74	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H-2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11852	24702	38193	2.33	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
11981	24833	38331	2.65	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12839	25452	31778	3.27	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
171	13272	26186	1.45	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
171	13272	26187	1.45	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
2323	15331	28334	1.03	3.0E-78	4502142	NT	Homo sapiens apoptosis inhibitor 3 (API3) mRNA
3828	16958		1.25	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
3888	16916	29793	0.9	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4198	16915	29793	0.71	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
10778	23664		5.84	3.0E-78	BE144795.1	EST_HUMAN	CMO-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA
11419	24335	37784	1.97	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-160200-114-g09 HT0367 Homo sapiens cDNA
3168	16216		2.84	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4100	17125		1.76	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
7880	20808	34110	1.2	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aag-g-10-0-JLr1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7880	20806	34111	1.2	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aag-g-10-0-JLr1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
8194	21101	34431	3.38	2.0E-78	BF688800.1	EST_HUMAN	602186529f1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
8618	21549	34890	2.95	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBFW08 5'
9020	21949	35304	2.16	2.0E-78	AI557509.1	EST_HUMAN	P2.1_16 B07.r tumor2 Homo sapiens cDNA 3'
9020	21949	35305	2.16	2.0E-78	AI557509.1	EST_HUMAN	P2.1_16 B07.r tumor2 Homo sapiens cDNA 3'
							q150H06.xt NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:1659961 3' similar to WFP.R90.1
11519	24428	37887	3.82	2.0E-78	AI197937.1	EST_HUMAN	CE06925 PROTEIN KINASE;
11564	24473	37940	2.05	2.0E-78	N66951.1	EST_HUMAN	za49f12.s1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:296823 3'
5488	18568	31414	3.22	1.0E-78	11417304	NT	Homo sapiens GAP-like protein (LOC51306), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7288	18457	31327	5.45	1.0E-78	AV648989.1	EST_HUMAN	AV648989 GLC Homo sapiens cDNA clone GLCBM001 3'
8737	21667		1.97	1.0E-78	U52373.1	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
12480	25224	31658	1.98	1.0E-78	11435903	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC83140), mRNA
4811	17812	30978	3.97	9.0E-79	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
5618	18694	31590	14.17	9.0E-79	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6587	19638	32818	2.33	9.0E-79	6454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
6905	19935	33152	1.07	9.0E-79	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
7738	26675		1.02	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
8008	20925	34242	1.07	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H. GS165L15.1), mRNA
8008	20925	34243	1.07	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H. GS165L15.1), mRNA
8061	20974	34260	0.61	9.0E-79	D30658.1	NT	Human T-cell mRNA for glycyl tRNA synthetase, complete cds
8920	21850	35204	0.53	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8920	21850	35205	0.53	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9615	22541	35911	6.45	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9615	22541	35912	6.45	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
10851	23737	37160	0.73	9.0E-79	11438843	NT	Homo sapiens hypothetical protein FLJ20335 (FLJ20335), mRNA
10901	23786	37212	1.11	9.0E-79	AF052346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10901	23786	37213	1.11	9.0E-79	AF052346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11945	24789	38286	3.28	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
11945	24789	38287	3.28	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
13023	25568	31760	2.04	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3805	16836	29722	0.9	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4609	17617	30478	0.97	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4609	17617	30479	0.97	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
3287	16344	28248	3.47	7.0E-79	BE619648.1	EST_HUMAN	601472766T1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE3875657 3'
9202	22130		0.6	6.0E-79	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12266	25076		3.13	6.0E-79	AA699828.1	EST_HUMAN	2194c04.s1 Soares fetal_liver_spleen_INFLS S1 Homo sapiens cDNA clone IMAGE462558 3' similar to
11927	24772	38270	2.77	5.0E-79	AL163282.2	NT	TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
3219	18267		0.95	4.0E-79	8922326	NT	Homo sapiens chromosome 21 segment HS21C082
333	13423	26339	2.27	3.0E-79	AF114488.1	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
1005	14054	26998	3.03	3.0E-79	AF232708.1	NT	Homo sapiens intercellular short isoform (ITSN) mRNA, complete cds
							Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cin) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3146	16196	28089	1.95	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5269	18255	31104	0.7	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5269	18255	31105	0.7	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5546	16624	31499	6.86	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5925	18992	32111	1.81	3.0E-79	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5954	19021	32141	0.94	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5954	19021	32142	0.94	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5977	19042	32164	3.79	3.0E-79	11426770	NT	Homo sapiens nefrin 1 (NTN1), mRNA
5977	19042	32165	3.79	3.0E-79	11426770	NT	Homo sapiens nefrin 1 (NTN1), mRNA
7049	20076	33308	0.83	3.0E-79	BE268893.1	EST_HUMAN	601112055F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352885 5'
7414	20113	33347	4.55	3.0E-79	AB014820.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7414	20113	33348	4.55	3.0E-79	AB014820.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8370	21274	34607	0.47	3.0E-79	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8742	21672	35015	0.99	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
10834	23720	37620	0.71	3.0E-79	AV698115.1	EST_HUMAN	AV698115 GKC Homo sapiens cDNA clone GKCAHE11 5'
11295	24215	37684	1.9	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
11295	24215	37666	1.9	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
307	13400		0.83	2.0E-79	H63129.1	EST_HUMAN	y4803.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208541 3'
657	13719	26630	2.39	2.0E-79	BE379926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
956	14006	26952	1.45	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1061	14105		1.37	2.0E-79	AI523747.1	EST_HUMAN	th18h07.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2118685 3'
2162	15174	28178	9.07	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2162	15174	28179	9.07	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2334	18342	28347	2.37	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
4262	17278	30147	1.41	2.0E-79	AI271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4801	17802	30669	0.68	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5868	18939		1.21	2.0E-79	AA312223.1	EST_HUMAN	EST182926 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
5928	18895	32114	0.78	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6491	19535	32713	1.06	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
7297	18466	31336	2.11	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7530	20469	33757	1.72	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7630	20469	33758	1.72	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8879	21610	34951	1.05	2.0E-79	4506442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
9082	22011	35368	2.37	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9325	22253	35617	0.74	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9325	22253	35618	0.74	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9556	22483	35843	0.85	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (H. sapiens) (LOC83981), mRNA
10594	23480	36907	1.72	2.0E-79	S72869.1	NT	H4(D10S1170) putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10594	23480	36908	1.72	2.0E-79	S72869.1	NT	H4(D10S1170) putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
11470	24383	37830	5.85	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
11470	24383	37831	5.85	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
12294	18432	31354	4.67	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12372	25155	31869	4.94	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12578	25279	31839	1.96	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6870	25656		2.98	1.0E-79	BF363071.1	EST_HUMAN	MFO-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA
6891	20018	33250	0.51	1.0E-79	A1613480.1	EST_HUMAN	h97e08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
6891	20018	33251	0.51	1.0E-79	A1613480.1	EST_HUMAN	TEKTIN C1.;
8820	21750	35096	0.92	1.0E-79	BE394211.1	EST_HUMAN	h97e08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
12048	24889	38393	1.84	1.0E-79	BF087405.1	EST_HUMAN	601311517F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632809 5'
3189	16238	29132	2.56	9.0E-80	AA725848.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
3189	16238	29133	2.56	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.a1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
10516	23403	36815	1.18	9.0E-80	BE798603.1	EST_HUMAN	ai23e05.a1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
11722	24624	38104	9.06	9.0E-80	11433924	NT	601861652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5'
11722	24624	38105	9.06	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3664	16598		1.68	8.0E-80	U94387.1	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
8048	20561	34276	2.7	8.0E-80	11422847	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
8048	20561	34277	2.7	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9338	22843	36231	1.41	8.0E-80	6005921	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9338	22843	36232	1.41	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7313	18431	31304	0.56	7.0E-80	AF127882.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
							Caallitrix jecchus olfactory receptor (CJA80) gene, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
925	13977	28923	1.89	8.0E-80	A1422197.1	EST_HUMAN	tf58d02.x1 NC1_QGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
1670	14700	27660	1.42	6.0E-80	U64898.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2318	15326	28326	1.84	6.0E-80	6631094	NT	Homo sapiens mitochondriome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2318	15326	28327	1.84	6.0E-80	6631094	NT	Homo sapiens mitochondriome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
3688	16702	26696	1	6.0E-80	AA349168.1	EST_HUMAN	EST59737 Infant adrenal gland II Homo sapiens cDNA 5' end
4383	17397	30284	1.07	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4383	17397	30265	1.07	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
6012	19075	32201	3.28	6.0E-80	11421462	NT	Homo sapiens melate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6312	19382	32532	2.97	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6474	19519	32695	4.13	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6524	19588		0.95	6.0E-80	7682393	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
6578	19619	32803	0.81	6.0E-80	M18533.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
9383	22311	36672	3.18	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9383	22311	36673	3.18	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9570	22497	36860	1.78	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9897	22812	36202	0.9	6.0E-80	AF161495.1	NT	Homo sapiens HSPC146 mRNA, complete cds
10375	23284	36886	1.93	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
11380	24296	37742	2.38	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11673	24577	38053	33.19	6.0E-80	AF228730.1	NT	Homo sapiens Cyf19 mRNA, complete cds
12125	24968	38471	1.44	6.0E-80	U76560.1	NT	Homo sapiens N-acetylglucosamine-6-phosphate mutase mRNA, complete cds
12171	25007	38510	1.48	6.0E-80	AF102265.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12382	25781		2.11	6.0E-80	AF240786.1	NT	Homo sapiens GST gene for cerebroside sulfoxidase, exon 1, 2, 3, 4, 5
12563	25273		7.19	6.0E-80	AB028600.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
13017	25894		3.01	6.0E-80	AJ133127.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
609	13674	26578	2.04	5.0E-80	4506228	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
860	13914	26858	1.19	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
860	13914	26859	1.19	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1217	14255		0.88	5.0E-80	X91647.1	NT	H. sapiens nrx1 gene (exon 12)
1475	14506		2.42	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2384	15389	28392	1.5	5.0E-80	U89359.1	NT	Human I(3)mb1 protein homolog mRNA, complete cds
2455	15459	28456	3.26	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar, (Top) Hit BLAST E Value	Top Hit Accession No	Top Hit Database Source	Top Hit Description
2842	15831	28827	0.93	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4123	17146	30020	1.09	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4123	17146	30021	1.09	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
5089	18080	30916	1.36	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8930	21850	35215	1.06	5.0E-80	9910293	NT	Mus musculus keratin complex 2, gene 8g (Krl2-8g), mRNA
8930	21850	35215	10.58	4.0E-80	F25915.1	EST_HUMAN	HSPD13.155 HM3 Homo sapiens cDNA clone e4000045F03
232	13330	36149	7.1	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4822	17823	30692	1.37	3.0E-80	BF085009.1	EST_HUMAN	PMO-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
6032	19094	32221	1.95	3.0E-80	AI091675.1	EST_HUMAN	TR:O35790 O35790 PIG-L
1821	14844	27819	5.8	2.0E-80	R35321.1	EST_HUMAN	y955a08.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:38060 5'
1886	14806	27801	1.03	2.0E-80	AI444821.1	EST_HUMAN	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2068	15083	28092	5.14	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_1 434 (synonym: hts2) Homo sapiens cDNA clone DKFZp434D1323 5'
6494	19538	32715	0.7	2.0E-80	AI023972.1	EST_HUMAN	wm49c10.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'
6494	19538	32716	0.7	2.0E-80	AI023972.1	EST_HUMAN	wm49c10.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'
7116	20320	33585	0.78	2.0E-80	AA882952.1	EST_HUMAN	nm80d01.s1 NCI CGAP_C08 Homo sapiens cDNA clone IMAGE:1090177 3'
7241	20150	33389	1.59	2.0E-80	11421930	NT	Homo sapiens Golgi transport complex protein (80 kDa) (GTC90), mRNA
7622	20557	33851	0.79	2.0E-80	T75215.1	EST_HUMAN	y086112.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:22851 5' similar to
9702	22627	36008	1.03	2.0E-80	AW984270.1	EST_HUMAN	SP-K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B :
10288	23178	36589	2.6	2.0E-80	AJ007379.1	NT	EST376343 IMAGE resequences, MAGH Homo sapiens cDNA
11304	24223	37671	7.87	2.0E-80	AA393362.1	EST_HUMAN	Homo sapiens GGT gene, exon 6
360	13447		1.72	1.0E-80	AL163303.2	NT	z170f12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
826	13881	26818	0.93	1.0E-80	AF231920.1	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
1988	14986		2.25	1.0E-80	AI732656.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
4615	17623	30486	0.9	1.0E-80	7662389	NT	Homo sapiens chromosome 21 unknown mRNA
4615	17623	30487	0.9	1.0E-80	7662389	NT	repetitive element :
5510	18589		5.69	1.0E-80	BE366815.1	EST_HUMAN	Homo sapiens KIAA0951 protein (KIAA0951), mRNA
6200	19256	32403	6.24	1.0E-80	L10347.1	NT	Homo sapiens KIAA0951 protein (KIAA0951), mRNA
6774	19808	33019	2.08	1.0E-80	5174540	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7573	20509	33787	1.38	1.0E-80	AJ224172.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
							Homo sapiens mRNA for lipophilin B

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8007	20924	34240	2.79	1.0E-80	A1848731.1	EST_HUMAN	wq25c05.x1 NCJ CGAP Kid11 Homo sapiens cDNA clone IMAGE:2472298 3'
8007	20924	34241	2.79	1.0E-80	A1848731.1	EST_HUMAN	wq25c05.x1 NCJ CGAP Kid11 Homo sapiens cDNA clone IMAGE:2472298 3'
8809	21739	35088	0.99	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type A (PTPRA), mRNA
9258	22186	35542	0.73	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type A (PTPRA), mRNA
9258	22186	35543	0.73	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type A (PTPRA), mRNA
9825	22737	36112	1.09	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
9825	22737	36113	1.09	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10908	23793	37222	0.85	1.0E-80	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11086	24027	37470	3.26	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
11086	24027	37471	3.26	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
12630	25312	31817	1.85	1.0E-80	11417901	NT	Homo sapiens meninoma (disrupted in balanced translocation) 1 (MN1), mRNA
12845	25457		2.03	1.0E-80	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11594	24503	37970	3.71	8.0E-81	BE394525.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
7623	20558	33852	2.87	7.0E-81	A1822115.1	EST_HUMAN	z681c08.x5 Scars fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:298918 3'
4494	17504	30369	3.68	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4494	17504	30370	3.68	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5465	18546	31386	1.78	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCI), member 3 (ABCA3), mRNA
5465	18546	31387	1.78	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCI), member 3 (ABCA3), mRNA
8029	20945	34261	0.49	6.0E-81	AF038660.1	NT	Homo sapiens chromosome 1p33-p34 beta-1.4-galactosyltransferase mRNA, complete cds
9778	22702	36087	1.53	6.0E-81	AA360017.1	EST_HUMAN	EST169129 Fetal lung II Homo sapiens cDNA 5' end
12763	25394	31808	1.54	6.0E-81	BF079022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
12763	25394	31807	1.54	6.0E-81	BF079022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2231	15241	28249	1.23	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8983	21913	35269	2.21	6.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8983	21913	35270	2.21	6.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10174	23065	38462	1.15	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
10174	23065	38463	1.15	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
12015	24857	38357	2.24	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
237	13335	26249	3.27	4.0E-81	AF252257.1	NT	Homo sapiens GRP2 binding protein mRNA, partial cds
3213	18261	29160	4.51	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3696	18728	29819	0.71	4.0E-81	AW004608.1	EST_HUMAN	w60h03.x1 NCL CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR-O43815 O43815 STRUTIN.
4257	17273	30140	1.8	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4257	17273	30141	1.8	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7653	20587	33883	0.81	4.0E-81	4757893	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2) mRNA
7798	20727	34029	0.42	4.0E-81	11420544	NT	Homo sapiens ets variant gene 1 (ETV1), mRNA
8864	21794	36146	2.83	4.0E-81	X06989.1	NT	Human mRNA for amyloid A(751) protein
9109	22037	35391	3.76	4.0E-81	U20187.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3
9109	22037	35392	3.75	4.0E-81	U20187.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3
9767	22691	36077	3.2	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10602	23488	36917	1.31	4.0E-81	11425281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10667	23553	36885	0.77	4.0E-81	11430065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
10667	23553	36986	0.77	4.0E-81	11430066	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11630	24536	38008	4.28	4.0E-81	4760085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
11630	24536	38007	4.28	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
12286	25836	31492	8.56	4.0E-81	11417892	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12286	25836	31493	8.56	4.0E-81	11417892	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12793	25420	31792	5.08	4.0E-81	11417871	NT	Homo sapiens beta-uridopropionase (LOC51733), mRNA
12793	25420	31793	5.08	4.0E-81	11417871	NT	Homo sapiens beta-uridopropionase (LOC51733), mRNA
12923	25498	31769	3.6	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1294	14327	27271	8.56	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1294	14327	27272	8.56	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2395	16400	28404	1.6	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3032	16084	28984	8.1	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (hepatin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3032	16084	28986	8.1	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (hepatin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2880	15935	28839	1.85	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2880	15935	28840	1.85	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3841	16870	29754	0.78	2.0E-81	AW611542.1	EST_HUMAN	hg65c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
8535	21466	34807	11.82	2.0E-81	8923839	NT	Homo sapiens hypothetical protein (LOC55586), mRNA
13052	16870	29754	5.38	2.0E-81	AW611542.1	EST_HUMAN	hg65c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
4636	17642	30505	2.08	1.0E-81	AA040370.1	EST_HUMAN	zka4h09.11 Soares_pregnant uterus_NHPIU Homo sapiens cDNA clone IMAGE:485925 5' similar to
4756	17761	30623	6.98	1.0E-81	BE047896.1	EST_HUMAN	PIR:S52437.S52437 CDP-diacylglycerol synthase - fruit fly
5284	18270	31118	1.03	1.0E-81	9968844	NT	tz45c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281526 5'
5417	18416	38582	2.56	1.0E-81	U87928.1	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
							Human aconitate hydratase (ACO2) gene, exon 3

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5538	18617	31487	3.74	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5538	18617	31488	3.74	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5692	18765	31689	0.71	1.0E-81	AA255669.1	EST_HUMAN	z85608.1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:882475 5' similar to SW:PR12_HUMAN P49843 DNA PRIMASE 58 KD SUBUNIT
5851	18922	32036	2.99	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
5851	18922	32037	2.99	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojuncin (CTNND2) mRNA, partial cds
6386	19435	32603	1.88	1.0E-81	BF674641.1	EST_HUMAN	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
6828	19861	33072	0.53	1.0E-81	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
6828	19861	33073	0.53	1.0E-81	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7042	20068	33302	0.94	1.0E-81	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
8242	21147	34480	7.73	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
8272	21177	34513	0.68	1.0E-81	AJ250408.1	NT	Homo sapiens GLI3 gene for GLI3 protein
10295	23165	36586	1.97	1.0E-81	BE58278.1	EST_HUMAN	601845051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
10295	23165	36597	1.97	1.0E-81	BE58278.1	EST_HUMAN	601845051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
10475	23363	36777	0.75	1.0E-81	BE564367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
							act14d06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:YB36_YEAST P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION
10604	23480	36919	1.19	1.0E-81	AA630784.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3638280 5'
10606	23492	36921	3.5	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3638280 5'
10606	23492	36922	3.5	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3638280 5'
10986	23870	37288	1.36	1.0E-81	AW897550.1	EST_HUMAN	CM3-NN0059-140400-147-012 NN0059 Homo sapiens cDNA
11379	24295	37741	1.91	1.0E-81	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11531	24441	37900	1.85	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11531	24441	37901	1.85	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11854	24798	38298	1.52	1.0E-81	BF204253.1	EST_HUMAN	60166714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12476	25221	31857	3.72	1.0E-81	11418138	NT	Homo sapiens photobulin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
13	13128	26014	3.89	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
110	13128	26014	2.9	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
283	13377	26292	1.76	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
839	13694	26831	3.17	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
912	13984	28911	1.72	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1509	14540	27502	1.39	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1684	14714	27676	1.75	8.0E-82	6719601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4342	17366	30221	0.96	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1469	14500		1.19	7.0E-82	BF035327.1	EST_HUMAN	601468531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882088 5'
2817	15806	28804	2	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000782 3'
4222	17238	30104	0.72	5.0E-82	AA515512.1	EST_HUMAN	nt68e11.s1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:925186 3'
1697	14727	27691	4.21	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5686	18759	31682	0.67	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-f08 HT0540 Homo sapiens cDNA
5986	18759	31683	0.67	4.0E-82	BF351691.1	EST_HUMAN	Human von Willebrand factor gene, exon 9
5984	19031	32152	0.63	4.0E-82	M28833.1	NT	we89g08.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2348318 3'
11047	23931	37371	0.52	4.0E-82	AI787613.1	EST_HUMAN	vp75609.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:075276
12138	24978	38479	3.37	4.0E-82	AI937300.1	EST_HUMAN	O75276 PKD1
12710	25362		3.85	4.0E-82	AF023701.2	NT	Homo sapiens preactin-1 gene, exons 1 and 2
297	13391	26309	13.28	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
728	13784	26709	2.41	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-070400-073-f02 BN0120 Homo sapiens cDNA
814	13669	26806	4.14	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
895	13948	26895	4.08	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1088	14132		19.09	3.0E-82	AA72848.1	EST_HUMAN	ai23e05.at Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1383	14415	27370	1.06	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1485	14516	27477	5.27	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1919	14940	27817	1.42	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
3316	16363		2.43	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
8731	21661	35007	2.85	3.0E-82	11425208	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9119	22047	35405	1.03	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
9119	22047	35406	1.03	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
10339	23228	36844	5.56	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10339	23228	36845	5.56	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
618	13653	26585	1.99	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
618	13683	26586	1.99	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1711	14739	27708	1.46	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M117 5'
3019	16071	28973	0.66	2.0E-82	AL163202	NT	Homo sapiens chromosome 21 segment HS21C001

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3838	18867	28750	1.74	2.0E-82	M86879.1	NT	H.sapiens plasminogen-apolipoprotein (a) gene family, exon for 1st kfringle 4 repeat
3916	16943	29822	1.21	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4107	17131	30005	0.65	2.0E-82	U76833.1	NT	Human integral membrane serine protease Seprease mRNA, complete cds
4333	17347	30212	1.27	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4673	17678	30547	1.19	2.0E-82	AB028018.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4673	17678	30548	1.19	2.0E-82	AB028018.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4978	17976	30837	2.71	2.0E-82	AF045555.1	NT	Homo sapiens whscr1 (WBSOR1) and whscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5215	18205	31049	1.37	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5215	18205	31050	1.37	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5286	18272	31120	1.58	2.0E-82	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
5657	18731	31636	2.59	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6416	19464	32638	4.53	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
8134	25986		0.95	2.0E-82	A1476428.1	EST_HUMAN	tm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
8313	21218	34554	0.87	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8880	21810	35163	0.72	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
9227	22155	35507	0.57	2.0E-82	7857340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
9227	22155	35508	0.57	2.0E-82	7857340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
10610	23486	36928	2.13	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10610	23486	36927	2.13	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11716	24618	38094	2.47	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11716	24618	38096	2.47	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11753	24654	38136	1.42	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11753	24654	38137	1.42	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
12313	25118		4.02	2.0E-82	N94950.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:305203 3'
12810	25432		2.98	2.0E-82	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:305203 3'
613	13678	26580	1.29	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1236	14272		1.33	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1312	14345	27291	3.39	1.0E-82	BE084396.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1313	14346	27292	0.83	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
9497	22425	35787	0.95	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
10739	23625		1.44	1.0E-82	BF515938.1	EST_HUMAN	U1H-BW1-ae-f03-0-U1.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
11186	24112	37860	1.65	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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Table 4
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5358	18339	31184	1.02	9.0E-83	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9274	22202	35559	5.49	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291501 5'
10767	23653	37085	0.74	9.0E-83	BE253347.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1436	14467	27423	3.49	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1708	15852	27703	9.51	8.0E-83	N66981.1	EST_HUMAN	z448f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
2908	15981		1.55	7.0E-83	AA684655.1	EST_HUMAN	nc12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element
4928	17928		7.82	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316 DJ207H1.1
6286	19337	32504	0.71	7.0E-83	11426657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
428	13497	26420	1.72	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GP1Ib) gene, exons 2-29
1810	14835	27808	1.34	6.0E-83	AW673088.1	EST_HUMAN	ht31h03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833626 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN HI0034.
3063	16115	29018	0.78	6.0E-83	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
3098	16149		0.88	6.0E-83	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3621	16657	29557	3.85	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5476	18557	31399	3.09	6.0E-83	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6256	19308	32472	1.14	6.0E-83	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7924	20847	34152	1.58	6.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocytic growth factor receptor) (MET), mRNA
10201	23082	36403	3.09	6.0E-83	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10289	23179	36590	0.92	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10289	23179	36591	0.92	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
11892	24805		2.7	6.0E-83	AA486105.1	EST_HUMAN	ab14ef10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element
12265	25083		3.23	6.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
974	14025		7.51	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2084	15856		1.14	5.0E-83	AF006305.1	NT	Homo sapiens 28S proteasome regulatory subunit (SUG2) mRNA, complete cds
3706	16736	29627	0.93	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3980	17008	29896	0.79	5.0E-83	4885190	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
5213	18203	31047	16.68	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5213	18203	31048	16.68	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
663	13725	26636	1.95	4.0E-83	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3573	16610	29513	1.07	4.0E-83	BE888078.1	EST_HUMAN	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
1025	14074		3.46	3.0E-83	AA368311.1	EST_HUMAN	EST179542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
2827	15816		1.98	3.0E-83	AA632654.1	EST_HUMAN	np87c07.e1 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR repetitive element;
6960	19892		0.7	3.0E-83	AI217223.1	EST_HUMAN	qf73e06.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1755882 3'
1822	14845	27820	1.28	2.0E-83	AA993492.1	EST_HUMAN	cd84g05.e1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216.;
1822	14845	27821	1.28	2.0E-83	AA993492.1	EST_HUMAN	cd84g05.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216.;
1940	14961	27939	5.63	2.0E-83	NG6951.1	EST_HUMAN	zsa48f12.e1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:295823 3'
2194	15205	28209	1.01	2.0E-83	AB033098.1	NT	Homo sapiens mRNA for KIAA1272 protein, partial cds
2895	16949	28849	1.39	2.0E-83	BE828694.1	EST_HUMAN	RC9-ET0046-280800-013-H12 ET0046 Homo sapiens cDNA
3313	16360		2.22	2.0E-83	11430834	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3842	16871		0.76	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4445	17466	30315	5.73	2.0E-83	AF202879.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4762	17767	30630	1.64	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4762	17767	30631	1.64	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5453	18634	31376	0.77	2.0E-83	U06679.1	NT	Human carcinoembryonic antigen gene family member 18 (CGM18) gene, exons A1 and B1
5658	18732	31637	0.44	2.0E-83	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
5658	18732	31638	0.44	2.0E-83	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6059	19121	32249	0.69	2.0E-83	11428081	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6192	19249	32395	1.19	2.0E-83	BE885401.1	EST_HUMAN	Homo sapiens membrane protein CH1 (CH1), mRNA
7050	20076	33309	0.44	2.0E-83	AF129533.1	NT	601507482F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909088 5'
7398	20767	34070	5.71	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein F55b (FBL3B) mRNA, partial cds
8312	21216	34562	0.47	2.0E-83	BF105097.1	EST_HUMAN	Homo sapiens F-box protein F55b (FBL3B) mRNA, partial cds
8425	21357	34695	0.65	2.0E-83	AB001025.1	NT	601822060F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:4042318 5'
8425	21357	34696	0.65	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain natriuretic receptor, complete cds
8666	21497	34840	1.73	2.0E-83	U06707.1	NT	Homo sapiens mRNA for brain natriuretic receptor, complete cds
8869	21819	35170	2.5	2.0E-83	AF011920.1	NT	Rattus norvegicus densin-180 mRNA, complete cds
8869	21819	35171	2.5	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
10537	23423	36839	2.2	2.0E-83	M22094.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
10537	23423	36839	2.2	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10617	23503	36937	1.55	2.0E-83	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
10686	23572	37002	1.08	2.0E-83	AW505600.1	EST_HUMAN	U1-HF-BNO-and-h-07-Q-U1.1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3081852 5'
11284	24205	37655	4.46	2.0E-83	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11365	24283	37726	1.74	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135.1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547J135 5'
11365	24283	37727	1.74	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135.1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547J135 5'
12842	25454		5.7	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1436	14466	27421	2.02	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/acyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1435	14466	27422	2.02	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/acyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1478	14509	27469	4.06	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1478	14509	27470	4.08	1.0E-83	AF105087.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
2032	15046	28046	1.48	1.0E-83	4503652	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2705	15699	28694	2.19	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3226	16274	29175	0.77	1.0E-83	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
3937	16965	29947	3.66	1.0E-83	AF053788.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4343	17357	30222	2.32	1.0E-83	Z25822.1	NT	H.sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
6993	20020	33253	1.7	1.0E-83	A027614.1	EST_HUMAN	ov89b08.x1 Soares_testis_NHTT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:U64241 QM PROTEIN (HUMAN);
3861	16890	29779	4.16	7.0E-84	BE901209.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1321	14354	27239	3.39	6.0E-84	BE839894.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
1321	14354	27300	3.39	6.0E-84	BE839894.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2420	15424	28425	7.2	6.0E-84	AA776574.1	EST_HUMAN	ae86a03.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5420	18418		1.83	6.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0322 5'
5708	18781	31711	1.68	6.0E-84	AA897339.1	EST_HUMAN	al47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone DKFZp434H0322 5'
5857	18928	32045	1.36	6.0E-84	11426718	NT	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5857	18928	32046	1.36	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC= scavenger receptor expressed by endothelial cells (SREC), mRNA
7893	20819	34125	3.46	6.0E-84	BE810371.1	EST_HUMAN	Homo sapiens acetyl LDL receptor; SREC= scavenger receptor expressed by endothelial cells (SREC), mRNA
8145	21054	34386	0.81	6.0E-84	AF038391.1	NT	PM0-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
8651	21582	34917	2.71	6.0E-84	BE701099.1	EST_HUMAN	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
737	13795	26720	0.75	6.0E-84	AA382811.1	EST_HUMAN	PM4-F10054-160600-004-e10 F10054 Homo sapiens cDNA
							EST86094 Testis 1 Homo sapiens cDNA 5' end

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3058	15110		1.25	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
6344	19394	32562					
11977	24820	38313	0.51	5.0E-84	AA167878.1	EST_HUMAN	zq39e07.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632100 5' similar to TR:G483915 G483916 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q ;
			2.94	5.0E-84	11428740	NT	Homo sapiens regulatory factor X_3 (influences HLA class II expression) (RFX3), mRNA
1434	14465	27420	1.66	4.0E-84	A1685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN Q43847 NARDILYSIN PRECURSOR ;
5065	18062	30913	0.98	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
5066	18063	30914	2.02	4.0E-84	AF069801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5444	18525	31251	0.46	4.0E-84	AF022835.1	NT	Homo sapiens multidrug resistance protein (MRP), exon 13
5754	18827	31926	1.59	4.0E-84	11386188	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5754	18827	31927	1.59	4.0E-84	11386188	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6520	19584	32746	3.17	4.0E-84	AF059850.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
8096	21008	34333	13.7	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9468	22398	35758	1.2	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9468	22396	35769	1.2	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
11355	24273	37715	4.55	4.0E-84	AB032956.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
336	13428	26342	1.32	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1974	14992	27975	1.69	3.0E-84	5493655	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2021	15039	28033	1.56	3.0E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger G2H2 type domains
3811	16841	29728	7.05	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
11314	24233		10.94	3.0E-84	A1683801.1	EST_HUMAN	wu2d05.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2620685 3' similar to gb:U05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2117	15130	28136	6.17	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2117	15130	28137	6.17	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2985	16037	28041	10.81	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
3003	16055	28969	1.37	2.0E-84	X89211.1	NT	H-sapiens DNA for endogenous retroviral like element
4905	17904	30773	0.91	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
4905	17904	30774	0.91	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
5710	18789	31720	0.91	2.0E-84	BF511575.1	EST_HUMAN	UI-H-B14-ad-e-02-Q-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084863 3'
5716	18789	31721	0.91	2.0E-84	BF511575.1	EST_HUMAN	UI-H-B14-ad-e-02-Q-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084863 3'
6928	19957	33178	1.03	2.0E-84	H63370.1	EST_HUMAN	yr86e11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:209324 3'
8635	21566		1.52	2.0E-84	A1298674.1	EST_HUMAN	qm87cd09.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895728 3'
8956	21886	35244	0.56	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8956	21888	35245	0.58	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9884	22799	36185	1.05	2.0E-84	AU120280.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
10252	23142	36551	0.64	2.0E-84	H22841.1	EST_HUMAN	ym49e11.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:51383 5' similar to SP-APOH_RAT
12502	25239	31863	1.66	2.0E-84	BF448000.1	EST_HUMAN	P26844 BETA-2-GLYCOPROTEIN I; nae30a02.x1 Lupski_sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ766G23.1;
12502	25239	31864	1.66	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ766G23.1;
332	13422	26338	1.98	1.0E-84	AF114498.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
571	13639	26548	6.27	1.0E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
743	13801	27297	3.78	1.0E-84	11427831	NT	Homo sapiens complement component 5 (C5), mRNA
1319	14352	27297	2.6	1.0E-84	AA984379.1	EST_HUMAN	am85b11.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1620885 3'
2067	15082	28081	2.16	1.0E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
3814	16844	29730	2.83	1.0E-84	AA720851.1	EST_HUMAN	nm12608.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4524	17533	30395	6.66	1.0E-84	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4812	17813	30679	2.35	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htae3) Homo sapiens cDNA clone DKFZp434N0323 5'
4812	17813	30680	2.35	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htae3) Homo sapiens cDNA clone DKFZp434N0323 5'
5019	17833	30395	3.24	1.0E-84	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6144	18203	32340	0.69	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
6431	19478	32655	1.2	1.0E-84	S73482.1	NT	uterine water channel=28 kDa erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
7207	20207	33452	2.17	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7207	20207	33453	2.17	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7466	20406	33682	2.62	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7887	20813	34119	4.29	1.0E-84	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7987	20815	34231	0.82	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
8044	20915	34231	1.92	1.0E-84	11430846	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
10064	22980	36502	2.69	1.0E-84	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15), mRNA
10280	23180	31346	0.54	1.0E-84	AF224511.1	NT	Homo sapiens Ca2+-binding protein CABP3 (CABP3) gene, exon 6 and partial cds
10309	18424	31346	1.79	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10309	18424	31349	1.79	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
12396	25169		3.39	1.0E-84	11417812	NT	Homo sapiens putative receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
12494	25235	31860	2.85	1.0E-84	11418185	NT	Homo sapiens acyltransferase 2, mitochondrial (ACO2), mRNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
993	14043		1.11	9.0E-95	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1100	14143	27080	1.81	9.0E-95	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1100	14143	27081	1.81	9.0E-95	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1600	14631	27590	15.16	9.0E-95	M33282.1	NT	Human plasminogen gene, exon 7
1600	14631	27591	15.16	9.0E-95	M33282.1	NT	Human plasminogen gene, exon 7
1701	14730	27696	2.32	9.0E-95	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3848	16877	29761	1.2	9.0E-95	7661923	NT	Homo sapiens KIAA0125 gene product (KIAA0125), mRNA
3868	16895	29779	0.92	9.0E-95	7019418	NT	Homo sapiens nucleolar GTPase (HUMAUANTIG), mRNA
4350	17364	30228	1.17	9.0E-95	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4985	17984	30842	1.14	9.0E-95	6501979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5021	18018	30877	1.53	9.0E-95	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1163	14204	27142	6.33	7.0E-95	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
12069	24910		3.45	7.0E-95	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11849	24699	38190	3.25	6.0E-95	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11849	24699	38191	3.25	6.0E-95	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2355	16382	28365	4.79	5.0E-95	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4540	17549		0.7	5.0E-95	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA11) mRNA, complete cds
5636	18712	31612	1.64	5.0E-95	BF035874.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
5636	18712	31613	1.64	5.0E-95	BF035874.1	EST_HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
11559	24468	37933	1.62	5.0E-95	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
13050	17549		3.97	5.0E-95	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA11) mRNA, complete cds
6388	19437	32804	1.62	4.0E-95	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6388	19437	32805	1.62	4.0E-95	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
7152	20260	33514	0.43	4.0E-95	A1628119.1	EST_HUMAN	1684901.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2285808 3'
11045	23929		1.92	4.0E-95	BE079263.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
1325	14359	27306	0.9	3.0E-95	AF098157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1804	14830	27797	3.64	3.0E-95	T97495.1	EST_HUMAN	ye33g09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
5007	18005	30863	1.11	3.0E-95	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5007	18005	30864	1.11	3.0E-95	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5083	18080	30926	1.05	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5588	18653	31539	1.37	3.0E-85	11436001	NT	Homo sapiens lacrimal proline rich protein (LPRP), mRNA
6322	18372	32540	0.67	3.0E-85	1142024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6374	19423	32588	6.53	3.0E-85	7662309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6374	19423	32588	6.53	3.0E-85	7662309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7284	20237		6.92	3.0E-85	A1404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7794	20723	34026	0.87	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621), mRNA
9075	22004	35358	1.05	3.0E-85	11525829	NT	Homo sapiens CGI-81 protein (LOC51108), mRNA
9529	22456	35818	3.8	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9846	22954	36343	0.91	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRPB2), mRNA
9846	22954	36344	0.91	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRPB2), mRNA
10961	23845	37271	0.71	3.0E-85	AF098642.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11939	24783	38280	2.49	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
12661	25519		1.63	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
989	14039	26983	3.68	2.0E-85	7857286	NT	Homo sapiens KIAA0829 protein Mex2 Interacting nuclear target (MINT) homolog (KIAA0829), mRNA
1066	14110	27049	2.1	2.0E-85	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1442	14473	27430	32.05	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1442	14473	27431	32.05	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2244	15254	28260	1.79	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2871	14367		6.52	2.0E-85	7857468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3088	16120	29021	0.97	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4443	17454	30313	5.87	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4680	17685	30553	0.82	2.0E-85	4826977	NT	Homo sapiens reelin (RELN) mRNA
5018	18016	30875	1.25	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5282	18268	31116	1.27	2.0E-85	4502212	NT	Homo sapiens arginase, liver (ARGT) mRNA
9813	22719	36102	0.99	2.0E-85	A1760820.1	EST_HUMAN	w167h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2388431 3' similar to contains element MSR1 repetitive element;
10175	23066	36494	0.94	2.0E-85	A1914459.1	EST_HUMAN	w149d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331461 3'
10755	23641	37075	1.14	2.0E-85	A1893384.1	EST_HUMAN	w184d12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2306	16314		2.32	1.0E-85	BE794306.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2416	15420	28421	7.32	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2416	15420	28422	7.32	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8297	21201	34537	0.52	1.0E-85	BE062951.1	EST_HUMAN	MRO-BT0284-221189-002-f03 BT0284 Homo sapiens cDNA
10300	23180	36601	2.55	1.0E-85	BE257917.1	EST_HUMAN	601109738F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3350553 5'
11361	24279	37721	2.15	1.0E-85	AA778785.1	EST_HUMAN	245f03.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11361	24279	37722	2.15	1.0E-85	AA778785.1	EST_HUMAN	245f03.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11435	24351	37798	3.41	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
11435	24351	37799	3.41	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
12184	25020	38522	1.47	1.0E-85	AI198420.1	EST_HUMAN	gi56a07.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:1860468 3'
12400	25316	31819	5.29	1.0E-85	11417862	NT	Homo sapiens calchectin binding protein 1 (KIAA0330), mRNA
12637	25316	31819	5.28	1.0E-85	11417862	NT	Homo sapiens calchectin binding protein 1 (KIAA0330), mRNA
1450	14481		13	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987690 5'
6366	19415	32580	0.82	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC83041), mRNA
12120	24961	38494	1.66	8.0E-86	4503224	NT	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
243	13340	26252	0.78	7.0E-86	7882247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
964	14014	26956	0.96	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
964	14014	26957	0.96	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
8437	19484	32659	0.96	7.0E-86	9968886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
8437	19484	32660	0.96	7.0E-86	9968886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7317	18485	31309	6.57	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
9303	22231	35591	2.95	7.0E-86	L38557.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15
10222	23113		1.77	7.0E-86	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10278	23168	36581	1.94	7.0E-86	11528307	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA
11399	24315	37761	1.6	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11399	24315	37762	1.6	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
1320	14353	27298	1.96	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (liponamide) (OGDH) mRNA
226	13323	26241	2.67	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
6268	19319	32483	10.62	4.0E-86	BE26843.1	EST_HUMAN	601176865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531963 5'
11687	13323	26241	1.88	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4938	17402	30271	0.79	3.0E-86	BE897703.1	EST_HUMAN	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5760	18862	31970	6.08	3.0E-86	AW340946.1	EST_HUMAN	xz92h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8838	21768	35114	1.23	3.0E-86	AV722329.1	EST_HUMAN	AV722329 HTB Homo sapiens cDNA clone HTBBS04 5'
10716	23602	37028	4.08	3.0E-86	BE886479.1	EST_HUMAN	601509896F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
10716	23602	37030	4.08	3.0E-86	BE886479.1	EST_HUMAN	601509896F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11868	23968	37404	5.29	3.0E-86	AI699240.1	EST_HUMAN	tur18602.x1 NCI_CGAP_Pf28 Homo sapiens cDNA clone IMAGE:2251371 3'
12374	25779		2.69	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636763 5'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
286	13380	26284	1.87	2.0E-96	AA306284.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' and
437	13508		2.2	2.0E-96	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1218	14256	27198	2.32	2.0E-96	N58977.1	EST_HUMAN	yz19a08.r1 Soares_multiple_sclerosis_2Nbl-HMSP Homo sapiens cDNA clone IMAGE:283478 5'
2207	15218	28222	7.73	2.0E-96	9635487	NT	Human endogenous retrovirus, complete genome
2287	15295	28303	1.89	2.0E-96	AB03103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3476	16516	29415	1.47	2.0E-96	AW566142.1	EST_HUMAN	EST378215 MAGE resequences, MAGI Homo sapiens cDNA
3809	18839	29725	3.26	2.0E-96	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3809	18839	29726	3.26	2.0E-96	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4124	17147		3.67	2.0E-96	AW515742.1	EST_HUMAN	hd87g08.x1 NCJ CGAP_GCB Homo sapiens cDNA clone IMAGE:2816542 3'
4902	17801	30769	3.36	2.0E-96	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
6087	19148	32283	1.42	2.0E-96	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6087	19148	32284	1.42	2.0E-96	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7429	25663	33367	0.83	2.0E-96	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8588	21519	34963	0.65	2.0E-96	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
9137	22065	35425	3.11	2.0E-96	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9137	22065	35426	3.11	2.0E-96	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9460	22388	35751	1.06	2.0E-96	10863878	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9858	22773	36160	1.66	2.0E-96	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10928	23813	37241	2.96	2.0E-96	11545946	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10928	23813	37242	2.96	2.0E-96	11545946	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10981	23865	37292	1.09	2.0E-96	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11342	24261	37701	1.95	2.0E-96	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
12788	25416	31789	3.57	2.0E-96	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12944	25610		3.21	2.0E-96	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1620	14650	27613	1.82	1.0E-96	4926855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3205	16253	29149	1.56	1.0E-96	5453949	NT	Homo sapiens fibulin 6 (FBLN6) mRNA
3282	16330	29235	2.89	1.0E-96	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3339	16385	29284	2.25	1.0E-96	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3339	16385	29285	2.25	1.0E-96	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4023	17050	29840	0.83	1.0E-96	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4023	17050	28941	0.83	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC81318), mRNA
4364	17378	30242	6.6	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4734	17739	30601	0.7	1.0E-86	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
5744	18817	31973	1.59	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5541	18620		1.67	9.0E-87	AI150703.1	EST_HUMAN	qb77c09.x1 Soares fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10;
7852	20778	34080	2.05	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7852	20778	34081	2.05	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
502	13572	26490	35.07	8.0E-87	X82245.1	NT	O. curticulus mRNA for elongation factor 1 alpha
2315	15323	28324	2.46	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3322779 3'
2315	15323	28325	2.46	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3322779 3'
8665	19703	32898	0.81	7.0E-87	AW890336.1	EST_HUMAN	MRO-NT0039-020500-004-a11 NT0039 Homo sapiens cDNA
8767	21697	35041	3.23	7.0E-87	BF352776.1	EST_HUMAN	IL3-HT0619-060700-188-D10 HT0619 Homo sapiens cDNA
8966	21344	34678	0.65	7.0E-87	BE712891.1	EST_HUMAN	IL6-HT0702-160800-103-406 HT0702 Homo sapiens cDNA
10573	23459	36879	4.06	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
10573	23459	36880	4.06	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
10947	25698		0.57	7.0E-87	AI081565.1	EST_HUMAN	alphaH01.s1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1660657 3'
11328	24247	37684	7.39	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
11328	24247	37685	7.39	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
3588	16625	29528	0.66	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
8938	19724	32924	1.45	6.0E-87	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
11167	24095		3.58	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC83102), mRNA
1185	14225	27183	1.73	5.0E-87	AA382811.1	EST_HUMAN	EST86094 Testis I Homo sapiens cDNA 5' end
12839	14225	27183	1.65	5.0E-87	AA382811.1	EST_HUMAN	EST86094 Testis I Homo sapiens cDNA 5' end
992	14042	26985	1.1	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1200	14239	27178	10.9	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
2043	15060	28061	1.8	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0458 protein, partial cds
3326	16564	29488	1.84	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
5631	18707	31606	14.18	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5957	19024	32144	0.47	4.0E-87	U85429.1	NT	Human transcription factor NFATx3 mRNA, complete cds
6280	18331	32497	4.49	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8122	21032	34359	0.45	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8122	21032	34360	0.45	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8243	21148	34481	0.83	4.0E-87	L48524.1	NT	Homo sapiens tuberin (TSC2) gene, exon 10
9769	22693	36079	0.51	4.0E-87	AF223470.1	NT	Homo sapiens KIAA0971-l protein (KIAA0971-l) mRNA, complete cds
11606	24515	37984	4.02	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11651	24557	38026	1.42	4.0E-87	AB040537.1	NT	Homo sapiens DDX10 mRNA for RNA helicase, complete cds
11651	24557	38027	1.42	4.0E-87	AB040537.1	NT	Homo sapiens DDX10 mRNA for RNA helicase, complete cds
12730	25824	31484	1.8	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12730	25824	31485	1.8	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12868	25470		48.71	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2826	15815	28810	3.44	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4), mRNA
2990	16042		0.86	2.0E-87	BF327920.1	EST_HUMAN	QV0-BN0148-050600-254-a03 BN0148 Homo sapiens cDNA
3850	16879	29764	0.9	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
6022	18019	30378	0.72	2.0E-87	BF376311.1	EST_HUMAN	CMO-TN0038-150900-552-H08 TN0038 Homo sapiens cDNA
5075	18072	30921	0.73	2.0E-87	BE175478.1	EST_HUMAN	RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
5958	18929	32047	11.67	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5958	18929	32048	11.67	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6583	19624		4.09	2.0E-87	BE567193.1	EST_HUMAN	601341383F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3683348 5'
6996	20023	33255	0.8	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
7088	20284	33553	0.87	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDSG04 3'
7537	20476	33764	1.3	2.0E-87	BE294432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7595	20531	33822	0.84	2.0E-87	11433046	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
7857	20784	34087	31.46	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
8140	21049	34380	34.31	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
8968	21898	35253	6.9	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
10304	23194		5.16	2.0E-87	BE631136.1	EST_HUMAN	601273316F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'
1210	15849		1.81	1.0E-87		NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
3773	16805	29692	3.82	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3788	16827	29714	2.03	1.0E-87	4768827	NT	Homo sapiens neuraxin III (NRXN3) mRNA
5260	18246	31097	0.98	1.0E-87	U50949.1	NT	Rattus norvegicus taste bud receptor protein TB 041 (TB 041) gene, complete cds
6471	19516	32691	2.57	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6471	19516	32692	2.57	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7541	20480	33768	0.52	1.0E-87	AF039517.1	NT	Homo sapiens corticotrophin-releasing factor type 1 receptor gene, exon 8
7541	20480	33769	0.52	1.0E-87	AF039517.1	NT	Homo sapiens corticotrophin-releasing factor type 1 receptor gene, exon 8

Table 4

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7547	20485	33774	0.87	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7797	20726	34028	1.26	1.0E-87	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7965	20887	34198	0.44	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
8261	21168	34501	0.51	1.0E-87	4505528	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
8693	21624	34967	9.05	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9468	22394	35755	1.44	1.0E-87	AB022818.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9468	22394	35756	1.44	1.0E-87	AB022818.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
10159	23050	36450	3.18	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-072-E02 BN0276 Homo sapiens cDNA
10159	23050	36451	3.18	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-072-E02 BN0276 Homo sapiens cDNA
10661	23747	37171	0.73	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' end
11437	24353		1.63	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12726	25058		1.95	1.0E-87	7657692	NT	Homo sapiens sulfotransferase-related protein (SULTY3), mRNA
13108	25623	31696	5.49	1.0E-87	AF169598.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
13108	25623	31697	5.49	1.0E-87	AF169598.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
947	13998	26941	2.32	9.0E-88	5453887	NT	Homo sapiens protease inhibitor 4 (kallistatin) (PI4) mRNA
1133	14175	27112	6.68	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1378	14410	27364	2.49	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
1378	14410	27365	2.49	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
2134	15147	28148	1.01	9.0E-88	7681701	NT	Homo sapiens DKFZP586P1522 protein (DKFZP586P1522), mRNA
3694	16726	29618	1.04	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4368	17382	30246	3.43	9.0E-88	X91029.1	NT	H. sapiens ECE-1 gene (exon 9)
4368	17382	30247	3.43	9.0E-88	X91029.1	NT	H. sapiens ECE-1 gene (exon 9)
5124	18120	30962	0.97	9.0E-88	AB026998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9572	22489	35863	3.09	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1852	14874		0.93	5.0E-88	7681887	NT	Homo sapiens KIAA00063 gene product (KIAA00063), mRNA
2887	16581	28682	3.6	5.0E-88	N89399.1	EST_HUMAN	K9718F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3043	16095	28997	0.65	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3054	16108	29011	0.68	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3054	16108	29012	0.68	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3448	16489		3.11	5.0E-88	AI693217.1	EST_HUMAN	wc68h08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element/contains element MER22 MER22 repetitive element
3596	16633	26538	0.82	5.0E-88	AF114486.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
7077	20283	33540	2.87	5.0E-88	U10932.1	EST_HUMAN	ym06b10.11 Soares infant brain T118 Homo sapiens cDNA clone IMAGE:47129 5'
8508	21439	34779	2.37	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9852	22767	36152	0.55	5.0E-88	BF680206.1	EST_HUMAN	602164658F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285775 5'
1357	14389	27343	1.33	4.0E-88	BF091228.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1357	14389	27344	1.33	4.0E-88	BF091228.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
7613	20548	33840	2.54	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
11921	24766	38262	1.93	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11921	24766	38263	1.93	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
755	13812	26739	0.85	3.0E-88	11645800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1834	14857		1.73	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2889	16041	28946	6.26	3.0E-88	N68951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen T1N1LS Homo sapiens cDNA clone IMAGE:296823 3'
4339	17353	30215	0.93	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4339	17353	30216	0.93	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4891	17599	31407	4.92	3.0E-88	11429360	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5482	18583	31958	2.94	3.0E-88	11429367	NT	Homo sapiens valosin-containing protein (VCP), mRNA
5779	18851	31958	3.42	3.0E-88	9968888	NT	Homo sapiens vral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
5903	18972	32090	3.64	3.0E-88	11420697	NT	Homo sapiens interleukin 13 (IL13), mRNA
6402	19450	32921	0.86	3.0E-88	11417370	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6680	25652	32915	0.82	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6680	25652	32916	0.82	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7419	20118	33365	15.09	3.0E-88	AF278265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7970	20892	34204	5.24	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
8499	21430	34771	10.36	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 6 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8774	21704	35049	1.76	3.0E-88	AF034374.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds
9668	21326	34659	0.78	3.0E-88	11528282	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
10439	23327	36744	0.78	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10438	23327	36745	0.78	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10463	23351	36767	1.32	3.0E-88	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12482	25226		5.29	3.0E-88	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA

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Table 4
Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1062	14108	27043	1.94	2.0E-88	7305198	NT	Homo sapiens Calsenlin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1647	14878	27641	2.21	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1775	14801	27769	3.81	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4532	17541	30403	2.13	2.0E-88	5031666	NT	Homo sapiens dynamin, axonemal, light polypeptide 4 (DNAL4), mRNA
6131	19190	32328	4.82	1.0E-88	AW139865.1	EST_HUMAN	UIH-B1-aea-4-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718760 3'
6131	19190	32327	4.82	1.0E-88	AW139865.1	EST_HUMAN	UIH-B1-aea-4-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718760 3'
6937	19868	33187	22.47	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6937	19868	33188	22.47	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7481	20421	33700	1.39	1.0E-88	AI969034.1	EST_HUMAN	wa70a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2476606 3'
7548	20486	33775	3.88	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP-B0272.2
8715	21646	34992	0.66	1.0E-88	AF135183.1	NT	CE00851 ;
9784	22748	36130	1.12	1.0E-88	AA190368.1	EST_HUMAN	Homo sapiens Recq helicase 5 (RECQ5) gene, alternative splice products, complete cds
10108	22989	36395	3.12	1.0E-88	AL043314.2	EST_HUMAN	zp87c02.r1 Strategene HeLa cell e3 037216 Homo sapiens cDNA clone IMAGE:627170 5' similar to
11137	24066	37511	1.6	1.0E-88	AA897611.1	EST_HUMAN	SW:POL.1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN ;
11878	23978	37416	3.31	1.0E-88	AA991479.1	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
12890	28347		4.6	1.0E-88	AL163246.2	NT	q62609.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1394873 3'
2784	15774	28770	2.06	8.0E-89	BE311557.1	EST_HUMAN	os81g03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612766 3' similar to gb:MI16342
7262	20171	33412	1.18	8.0E-89	11421514	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
456	13528	26450	1.22	7.0E-89	7657213	NT	Homo sapiens chromosome 21 segment HS21C046
456	13528	26451	1.22	7.0E-89	7657213	NT	60T142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508185 5'
4983	17992	30849	3.73	7.0E-89	4557390	NT	Homo sapiens similar to serpin domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
5042	18039	30895	7.08	7.0E-89	AL045748.1	EST_HUMAN	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5616	18692	31587	1.17	7.0E-89	X99832.1	NT	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA
5616	18692	31588	1.17	7.0E-89	X99832.1	NT	DKFZp434E246_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E246 5'
6600	19841	32822	1.05	7.0E-89	7549808	NT	H. sapiens CLN3 gene, complete CDS
6600	19841	32823	1.05	7.0E-89	7549808	NT	H. sapiens CLN3 gene, complete CDS
7920	20843	34147	1.87	7.0E-89	11420764	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
8459	21390	34730	0.52	7.0E-89	11417118	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
8459	21390	34731	0.52	7.0E-89	11417118	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
11011	23896	37326	1.07	7.0E-89	X62048.1	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
							H. sapiens Wee1 hu gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11011	23895	37329	1.07	7.0E-89	X62048.1	NT	H.sapiens Wee1 hu gene
11024	23908	37348	2.15	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
11024	23908	37349	2.15	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
1050	14094	27033	0.83	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
2228	15238	28245	1.24	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2458	15462	28458	1.4	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2458	15462	28459	1.4	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
3586	16823	29528	1.14	6.0E-89	7681817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4749	17754	30813	3.61	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4749	17754	30814	3.61	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5209	18199	31042	3.43	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5209	18199	31043	3.43	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
8026	20942	34257	1.31	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-080600-219-g03 NT0022 Homo sapiens cDNA
11581	24490	37859	1.75	4.0E-89	A1798872.1	EST_HUMAN	we91c03.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348452 3'
5375	18367	31197	1.37	3.0E-89	BF331740.1	EST_HUMAN	RC5-BT0624-290600-015-H09 BT0624 Homo sapiens cDNA
7500	20438	33721	1.26	3.0E-89	A1217359.1	EST_HUMAN	qh17b06.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844915 3'
11239	24165	37611	1.54	3.0E-89	N57357.1	EST_HUMAN	yw86e11.1 Soares_placenta_8tbcweeks_2NtHP8tbcw Homo sapiens cDNA clone IMAGE:259148 5' similar to SW:PI4K_HUMAN P42356 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA;
131	13502	26428	0.7	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
131	13502	26427	0.7	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
431	13502	26428	0.83	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
431	13502	26427	0.83	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
553	13622	26530	0.94	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2923	15976	28874	1.9	2.0E-89	A1222006.1	EST_HUMAN	qg96c08.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
3613	16650	29550	0.88	2.0E-89	AA759149.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
3613	16650	29551	0.88	2.0E-89	AA759149.1	EST_HUMAN	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4243	17259	30125	1.06	2.0E-89	AF089897.1	NT	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4251	17267	30135	6.06	2.0E-89	X58742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4251	17267	30136	5.06	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4251	17267	30138	5.06	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4458	17469	30328	0.78	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4617	17623	30489	1.32	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5527	18506		0.93	2.0E-89	BE641744.1	EST_HUMAN	601065906F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5669	18743	31653	4.81	2.0E-89	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
5999	19084	32181	1.41	2.0E-89	U03985.1	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
6454	19499	32873	0.71	2.0E-89	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8120	21031	34358	5.52	2.0E-89	U81004.1	NT	Human GT24 (GT24) mRNA, partial cds
8513	21444	34786	2.59	2.0E-89	11428801	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8988	21917	35272	0.98	2.0E-89	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
9795	22759	36145	0.77	2.0E-89	AB037754.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10326	23215	36627	0.6	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
10328	23215	36628	0.6	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
11812	24733	38224	2.45	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
12003	24845	38342	4.22	2.0E-89	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
12139	24979	38480	1.86	2.0E-89	U10692.1	NT	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds
13109	25624		2.82	2.0E-89	AB012722.2	NT	Homo sapiens mRNA for kinesin-like protein, complete cds
12009	24851	38350	7.24	1.0E-89	BF196052.1	EST_HUMAN	h61409.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 054778 SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;
12009	24851	38351	7.24	1.0E-89	BF196052.1	EST_HUMAN	h61409.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 054778 SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;
8805	21735	35084	1.43	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8805	21735	35085	1.43	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1090	14134	27070	3.02	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1091	14134	27070	2.48	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1358	15898	27345	3.76	8.0E-90	BE670561.1	EST_HUMAN	7e36708.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1358	15898	27346	3.76	8.0E-90	BE670561.1	EST_HUMAN	7e36708.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
9123	22051	35411	0.63	8.0E-90	BE177830.1	EST_HUMAN	RC1.H10598-120400-022408 HT0598 Homo sapiens cDNA
11143	24072	37518	1.58	8.0E-90	AJ222095.1	EST_HUMAN	qg86c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb.J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11143	24072	37519	1.58	8.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
861	13915		3.4	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8994	21923		2.01	7.0E-90	AA782977.1	EST_HUMAN	alc3d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
9518	22445	35808	2.33	7.0E-90	BE962625.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9518	22445	35808	2.33	7.0E-90	BE962625.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10635	23521	36955	2.02	7.0E-90	H68949.1	EST_HUMAN	yf86s04.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10635	23521	36955	2.02	7.0E-90	H68949.1	EST_HUMAN	SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10934	23819	37246	0.68	7.0E-90	BF526089.1	EST_HUMAN	SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
3116	16167	29051	1.24	6.0E-90	X91926.1	NT	602071208F1 NCL_CGAP_Birt64 Homo sapiens cDNA clone IMAGE:4214257 5'
3116	16157	29062	1.24	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4326	17340	30205	8.58	6.0E-90	8922398	NT	H. sapiens ECE-1 gene (exon 6)
4326	17340	30205	8.58	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6214	19259	32421	3.28	6.0E-90	U77700.1	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6214	19259	32421	3.28	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8002	21832	35186	3.54	6.0E-90	4504794	NT	Homo sapiens HsGCN1 mRNA, partial cds
8002	21832	35187	3.54	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
165	13268		19.05	5.0E-90	AB035344.1	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
1220	14258	27198	6.75	5.0E-90	U80226.1	NT	Homo sapiens TClb gene, exon 1-10b
							Human gamma-aminobutyric acid transaminase mRNA, partial cds
1843	14866	27847	1.44	5.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
1843	14866	27848	1.44	5.0E-90	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
2590	15588	28582	2.66	5.0E-90	AF114487.1	NT	Homo sapiens intercalin long isoform (ITSN) mRNA, complete cds
4856	17631	30529	2.27	5.0E-90	4508364	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
5785	18857	31965	2.88	5.0E-90	Z18411.1	NT	H. sapiens mRNA encoding phospholipase c
5803	18875		0.58	5.0E-90	AF008915.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
5891	18960	32070	1.08	5.0E-90	AB016617.1	NT	Homo sapiens ELKS mRNA, complete cds

Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5974	18557	31965	2.12	5.0E-90	Z18411.1	NT	H. sapiens mRNA encoding phospholipase c
7034	20060	33293	0.57	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7034	20060	33294	0.57	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7582	20518	33808	1.98	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7582	20518	33807	1.98	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7998	20914	34230	9.54	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
8869	21799	35164	5.19	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10205	23096	36498	1.57	5.0E-90	11419429	NT	Homo sapiens similar to octonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10773	23659	37088	0.92	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10927	23812	37240	13.14	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10983	23867	37294	0.59	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10983	23867	37295	0.59	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
11353	24271	37713	4.85	5.0E-90	D49387.1	NT	Human mRNA for NADP dependent leukotiene b4 12-hydroxylase, partial cds
12227	25061	38559	1.41	5.0E-90	X98411.1	NT	H. sapiens mRNA for myosin-IE
12662	25520		3.16	5.0E-90	AI523360.1	EST_HUMAN	ar78h05.x1 Barstead acra HPLRB0 Homo sapiens cDNA clone IMAGE:2128761 3'
322	13414	26331	1.88	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
322	13414	26332	1.88	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1113	14155	27094	3.1	4.0E-90	4505318	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1715	14743	27712	6.89	4.0E-90	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
3037	16089	28990	0.97	4.0E-90	AF007544.1	NT	Homo sapiens prostate-specific membrane antigen (PSM) gene, complete cds
4767	17772	30839	2.34	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4913	17912	30780	2.12	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4932	17931	30780	2.22	4.0E-90	M85967.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
8435	21387	34707	0.91	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-amy-b-04-Q-U1.s1 NCJ CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
8435	21387	34708	0.91	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-amy-b-04-Q-U1.s1 NCJ CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
12056	24897	38402	16	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
229	13327	26244	3.32	2.0E-90	BE637913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1201	14240	27180	4.64	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1201	14240	27181	4.64	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3914	16942	29821	2.52	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares placenta 8to9weeks 2NbHP8to9w Homo sapiens cDNA clone IMAGE:1713410 3'
5017	18015	30874	10.91	2.0E-90	6729855	NT	similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3 ; Homo sapiens GRB2-related adaptor protein (GRAP) mRNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5984	19049	32173	0.53	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5984	19049	32174	0.53	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5993	19059	32185	3.94	2.0E-90	AW672696.1	EST_HUMAN	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE2898881 5' similar to TR:O76208 O76208 HYPOTHETICAL 36.6 KD PROTEIN.;
10308	23198	36607	1.79	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67KD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10308	23198	36608	1.79	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67KD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10466	23354	36768	0.98	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
10466	23354	36769	0.98	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11802	24002	37441	3.66	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
296	13390	26308	3.61	1.0E-90	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nadn-ii, Alzheimer disease) (APP), mRNA
395	15844	26398	1.36	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
396	15844	26398	1.37	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
719	13777	26698	1.78	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
719	13777	26699	1.78	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
753	13810	26736	7.36	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
753	13810	26737	7.36	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1137	14179		1.85	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1332	14366	27315	3.13	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1332	14366	27316	3.13	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1694	14724		1.02	1.0E-90	BE379884.1	EST_HUMAN	60115953F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE3511118 5'
1920	14941	27918	2.41	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2898	15950	28850	9.01	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3918	16946	29826	1.12	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3918	16946	29827	1.12	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4530	17539	30401	1.4	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5872	18942	32058	2.04	1.0E-90	AB014833.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6050	19112	32241	0.86	1.0E-90	11426910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6849	19881	33085	0.42	1.0E-90	11419408	NT	Homo sapiens cytochrome P450, 51 (lanosterol 14-alpha-demethylase) (CYP51), mRNA
7428	20127	33366	0.67	1.0E-90	U91934.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7687	20620	33920	0.63	1.0E-90	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8124	21034	34363	2.37	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
9380	22308	35669	3.97	1.0E-90	11422096	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9833	22739		0.89	1.0E-90	AF163894.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9856	22771	36157	1.57	1.0E-90	11422109	NT	Homo sapiens CGL-15 protein (LOC51006), mRNA
9856	22771	36158	1.57	1.0E-90	11422109	NT	Homo sapiens CGL-15 protein (LOC51006), mRNA
11477	24380	37840	1.49	1.0E-90	J04474.1	NT	Human branched chain alpha-keto acid dehydrogenase mRNA, 3' end
4292	17306	30175	7.85	8.0E-91	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
1484	14495	27456	1.24	7.0E-91	AF053788.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
8881	21811	35164	1.58	7.0E-91	11419234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
10789	23875	37105	0.71	7.0E-91	AI904151.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
3334	16572	28476	1.56	5.0E-91	AA702794.1	EST_HUMAN	z90b04.s1 Soares_fetal_liver_spleen_1NPLS.S1 Homo sapiens cDNA clone IMAGE:448015 3'
4637	17643	30506	1.14	5.0E-91	AU143539	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4637	17643	30507	1.14	5.0E-91	AU143539	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4923	17922	30785	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4923	17922	30786	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6803	19933	33151	1.02	5.0E-91	AI878985.1	EST_HUMAN	au49f09.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW:ASPG FLAME Q47898 N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR;
8783	21713	35060	1.53	5.0E-91	BF314682.1	EST_HUMAN	601601624F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4130933 5'
9319	22247	35609	1.77	5.0E-91	AV649878	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
9319	22247	35610	1.77	5.0E-91	AV649878	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
3246	16294	29197	1.57	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3246	16294	29198	1.57	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
11368	24286	37731	1.65	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12442	25197	31846	3.04	4.0E-91	M77694.1	EST_HUMAN	EST01579 Hippocampus, Strathgery (cat. #836205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12442	25197	31882	3.04	4.0E-91	M77694.1	EST_HUMAN	EST01579 Hippocampus, Strathgery (cat. #836205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
1640	14671	27634	1.85	3.0E-91	11430183	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1640	14671	27635	1.85	3.0E-91	11430183	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1614	15653	27812	1.31	3.0E-91	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLOON mRNA, complete cds
2158	15168	28170	1.99	3.0E-91	BE205792.1	EST_HUMAN	bb48b02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3009963 3' similar to TR:O28061 O28061 2-DEOXY-D-GLUCONATE 3-DEHYDROGENASE; contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2708	15702	28697	2.4	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
2708	15702	28698	2.4	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
3388	18431	29335	1.12	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3523	16561	29464	3.48	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3523	16561	29465	3.48	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3853	16882	29767	0.72	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4703	17708	30571	4.4	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5101	18098	30945	1.29	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5101	18098	30946	1.29	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6884	18953	32068	1.52	3.0E-91	11434864	NT	Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA
6659	19601		3.02	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6865	19697	33112	3.37	3.0E-91	11497811	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6865	19697	33113	3.37	3.0E-91	11497811	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
8087	20999	34320	3.75	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8525	21456	34798	0.55	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8330	22258	35622	2.74	3.0E-91	D16494.1	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9828	22734	36116	0.94	3.0E-91	AB011166.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
11328	24245	37683	1.56	3.0E-91	AB032179.2	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
12672	25338	31823	1.51	3.0E-91	AF240788.1	NT	Homo sapiens EHM2 mRNA, complete cds
12889	15702	28697	9.92	3.0E-91	AF169555.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12889	15702	28698	9.92	3.0E-91	AF169555.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
51	13168	26065	2.07	1.0E-91	AL163284.2	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
1273	14307	27258	4.77	1.0E-91	AW449746.1	EST_HUMAN	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
5598	18674	31552	0.88	1.0E-91	11434402	NT	Homo sapiens chromosome 21 segment HS21C084
7159	20237	33522	1.7	1.0E-91	BF348182.1	EST_HUMAN	UI-H-B13-aks-d-01-Q.U1.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
7159	20237	33523	1.7	1.0E-91	BF348182.1	EST_HUMAN	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
8399	21302	34633	0.49	1.0E-91	M20453.1	NT	602022098F1 NCI CGAP Bmr67 Homo sapiens cDNA clone IMAGE:4157804 5'
1269	14304	27252	7.34	9.0E-92	AJ001689.1	NT	602022098F1 NCI CGAP Bmr67 Homo sapiens cDNA clone IMAGE:4157804 5'
1269	14304	27253	7.34	9.0E-92	AJ001689.1	NT	Human nucleus-encoded mitochondrial aldehyde dehydrogenase 2 (ALDH2) gene, exon 10
6361	18343	31187	1.21	9.0E-92	AB020540.1	NT	Homo sapiens NKG2D gene, exon 10
							Homo sapiens NKG2D gene, exon 10
							Homo sapiens mRNA for KIAA0833 protein, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5649	18723	31629	3.69	9.0E-92	J03007.1	NT	Human Na ⁺ K ⁺ ATPase alpha-subunit mRNA, partial cds
5799	18871	31979	2.82	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20280 (FLJ20280), mRNA
6724	19760	32967	4.13	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
8946	21876	35236	1.2	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8946	21876	35237	1.2	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9814	22720	36103	2.3	9.0E-92	11422088	NT	Homo sapiens Brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
95	13208	26120	6.86	8.0E-92	W26367.1	EST_HUMAN	26367 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
305	13398	26318	2.99	8.0E-92	BE386363.1	EST_HUMAN	901273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
5577	18655	31632	0.76	8.0E-92	AB046820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds
5688	18781	31885	0.63	8.0E-92	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
8826	19659	33071	1.03	8.0E-92	AJ000379.1	NT	Homo sapiens MCP-4 gene
8830	19853	33076	0.91	8.0E-92	AF179428.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
8241	21146	34478	7.75	8.0E-92	X69536.1	NT	H. sapiens gene for Inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
8241	21146	34479	7.75	8.0E-92	X69536.1	NT	H. sapiens gene for Inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
8670	21601		0.67	8.0E-92	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8895	21924	35278	4.05	8.0E-92	L04189.1	NT	Human lens membrane protein (mp19) gene, exon 11
8895	21924	35279	4.05	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8088	22017	35373	0.9	8.0E-92	11428569	NT	Homo sapiens transcription termination factor RNA polymerase II (TTF2), mRNA
9614	22540	35910	3.04	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10529	23415	36829	1.11	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
11243	24168	37615	3.46	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11799	24721	38214	1.39	8.0E-92	4503340	NT	Homo sapiens dihydropyrimidine S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
26	13142	26029	0.91	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
255	15870	26267	1.11	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
255	15870	26268	1.11	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
612	13677		1.34	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Sepsis truncated isoform mRNA, complete cds
1306	14339	27287	0.8	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2202	15213	28215	1.33	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2202	15213	28216	1.33	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2599	15597	28592	1.79	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
2772	15764	28756	1.86	7.0E-92	5005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2801	15790	28789	1	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3394	18401	29339	0.72	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3394	18401	29340	0.72	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4701	17706	30569	1.67	7.0E-92	ST1824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4701	17706	30570	1.67	7.0E-92	ST1824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5321	18305	31155	1.04	7.0E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5442	18624	31249	4.92	7.0E-92	AA446206.1	EST_HUMAN	z668412.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'
1610	14640		0.89	5.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
5376	18358		0.93	4.0E-92	BE205702.1	EST_HUMAN	bb49b02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3009963 3' similar to TR:O28061 O28061 2-DEOXY-D-GLUCONATE 3-DEHYDROGENASE contains Alu repetitive element;
2816	15805	28803	2.34	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902639 5'
4546	17555		0.94	3.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6091	19162	32288	7.97	3.0E-92	AA376336.1	EST_HUMAN	EST191020 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to ribosomal protein S13
11203	24129	37576	2	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
11203	24129	37577	2	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
27	13143	26030	1.67	2.0E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
152	13252	26170	24.89	2.0E-92	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
190	13288	26202	2.91	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D.J462023.2), mRNA
190	13288	26203	2.91	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D.J462023.2), mRNA
773	13630	26762	16.21	2.0E-92	BE289180.1	EST_HUMAN	60118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
773	13630	26763	16.21	2.0E-92	BE289180.1	EST_HUMAN	60118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1743	14770		1.65	2.0E-92	S78653.1	NT	migras-related [human, Genomic, 2416 nt]
1951	14971	27952	1.3	2.0E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1951	14971	27953	1.3	2.0E-92	AI818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1978	14998	27990	0.95	2.0E-92	4507464	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1978	14998	27991	0.95	2.0E-92	4507464	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2062	16078	28078	5.02	2.0E-92	4506960	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2707	15701	28086	34.53	2.0E-92	6912457	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
3677	16710	29600	0.91	2.0E-92	AF231919.1	NT	Homo sapiens syndecan 4 (emphiglycan, ryndocan) (SDC4) mRNA
3677	16710	29601	0.91	2.0E-92	AF231919.1	NT	Homo sapiens caldesin binding protein 1 (KIAA0330), mRNA
3677	16710	29601	0.91	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3752	16784	29673	7.66	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4386	17400	30268	1.33	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4868	17868	30732	0.87	2.0E-92	AF136623.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
5115	18112		5.25	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414_r1_434 (synonym: ites3) Homo sapiens cDNA clone DKFZp434C0414.5'
5369	18351		0.97	2.0E-92	4759169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
5967	19034	32155	0.73	2.0E-92	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6556	19598		2.77	2.0E-92	4504756	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
6900	19930	33147	2.48	2.0E-92	AB028991.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7876	20803		0.59	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7809	20803		0.59	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
9414	22342	35707	1.41	2.0E-92	AW340174.1	EST_HUMAN	h02h02.x1 Scores: NFI_T_GBC S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711
11199	24125	37571	6.13	2.0E-92	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
11448	24382	37810	1.5	2.0E-92	11434759	NT	Homo sapiens zinc finger protein 198 (ZNF198), mRNA
11488	24398	37848	1.47	2.0E-92	5803103	NT	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
11584	24493	37961	1.57	2.0E-92	AW836290.1	EST_HUMAN	CM4-LT0026-161299-062-g06 LT0026 Homo sapiens cDNA
11584	24493	37962	1.57	2.0E-92	AW836290.1	EST_HUMAN	CM4-LT0026-161299-062-g06 LT0026 Homo sapiens cDNA
12770	25399	31810	4.57	2.0E-92	AB029016.1	NT	Homo sapiens mRNA for KIAA1083 protein, partial cds
13009	16701	28696	89.73	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1874	14895	27878	1.26	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Scores: placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1874	14895	27879	1.26	1.0E-92	R78078.1	EST_HUMAN	y80e08.r1 Scores: placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2087	15101	28101	27.09	1.0E-92	4506688	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8822	21752	35098	0.65	1.0E-92	BE438825.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
9707	22692	38011	3.01	1.0E-92	AI380356.1	EST_HUMAN	tg01b02.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:P.TNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element;
9707	22692	38012	3.01	1.0E-92	AI380356.1	EST_HUMAN	tg01b02.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:P.TNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element;
2042	15059	28060	2.7	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2056	15073		9.46	9.0E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2695	15689		2.12	9.0E-93	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3879	16712	28603	1.1	9.0E-93	BE388571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
12074	24915		8.72	9.0E-93	11418528	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
6712	19748	32951	0.42	8.0E-93	AW014042.1	EST_HUMAN	U1-H-B10-aah-h-08-q-U1.a7 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6712	19748	32952	0.42	8.0E-93	AW014042.1	EST_HUMAN	U1-H-B10-aah-h-08-q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6876	18907	33122	3.08	8.0E-93	BF036384.1	EST_HUMAN	601460321F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863908 5'
265	13360	26275	6.07	7.0E-93	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
6213	19268	32419	0.44	6.0E-93	11450204	NT	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
6213	19268	32420	0.44	6.0E-93	11450204	NT	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
6977	20004	33236	1.12	6.0E-93	AB033098.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7245	20154	33394	1.24	6.0E-93	AF085771.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
1408	14439	27393	1.26	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1432	14463	27416	2.43	5.0E-93	A1674184.1	EST_HUMAN	wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'
1432	14463	27417	2.43	5.0E-93	A1674184.1	EST_HUMAN	wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'
1493	14524		0.97	5.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3280	16328	29233	2.06	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
3978	17006	29894	1.01	5.0E-93	8923209	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
6010	19073	32199	1.01	5.0E-93	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
6347	18997		1.33	5.0E-93	AF045555.1	NT	Homo sapiens wbc01 (WBC01) and wbc05 (WBC05) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
8174	21081	34411	3.39	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
9166	22094	35452	0.79	5.0E-93	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9166	22094	35453	0.79	5.0E-93	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
10149	23040	36439	2.26	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10323	23212	36524	1.09	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10572	23458	36878	1.31	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
11264	24187	37636	2.87	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12678	25621	31724	2.04	6.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
90	13203		8.04	4.0E-93	AA459933.1	EST_HUMAN	z50e09.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:785688 3' similar to SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM;
467	13538	26460	1.62	4.0E-93	4557879	NT	Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
467	13538	26461	1.62	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
798	13553	26788	1.44	4.0E-93	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1) mRNA
798	13553	26789	1.44	4.0E-93	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1) mRNA
1211	14249	27180	1.44	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1893	15011	28001	3.66	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2850	15645	28645	2.18	4.0E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3628	16862	28562	0.83	4.0E-93	7705398	NT	Homo sapiens tumor antigen SLP-3p (HCC8), mRNA
4132	17154	30031	2	4.0E-93	4504854	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5150	16862	28562	0.69	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-3p (HCC8), mRNA
5940	18911	32027	4.31	4.0E-93	T46864.1	EST_HUMAN	y694c12.1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN ,
11573	24482	37950	5.62	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKC Homo sapiens cDNA clone GKORF07 5'
3720	16752	29639	2.98	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332036 5'
3720	16752	29640	2.98	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332036 5'
4335	17349		1.6	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
6844	19876	33091	1.21	3.0E-93	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
11240	24166	37612	3.7	3.0E-93	AI824829.1	EST_HUMAN	wb02d05.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2304489 3'
203	13302	26217	7.85	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
203	13302	26218	7.85	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
343	13433	26348	8.36	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
344	13433	26348	7.2	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1638	14669	27632	2.36	2.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
2144	15157	28169	1.07	2.0E-93	U40763.1	NT	Human CLK-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2509	15510	28513	1.06	2.0E-93	BE252882.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3958220 5'
5602	18678	31568	5.33	2.0E-93	AW984386.1	EST_HUMAN	EST1376458 IMAGE resequences, MAGI Homo sapiens cDNA
5613	18689	31584	0.6	2.0E-93		NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5733	18806		0.75	2.0E-93	BF351459.1	EST_HUMAN	QV3-HT0513-280300-126-H04 HT0513 Homo sapiens cDNA
5833	18904	32019	1.55	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC61318), mRNA
5848	18919	32033	0.59	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-86
6980	20007		1.3	2.0E-93	AV502002.1	EST_HUMAN	UHF-BNO-eks-g-09-q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076329 5'
12655	25328		2.39	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12900	25488		5.72	2.0E-93	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3862086 5'

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108	13219	26131	5.79	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
108	13219	26132	5.79	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
541	13610	26520	14.12	1.0E-93	7657018	NT	Homo sapiens hypothetical protein (D1328E19.C1.1), mRNA
621	13686	26589	4.04	1.0E-93	A146755.1	EST_HUMAN	Q8408.X1 NCL CGAP_GLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 ZINC FINGER PROTEIN ;
897	13950	26897	6.3	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1195	14234	27173	0.88	1.0E-93	4503872	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD87, mRNA
1265	14299	27246	5.85	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1265	14299	27246	5.85	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1374	14408	27359	1.52	1.0E-93	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2360	15367	28371	1.19	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2487	15489	28490	3.95	1.0E-93	AF055006.1	NT	Homo sapiens MHC class 1 region
2532	15533		0.97	1.0E-93	AL137200.1	NT	Novel human gene mapping to chromosome 1
2870	14355	27301	1.81	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2870	14355	27302	1.81	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2976	16028	28930	1.19	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3262	18310		1.27	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4536	17545	30408	1.87	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5768	18831	31631	2.06	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5758	18831	31632	2.06	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5973	19039	32161	0.94	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6137	19196	32334	8.81	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6438	19485	32681	0.9	1.0E-93	7662241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
7100	20306	33585	2.19	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7621	20568	33850	3.47	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8836	21766	35113	2.04	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
9107	22035	35389	1.33	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEMD protein
9208	22136	35493	1.58	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9575	22502	35865	0.65	1.0E-93	AB023228.1	NT	Homo sapiens mRNA for KIAA1011 protein, partial cds
9575	22502	35866	0.65	1.0E-93	AB023228.1	NT	Homo sapiens mRNA for KIAA1011 protein, partial cds
9984	21342	34677	2.49	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9988	21346	34681	1.21	1.0E-93	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
10116	23007	36401	4.95	1.0E-93	X13474.1	NT	Human PresA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
10116	23007	36402	4.95	1.0E-93	X13474.1	NT	Human PresA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
10246	23137	36542	0.74	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10643	23629	36962	0.67	1.0E-93	11433646	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
12266	25719	31666					gn03c12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP.T18B4.4 CE13742;
12812	25434		1.85	1.0E-93	AI268262.1	EST_HUMAN	Homo sapiens GGT1 gene, exon 1
12895	25485		2.33	1.0E-93	AJ230125.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
			3.64	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
13048	25841		2.21	1.0E-93	AF240788.1	NT	Homo sapiens chromosome 21 segment HS21C009
11064	23948		1.39	6.0E-94	AL163209.2	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
4045	17072	29958	1.85	6.0E-94	AF142482.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5552	18630	31508	3.94	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5552	18630	31509	3.94	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6283	19334	32500	18.24	5.0E-94	AA722434.1	EST_HUMAN	cg87g06.s1 Soares_fetal_tetus_NB2HF8_9w Homo sapiens cDNA clone IMAGE:409594 3'
7354	20350	33617	1.39	5.0E-94	AI015900.1	EST_HUMAN	cg83g05.s1 Soares_fetal_tetus_NB2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'
9198	22126	35482	0.98	5.0E-94	BF529115.1	EST_HUMAN	602042163F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180023 5'
11410	24326	37775	1.96	5.0E-94	11423962	NT	Homo sapiens adenylylase kinase 2 (AK2), mRNA
11410	24326	37776	1.96	5.0E-94	11423962	NT	Homo sapiens adenylylase kinase 2 (AK2), mRNA
12555	25946	31375	3.09	5.0E-94	T89398.1	EST_HUMAN	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
13063	25569		1.6	5.0E-94	D26217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
1857	14869		5.75	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
3739	16771	29657	1.11	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3739	16771	29658	1.11	4.0E-94	AW197851.1	EST_HUMAN	xn89f12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2701679 3'
							tr41f10.x1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE ;
4831	17832	30702	3.28	4.0E-94	AI591312.1	EST_HUMAN	
6741	19775	32987	1.64	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6741	19775	32988	1.64	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7240	20149		1.04	4.0E-94	L27386.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
11548	24457	37920	1.46	4.0E-94	AB004929.1	NT	Homo sapiens gene for Smad 3, exon 8
11887	23987	37425	1.41	4.0E-94	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12177	25013	38518	10.28	4.0E-04	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
634	13695	26800	1.37	3.0E-04	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
744	13802	26728	12.12	3.0E-04	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1768	14794	27764	1.98	3.0E-04	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein 352 precursor, mRNA, complete cds
1768	14794	27765	1.98	3.0E-04	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein 352 precursor, mRNA, complete cds
1797	14823	27791	2.94	3.0E-04	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2094	15108	28110	1.05	3.0E-04	11427779	NT	Homo sapiens hepatic leukemia factor (HLF), mRNA
2094	15108	28111	1.05	3.0E-04	11427779	NT	Homo sapiens hepatic leukemia factor (HLF), mRNA
4285	17299	30166	0.77	3.0E-04	AA464805.1	EST_HUMAN	zw63g08.l1 Soares fetal testis N52HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
4422	17433	30294	0.78	3.0E-04	AA781836.1	EST_HUMAN	al59h06.s1 Soares testis_NHT Homo sapiens cDNA clone 1375183 3'
5878	18947	32084	4.02	3.0E-04	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6391	19440	32607	1.17	3.0E-04	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6722	19758	32955	4.23	3.0E-04	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
8290	21194	34531	0.4	3.0E-04	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8777	21707	35053	1.02	3.0E-04	AF152308.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
9149	22077	35438	5.3	3.0E-04	AB014578.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
10120	23011	36408	5.12	3.0E-04	AF087942.1	NT	Homo sapiens glycoheparin-1L mRNA, complete cds
11544	24463	37916	1.8	3.0E-04	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
12061	24902	38405	3.18	3.0E-04	11436925	NT	Homo sapiens anaphase-promoting complex 10 (APC10), mRNA
12104	24945	38448	2.06	3.0E-04	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
10273	23163	36574	0.73	2.0E-04	AB103933.1	EST_HUMAN	w30h1.1 x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
10273	23163	36575	0.73	2.0E-04	AB103933.1	EST_HUMAN	w30h1.1 x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
199	13289	26177	1.45	1.0E-04	BE285714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3138	16188	26080	2.44	1.0E-04	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3138	16188	26081	2.44	1.0E-04	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
6308	19358	32529	0.55	1.0E-04	AE000269.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6518	19562	32743	0.72	1.0E-04	AL040518.1	EST_HUMAN	DKFZp434G0314_j1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G0314 5'
6527	19571	32754	0.64	1.0E-04	H08270.1	EST_HUMAN	y8702.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'
6797	18830	33040	0.62	1.0E-04	AV725992.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone HTCCBF05 5'
9798	22762	36147	2.3	1.0E-04	11428740	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
10308	23168	36606	1.83	1.0E-04	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872089 5'
11505	24415	37869	3.56	1.0E-04	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11762	24863	38148	2.42	1.0E-94	A1272244.1	EST_HUMAN	ap22e02.x1 Schiller oligodendroglioma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR-Q62845
12668	13259	26177	1.57	1.0E-94	BE295714.1	EST_HUMAN	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ;
12668	13259	26177	2.02	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1495	14526	27488	1.86	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3169	18247	29142	1.25	9.0E-95	7662027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3169	18247	29143	1.25	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5590	18656	31543	1.22	9.0E-95	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5590	18656	31544	1.22	9.0E-95	X82569.1	NT	M.musculus glyt1 gene (exons 1c and 2)
8827	21757	35101	1.71	9.0E-96	AF274753.1	NT	M.musculus glyt1 gene (exons 1c and 2)
154	13254	26172	12.12	8.0E-95	AF154830.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
7280	20233	33483	0.8	8.0E-95	11419378	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
7611	20546	33838	1.62	8.0E-95	11426529	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
7611	20546	33839	1.62	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8775	21705	35050	2.05	8.0E-95	AF032897.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8904	22892	36277	2.2	8.0E-95	11420944	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
9904	22892	36278	2.2	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10362	23251	36671	3.15	8.0E-95	5174644	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10391	23280		3.34	8.0E-95	AB037816.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10730	23618	37043	0.75	8.0E-95	8945523	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
11166	24085	37632	1.58	8.0E-95	AF112152.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
11915	24762	38259	1.42	8.0E-95	10964024	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
12663	25468		26.36	8.0E-95	AA629056.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
295	13389	26308	8.44	7.0E-95	D87676.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
295	13389	26307	8.44	7.0E-95	D87676.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4473	17484	30344	5.63	7.0E-95	M95708.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4521	17530		0.83	7.0E-95	AL163246.2	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
8183	18175	31020	1.02	7.0E-95	M95929.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9758	22682	36068	0.93	4.0E-95	BE439625.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
223	13222	26238	15.69	3.0E-95	AV648361.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
6628	18704	31603	1.88	3.0E-95	BF526041.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5871	25634	32567	0.7	3.0E-95	4503354	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
7528	20467	33755	1.72	3.0E-95	AA412321.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7528	20487	33756	1.72	3.0E-05	AA412321.1	EST_HUMAN	z897d01.r1 Soares testis NIH_Homo sapiens cDNA clone IMAGE:730273 5'
7760	20690	33988	1.29	3.0E-05	AW958121.1	EST_HUMAN	EST1370191 MAGE resequences, MAGE Homo sapiens cDNA
7760	20690	33989	1.29	3.0E-05	AW958121.1	EST_HUMAN	EST1370191 MAGE resequences, MAGE Homo sapiens cDNA
9893	22808	36196	1.5	3.0E-05	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9893	22808	36197	1.5	3.0E-05	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10267	23157	36568	0.81	3.0E-05	BF213446.1	EST_HUMAN	601845212F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4070451 5'
11316	24235	37680	1.79	3.0E-05	R63190.1	EST_HUMAN	y687g11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194468 5'
965	14016	26959	5.54	2.0E-05	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
1671	14701	27661	1.84	2.0E-05	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1671	14701	27662	1.84	2.0E-05	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1656	14976	27958	5.45	2.0E-05	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1559	14978	27962	1.79	2.0E-05	BE398873.1	EST_HUMAN	601312161F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3658862 5'
2450	15454	28480	1.23	2.0E-05	5453666	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2450	15454	28451	1.23	2.0E-05	5453666	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2489	15491	28491	3.88	2.0E-05	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2539	15539	28538	2.59	2.0E-05	4768423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2865	14015	26958	13.24	2.0E-05	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
3200	16248	29144	1.97	2.0E-05	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3623	16659	29568	4.18	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3623	16659	29569	4.18	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3662	16715	29606	1.27	2.0E-05	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3813	16843	29729	0.68	2.0E-05	AI290284.1	EST_HUMAN	qnt01c02.x1 Soares_Nh-HMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705;
4469	17480	30339	1.16	2.0E-05	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5169	18161	31009	3.08	2.0E-05	7681979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5668	18742	31651	5.72	2.0E-05	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5668	18742	31652	5.72	2.0E-05	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5898	18965	32082	1.2	2.0E-05	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5906	18965	32083	1.2	2.0E-05	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5940	19007	32127	0.67	2.0E-05	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6382	19431	32599	3.74	2.0E-05	M69724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6720	18756	32982	0.87	2.0E-05	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6720	19756	32983	0.87	2.0E-05	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6852	19884	33098	2.63	2.0E-05	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 8 (DNAH8) mRNA, complete cds
7069	20275	33530	1.38	2.0E-05	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9885	22811	35985	0.92	2.0E-05	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10669	23755	37182	0.55	2.0E-05	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
11166	24094	37642	1.9	2.0E-05	4757653	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRIA) mRNA
12123	24964	38468	1.59	2.0E-05	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12123	24964	38469	1.59	2.0E-05	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12642	25318	31821	2.54	2.0E-05	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12744	25384		1.52	2.0E-05	11417860	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
13010	25558	31759	5.79	2.0E-05	11418194	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5809	18881	31988	8.43	1.0E-05	AA284651.1	EST_HUMAN	z123h04.r1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1057084 G1057084 F55H2.6
5809	18881	31989	8.43	1.0E-05	AA284651.1	EST_HUMAN	z123h04.r1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1057084 G1057084 F55H2.6
7937	20859	34167	4.82	1.0E-05	BF370000.1	EST_HUMAN	RC6-FN0019-250600-011-G11 FN0019 Homo sapiens cDNA
7937	20859	34168	4.82	1.0E-05	BF370000.1	EST_HUMAN	RC6-FN0019-250600-011-G11 FN0019 Homo sapiens cDNA
9996	22813	36203	0.65	1.0E-05	R17806.1	EST_HUMAN	y09b08.r1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:31763 5'
8772	21702	36048	1.79	9.0E-06	BE897269.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3822423 5'
465	15874	26457	0.66	8.0E-06	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
465	15874	26458	0.66	8.0E-06	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
6701	18774		2.77	8.0E-06	AW836047.1	EST_HUMAN	PMO-LT0019-090300-002-d09 LT0019 Homo sapiens cDNA
3963	17011	29899	0.83	7.0E-06	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
3363	16407	29308	0.66	6.0E-06	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21O001
3541	16579	29482	3.39	6.0E-06	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
5835	18906	32021	0.65	6.0E-06	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
11978	24821	38314	2.6	6.0E-06	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11978	24821	38315	2.6	6.0E-06	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12021	24863	38364	2.51	6.0E-06	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
340	13430	26344	2.63	5.0E-06	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
867	13920	26865	3.73	5.0E-06	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
867	13920	26866	3.73	5.0E-06	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2603	15659		1.5	5.0E-06	11416767	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
3073	16125	29023	0.93	5.0E-06	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
4018	17045	29935	1.18	5.0E-06	4788387	NT	Homo sapiens fibroblast growth factor 14 (FGF14), mRNA
5012	18010		1.13	5.0E-06	X60812.1	NT	H. sapiens DNA for monamine oxidase type A (7) (partial)
6942	19971	33184	0.99	5.0E-06	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
7009	20036	33269	0.5	5.0E-06	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleosidase (dNT-2 gene), exons 1-5
7089	20285	33554	4.1	5.0E-06	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7089	20295	33555	4.1	5.0E-06	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7368	20362	33632	1.01	5.0E-06	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7938	20860	34169	1.45	5.0E-06	AB024334.1	NT	Homo sapiens mRNA for 14-3-3 gamma, complete cds
8684	21615	34957	2.03	5.0E-06	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8684	21615	34958	2.03	5.0E-06	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
12217	25051	38550	1.69	5.0E-06	D83776.1	NT	Human mRNA for KIAA0181 gene, partial cds
4287	17301		5.4	3.0E-06	H68556.1	EST_HUMAN	yr87h12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5'
438	13509		2.7	2.0E-06	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
771	13828	26759	2.09	2.0E-06	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7868	20795	34097	0.62	2.0E-06	BF369731.1	EST_HUMAN	QV4-GN0120-260900-427-b12 GN0120 Homo sapiens cDNA
7868	20795	34098	0.62	2.0E-06	BF369731.1	EST_HUMAN	QV4-GN0120-260900-427-b12 GN0120 Homo sapiens cDNA
9632	22469		4.83	2.0E-06	AV689481.1	EST_HUMAN	AV689481 GKC Homo sapiens cDNA clone GKCfMD07 5'
12364	25151		2.4	2.0E-06	AW249440.1	EST_HUMAN	2819351.5 Splice NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819351 5'
945	13706	26612	0.7	1.0E-06	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
945	13706	26613	0.7	1.0E-06	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
694	13754	26671	2.14	1.0E-06	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1805	14831	27798	1.86	1.0E-06	AW955054.1	EST_HUMAN	EST387124 MAGC resequences, MAGC Homo sapiens cDNA
1805	14831	27799	1.86	1.0E-06	AW955054.1	EST_HUMAN	EST387124 MAGC resequences, MAGC Homo sapiens cDNA
2242	16252	28257	1	1.0E-06	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2242	16252	28258	1	1.0E-06	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2283	15857	28300	1.19	1.0E-06	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
5398	18380		35.82	1.0E-06	5453913	NT	Homo sapiens phospholipid transfer protein (PLTP), mRNA
7303	18472	31293	1.08	1.0E-06	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7402	20101	33336	0.67	1.0E-06	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8791	21721	35068	1.04	1.0E-06	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA

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8791	21721	35088	1.04	1.0E-96	7681803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
9275	22203	35560	26.87	1.0E-98	11419428	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
9409	22937	35701	2.74	1.0E-96	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10655	23541	36974	1.56	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
10655	23541	36975	1.56	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
12353	13706	26612	2.1	1.0E-96	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12353	13706	26613	2.1	1.0E-96	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3374	16418	26320	0.99	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
7989	20908		3.62	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
9489	22417	35778	0.94	6.0E-97	BE698012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
9489	22417	35780	0.94	6.0E-97	BE698012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
8593	21524	34869	1.79	5.0E-97	AL043314.2	EST_HUMAN	DKFZp344N0323_r1.434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
8721	21651	34998	10.22	5.0E-97	AA416026.1	EST_HUMAN	z97e12.s1 Soares NIH-MIPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
10200	23091	36492	3.17	5.0E-97	BF154912.1	EST_HUMAN	G1304125 PMS4 MRNA
11978	24822	38316	1.87	5.0E-97	BE148597.1	EST_HUMAN	RCO-BT0812-250900-032-a09 BT0812 Homo sapiens cDNA
11978	24822	38317	1.87	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
987	14018	26962	1.56	4.0E-97	BE004436.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
1926	14947	27023	1.18	4.0E-97	5453572	NT	CMD-BND106-170300-289-a08 BND106 Homo sapiens cDNA
5757	18630	31930	42.37	4.0E-97	4657326	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6070	19131	32284	0.53	4.0E-97	U09002.1	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein 1) (APOH) mRNA
6070	19131	32265	0.53	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (HNR2A) mRNA, complete cds
7136	20244	33495	6	4.0E-97	Y11339.2	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (HNR2A) mRNA, complete cds
7136	20244	33496	6	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7366	20360	33629	1.03	4.0E-97	7710125	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7422	20121	33358	0.94	4.0E-97	11422165	NT	Homo sapiens cyclic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8113	25683		0.47	4.0E-97	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
8400	21303	34634	0.42	4.0E-97	10947053	NT	Homo sapiens ankryrin 2, neuronal (ANK2), transcript variant 2, mRNA
8400	21303	34635	0.42	4.0E-97	10947053	NT	Homo sapiens ankryrin 2, neuronal (ANK2), transcript variant 2, mRNA
8713	21844	34990	0.83	4.0E-97	4557708	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8931	21881	35216	1.46	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA

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Probe- SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9179	22107	35485	0.85	4.0E-97	11423233	NT	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA
9780	22754	36136	1.22	4.0E-97	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9780	22754	36137	1.22	4.0E-97	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11604	24513	37981	1.84	4.0E-97	11853122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11604	24513	37982	1.84	4.0E-97	11853122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11867	23957	37403	1.99	4.0E-97	AB042557.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
12524	25248		7.05	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
262	13358	28273	1.31	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
899	13952	28899	7.56	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
899	13952	28900	7.56	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1400	15901	27453	1.43	3.0E-97	4759813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2462	15939	28463	2.08	3.0E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3212	16280	29159	14.55	3.0E-97	K02212.1	NT	Human alpha-1-antitrypsin gene (S variant), complete cds
3305	16352	29255	1.17	3.0E-97	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
3894	16623	29789	0.92	3.0E-97	AF138523.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
4892	17891	30757	4.56	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6695	19731	32931	2.44	1.0E-97	BE568486.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
7227	20135	33376	0.55	1.0E-97	5453881	NT	Homo sapiens phosphatase kinase, gamma 1 (muscle) (PHKG1) mRNA
9977	21335	34670	0.69	1.0E-97	AW379976.1	EST_HUMAN	RC0-HT0258-211199-011-g05 HT0258 Homo sapiens cDNA
9977	21335	34671	0.69	1.0E-97	AW379976.1	EST_HUMAN	RC0-HT0258-211199-011-g05 HT0258 Homo sapiens cDNA
10284	23174	36558	1.39	1.0E-97	R10887.1	EST_HUMAN	Y38c08.s1 Soares fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:129134 3'
11148	24077	37525	3.9	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11148	24077	37526	3.9	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11754	24655	38138	1.73	1.0E-97	AA553761.1	EST_HUMAN	nk28g02.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014962 3'
11900	24000	37438	6.95	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11900	24000	37439	6.95	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
926	13978	26924	3.7	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
4784	17789		0.92	9.0E-98	8400716	NT	Homo sapiens nebulin (NEB), mRNA
6557	19599		0.72	9.0E-98	AJ250713.1	NT	Homo sapiens GLDN12 gene for claudin-12
7669	20503	33001	0.54	9.0E-98	7651871	NT	Homo sapiens leucyl-tRNA synthetase, mitochondrial (KIAA0028), mRNA
7784	20713	34015	0.52	9.0E-98	11419408	NT	Homo sapiens A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), mRNA
8503	21434	34775	7.2	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA

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8503	21434	34776	7.2	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9660	22596	35957	4.34	9.0E-98	X06999.1	NT	Human mRNA for amyloid A4(751) protein
9765	22639	36074	5.67	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9832	22738	36120	1.63	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9876	22793		1.16	9.0E-98	AF057726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9906	22894	36280	1.13	9.0E-98		NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9906	22894	36281	1.13	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10753	23639	37072	0.64	9.0E-98	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10852	23738	37161	0.71	9.0E-98	11431544	NT	Homo sapiens protease-activated receptor 3 (PAR3), mRNA
11442	24336	37607	2.32	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11442	24358	37808	2.32	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12539	13978	26624	5.11	9.0E-98	BE080973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
25	13141		0.77	8.0E-98	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1581	14611	27573	1.53	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1581	14611	27574	1.53	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1756	14783	27753	4.42	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1756	14783	27754	4.42	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3654	16990	29585	1.27	8.0E-98	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3654	16990	29586	1.27	8.0E-98	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3860	16889	29774	11.61	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
6319	19369	32538	1.62	5.0E-98	BE885873.1	EST_HUMAN	601607503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 5'
5406	18387		1	4.0E-98	AA001786.1	EST_HUMAN	zh84f12.r1 Soares fetal liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
2191	16202	28207	1.1	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone B
2861	15648	28648	2.92	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2798	15787		4.29	3.0E-98	AA077498.1	EST_HUMAN	7518101 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7518101
7275	20228	33476	0.41	3.0E-98	9906846	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7278	20231	33480	2.2	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7278	20231	33481	2.2	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
9311	22239	35000	4.21	3.0E-98	H46898.1	EST_HUMAN	yo17g06.r1 Soares adult brain N2b5fHB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9837	22742	36123	0.74	3.0E-98	8922096	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
10395	23284	36704	1.47	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone B

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10395	23284	36705	1.47	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone IB
10952	23835	37263	0.84	3.0E-98	BE900454.1	EST_HUMAN	601873686F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956617 5'
11391	24307	37753	12.18	3.0E-98	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
13058	25585		2.5	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
759	13816	28745	0.73	2.0E-98	BE281694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2092	15106	28107	3.88	2.0E-98	BE294281.1	EST_HUMAN	601172659F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2253	15283	28272	2.38	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4398	17412	30278	0.85	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4449	17459	30318	4.13	2.0E-98	4758331	NT	Homo sapiens fatty acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4940	17939	30795	1.54	2.0E-98	AF218602.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4940	17939	30796	1.54	2.0E-98	AF218602.1	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
5561	18639	31518	5.74	2.0E-98	7708512	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
6048	19977	33200	1.07	2.0E-98	4505798	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8071	20984	34298	1.38	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8071	20984	34300	1.38	2.0E-98	11431271	NT	Homo sapiens KIAA0104 gene product (KIAA0104), mRNA
8288	21193	34530	0.42	2.0E-98	11431048	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
9169	22097	35458	4.11	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
9169	22097	35457	4.11	2.0E-98	11428813	NT	Homo sapiens NKAT4b mRNA, complete cds
9249	22177	35531	0.67	2.0E-98	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
10066	22982	36373	1.49	2.0E-98	X12664.1	NT	Homo sapiens arginase gene exon 3 (EC 3.5.3.1)
10897	23782		1.9	2.0E-98	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
11644	24550	38022	4.75	2.0E-98	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
428	13499	26423	21.4	1.0E-98	AI862007.1	EST_HUMAN	hw38604.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN
477	13548	26468	1.83	1.0E-98	AW99811.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A. ;
1820	14843	27818	17.08	1.0E-98	N49818.1	EST_HUMAN	PMD-BN0065-100300-001-c05 BN0065 Homo sapiens cDNA
5500	18679	31427	3.23	1.0E-98	AA105854.1	EST_HUMAN	y23105.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:243585 5' similar to
5761	18834	31936	0.92	1.0E-98	BE390627.1	EST_HUMAN	PIR-S64204 S64204 ribosomal protein L29 - human ;
5761	18834	31937	0.92	1.0E-98	BE390627.1	EST_HUMAN	z498c09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562
9550	22477	35635	0.72	1.0E-98	AF141349.1	NT	G806562 NEBULIN ;
							601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
							601284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
							Homo sapiens beta-tubulin mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9560	22477	36836	0.72	1.0E-99	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
6030	19092	32219	0.99	9.0E-99	AI005004.1	EST_HUMAN	QV.BT073-191298-012 BT073 Homo sapiens cDNA
6030	19092	32220	0.99	9.0E-99	AI005004.1	EST_HUMAN	QV.BT073-191298-012 BT073 Homo sapiens cDNA
6275	19326	32493	4.39	9.0E-99	AW968635.1	EST_HUMAN	EST380711 MAGC resequencing, MAGJ Homo sapiens cDNA
11562	24471	37937	2.81	9.0E-99	AI476829.1	EST_HUMAN	trn6sh07.x1 NCLCGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BIID_HUMAN
11562	24471	37938	2.81	9.0E-99	AI476829.1	EST_HUMAN	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
9286	22214	36572	0.99	8.0E-99	9635487	NT	Human endogenous retrovirus, complete genome
6047	19109	32239	9.01	7.0E-99	AF035808.1	NT	Homo sapiens oscillin (HLN) gene, exon 5
12037	24879	38385	2.78	7.0E-99	AF001886.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
494	13664	26483	0.76	6.0E-99	U10901.1	NT	Human G2 protein mRNA, partial cds
3958	16988	29872	1.78	6.0E-99	AW676364.1	EST_HUMAN	EST388473 MAGC resequencing, MAGN Homo sapiens cDNA
4862	17884	30728	1	6.0E-99	4502660	NT	Homo sapiens CD34 antigen (CD34) mRNA
6884	18914	33130	0.74	6.0E-99	7708136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
6974	20001	33232	0.98	6.0E-99	L43810.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6974	20001	33233	0.98	6.0E-99	L43810.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8983	21614	34956	1.32	6.0E-99	X99101.1	NT	H. sapiens mRNA for estrogen receptor
8700	21631	34978	0.72	6.0E-99	6801689	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8924	22252	35616	2.86	6.0E-99	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
9422	22350	35715	4.44	6.0E-99	AF080255.1	NT	Homo sapiens lodeslar protein mRNA, complete cds
9422	22350	35716	4.44	6.0E-99	AF080255.1	NT	Homo sapiens lodeslar protein mRNA, complete cds
9479	22407	35767	0.67	6.0E-99	11431994	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
9479	22407	35768	0.67	6.0E-99	11431994	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 1 (ITPR1), mRNA
11162	24090	37638	3.79	6.0E-99	11528299	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
11888	23988	37426	1.56	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
11888	23988	37427	1.56	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
945	13996	26937	3.34	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
945	13996	26938	3.34	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
1980	14998	27983	1.42	5.0E-99	Y11355.1	NT	H. sapiens IMPA gene, exon 8
4879	17684	30562	1.67	5.0E-99	AF009690.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S9A2 to TCRBV12S2 region
12654	25269		1.88	5.0E-99	BE890177.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
8898	21826		5.75	3.0E-99	M95586.1	NT	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1287	14802		10.54	2.0E-09	AW274792.1	EST_HUMAN	xp00606.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN
3303	16350	29264	1.26	2.0E-09	M80938.1	NT	LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN); Human Ku (p70p80) subunit mRNA, complete cds
4659	17664	30532	1.03	2.0E-09	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
8127	21037	34386	0.55	2.0E-09	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
9265	22193	35551	10.25	2.0E-09	W23507.1	EST_HUMAN	zb46406.r1 Soares Fetal_Jung_Nb-IL19W Homo sapiens cDNA clone IMAGE:306835 5' similar to
9695	22620	35998	0.8	2.0E-09	R78254.1	EST_HUMAN	gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN); y81b09.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145625 5'
11549	24458	37821	3.92	2.0E-09	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
12104	25029	38530	3.81	2.0E-09	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
336	13426	26341	1.54	1.0E-09	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
400	13482	26402	0.94	1.0E-09	11526180	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
1443	14474	27432	1.48	1.0E-09	M30938.1	NT	Human Ku (p70p80) subunit mRNA, complete cds
1678	14608	27568	1.51	1.0E-09	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1578	14608	27569	1.51	1.0E-09	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1942	14963	27941	1.34	1.0E-09	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1942	14963	27942	1.34	1.0E-09	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3134	16184	29077	1.52	1.0E-09	J03171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4487	17498	30358	2.78	1.0E-09	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4487	17498	30359	2.78	1.0E-09	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5949	19016	32136	0.49	1.0E-09	7562349	NT	Homo sapiens cell recognition molecule Casp2 (KIAA0869), mRNA
7115	20319	33583	1.42	1.0E-09	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7115	20319	33584	1.42	1.0E-09	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7499	25571	33720	0.83	1.0E-09	X08022.1	NT	H. sapiens EB-AP gene exon 2
9741	22865		1.12	1.0E-09	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
10050	22966	36355	1.71	1.0E-09	AW340174.1	EST_HUMAN	hd02102.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
11577	24486	37854	1.42	1.0E-09	7427514	NT	O02711 PRO-POLYDUTPASE POLYPROTEIN ; Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11577	24486	37855	1.42	1.0E-09	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11631	24537	38008	1.59	1.0E-09	5801979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11816	24737	38228	3.26	1.0E-09	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12336	25131		5.36	1.0E-09	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1	13118	26004	1.25	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	13118	26004	1.48	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
71	13186	26093	1.3	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
71	13186	26094	1.3	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
89	13202	26116	1	1.0E-100	AW276237.1	EST_HUMAN	x78011.x1 NCL CGAP_Bn53 Homo sapiens cDNA clone IMAGE:2824605 3'
179	13278	26184	1.08	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
337	13427	26343	25.73	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
363	13460	26362	2.75	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (caif836206) Homo sapiens cDNA clone HFBOR32
460	13532		1.45	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
512	13583		16.09	1.0E-100	X89631.1	NT	G.gallia DNA for ZNF80 gene homolog
532	13601	26512	1.33	1.0E-100	BE180609.1	EST_HUMAN	RC3-HT0625-040600-022-b09 HT0625 Homo sapiens cDNA
1046	14080	27028	2.5	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1046	14090	27029	2.5	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1568	14599		1.67	1.0E-100	AW207595.1	EST_HUMAN	U1-HB11-afk-c-07-Q-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722184 3'
1573	14603	27563				EST_HUMAN	q62709.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764633 3' similar to SW:CYT_COTJA
2257	15287		1.63	1.0E-100	AI200857.1	EST_HUMAN	p81081 CYSTATIN 1
2461	15465	28462	1.28	1.0E-100	D83348.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2756	15747	28742	1.01	1.0E-100	X62468.1	NT	H.sapiens mRNA for IFN-gamma (pK-O)
3064	16116		1.48	1.0E-100	D11078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4306	17320	30189	3.79	1.0E-100	AF067354.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4306	17350	30213	1.64	1.0E-100	AF067354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
5225	18214	31058	2.49	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5225	18214	31060	3.7	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5352	18335		3.7	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5472	18553	31395				EST_HUMAN	zh50e11.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415632 5' similar to gb:M24847 SODIUM/GLUCOSE COTRANSPORTER (HUMAN);
5698	18771	31699	1.08	1.0E-100	W78748.1	EST_HUMAN	gb:M24847 SODIUM/GLUCOSE COTRANSPORTER (HUMAN);
5909	18963	32086	1.65	1.0E-100	BF244218.1	EST_HUMAN	xa82f01.x1 NCL CGAP_CVL1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433
5952	19019	32139	1	1.0E-100	AW075983.1	EST_HUMAN	PROTEIN PIP5-1.2 (HUMAN);
6051	19113	32242	1.97	1.0E-100	AU118182.1	EST_HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
6404	19452	32623	1.4	1.0E-100	AF135116.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
			6.47	1.0E-100	X14690.1	NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
			1.06	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6404	19452	32624	1.08	1.0E-100	4567668	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6773	19807	33018	5.1	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6833	19865	33079	0.61	1.0E-100	AU136800.1	EST_HUMAN	AU136800 PLACE1 Homo sapiens cDNA clone PLACE1005089 5'
6982	20009	33240	1.33	1.0E-100	R10887.1	EST_HUMAN	M38c08.s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:129134 3'
7076	20281	33537	0.86	1.0E-100	7352479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7158	20266	33520	1.07	1.0E-100	AA496841.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
7158	20266	33521	1.07	1.0E-100	AA496841.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.;
7213	20213	33459	1.17	1.0E-100	BF376478.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
7213	20213	33460	1.17	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.;
7221	20220	33468	7.16	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
9098	20203	35381	5.23	1.0E-100	BF103853.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
9131	20259	35381	1.74	1.0E-100	AL163203.2	NT	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
9568	22483	35855	0.61	1.0E-100	AU116951.1	EST_HUMAN	Human mRNA for kidney epidermal growth factor (EGF) precursor
9568	22463	35856	0.61	1.0E-100	AU116951.1	EST_HUMAN	601847357F1 NIH_MGC 61 Homo sapiens cDNA clone IMAGE:3931310 5'
9774	22688	36084	3.54	1.0E-100	AB040918.1	NT	Homo sapiens chromosome 21 segment HS21C003
9850	22958		1.72	1.0E-100	AI972388.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9867	21325	34858	2.43	1.0E-100	AW988611.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
10019	22919		0.98	1.0E-100	AU1127720.1	EST_HUMAN	Homo sapiens mRNA for KIAA1626 protein, partial cds
10112	23003	36389	2.4	1.0E-100	AB046846.1	NT	PMO-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
10112	23003	36400	2.4	1.0E-100	AB046846.1	NT	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
10358	23247	36666	1.61	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1626 protein, partial cds
10358	23247	36667	1.61	1.0E-100	AW630487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1626 protein, partial cds
10949	23833	37260	0.7	1.0E-100	BF347519.1	EST_HUMAN	hh83c11.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2868398 5'
11035	23918		2.16	1.0E-100	Y10391.1	NT	hh83c11.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2868398 5'
11198	24124	37570	7.02	1.0E-100	BF327282.1	EST_HUMAN	602020554F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156165 5'
11792	24714	38204	4.74	1.0E-100	AF111170.3	NT	Human endogenous retrovirus HERV-K, pol gene
11792	24714	38205	4.74	1.0E-100	AF111170.3	NT	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
12059	24900		1.59	1.0E-100	AW875464.1	EST_HUMAN	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
12106	24947		1.82	1.0E-100	AF266285.1	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
12168	25004	38508	1.9	1.0E-100	AA115605.1	EST_HUMAN	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
12168	25004	38507	1.8	1.0E-100	AA115605.1	EST_HUMAN	QV2-PT0012-010300-070-d04 PT0012 Homo sapiens cDNA
							Homo sapiens golgin-like protein (GLP) gene, complete cds
							z489a03.r1 Soares_pregnant_uterus_Nib-IPIU Homo sapiens cDNA clone IMAGE:489984 5'
							z489a03.r1 Soares_pregnant_uterus_Nib-IPIU Homo sapiens cDNA clone IMAGE:489984 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12263	25081	38572	12.92	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12544	25263	31836	2.34	1.0E-100	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
13093	26610	31734	5.72	1.0E-100	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
80	13184	26108	6.71	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
80	13184	26107	6.71	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
710	13769	26985	2.27	1.0E-101	AB007815.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
727	13785	26710	5.49	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
727	13785	26711	5.49	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
797	13852	26787	1.79	1.0E-101	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
878	13931	26878	2.73	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, (GART) mRNA
953	14003	26948	0.92	1.0E-101	Z20556.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
1012	14061	27006	12.07	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4287281 5'
1078	14123	27060	1.56	1.0E-101	AJ221878.1	EST_HUMAN	q99909 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1605	14636	27598	1.33	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1605	14636	27598	1.33	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1960	14978	27983	5.95	1.0E-101	4502998	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2069	15084	28083	1.34	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-100900-016-h08 ST0281 Homo sapiens cDNA
2372	15922	28379	1.41	1.0E-101	5729892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2659	15855	28655	5.44	1.0E-101	X72993.1	NT	H. sapiens EWS gene, exon 5
2792	15781	28778	1.4	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2792	15781	28778	1.4	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2996	16048	28779	1.4	1.0E-101	AJ237744.1	NT	Homo sapiens genomic downstream Rhesus box
3247	16295	28199	11.84	1.0E-101	AJ252312.1	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3287	16334	28365	3.12	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862086 5'
3438	16479	28365	1.85	1.0E-101	AW965656.1	EST_HUMAN	EST377629 MAGI resequences, MAGI Homo sapiens cDNA
3460	15781	28778	1.81	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3460	15781	28779	1.81	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3946	16974	29857	5.13	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5165	18157	31004	1.22	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5165	18157	31005	1.22	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5501	18580	31428	1	1.0E-101	AW965139.1	EST_HUMAN	EST377212 MAGI resequences, MAGI Homo sapiens cDNA
6235	19289	32448	4.32	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6235	19289	32449	4.32	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6992	20019	33252	1.09	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7649	20883		1.07	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7704	20836	33932	4.43	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEO3) mRNA, alternative splice form 4, partial cds
7704	20836	33933	4.43	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEO3) mRNA, alternative splice form 4, partial cds
7896	20822	34127	18.05	1.0E-101	AW008476.1	EST_HUMAN	w55f12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
8009	20926		1.92	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349801 5'
8184	21081	34423	7.79	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
8492	21423	34762	0.77	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
8492	21423	34763	0.77	1.0E-101	BE275821.1	EST_HUMAN	601121621F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
8633	21564	34901	2.89	1.0E-101	BF029174.1	EST_HUMAN	601764686F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3968837 5'
8897	21827	35178	0.6	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8897	21827	35179	0.6	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9362	22489	35850	1.19	1.0E-101	AA036800.1	EST_HUMAN	zk23g08.r1 Soares_pregnant_liverus_NbHPU Homo sapiens cDNA clone IMAGE:471998 5' similar to PIR:S54640 S54640 YD9335.03c protein - yeast;
9870	22785	36174	0.89	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9870	22785	36175	0.89	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9894	21351	34688	19.03	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9994	21351	34689	19.03	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
10008	22825	36213	21.09	1.0E-101	9846462	NT	Human mRNA for pancreatic gamma-glutamyltransferase
10277	23167	36578	7.02	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10277	23167	36580	7.02	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10408	23295	36715	0.85	1.0E-101	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10593	23778	37205	2.04	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10921	23808	37233	1.43	1.0E-101	A1570283.1	EST_HUMAN	bb77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10921	23808	37234	1.43	1.0E-101	A1570283.1	EST_HUMAN	bb77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
11026	23910	37351	0.86	1.0E-101	BE973848.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
11026	23910	37352	0.86	1.0E-101	BE973848.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
11313	24232	37679	1.68	1.0E-101	S38327.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt segment 8 of 9]

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11551	24450	37823	1.43	1.0E-101	AB020626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
12176	25012	38516	1.4	1.0E-101	AI908168.1	EST_HUMAN	RC-BT163-230499-085 BT163 Homo sapiens cDNA
12176	25012	38517	1.4	1.0E-101	AI908168.1	EST_HUMAN	RC-BT163-230499-085 BT163 Homo sapiens cDNA
12701	25418		28.93	1.0E-101	AW939031.1	EST_HUMAN	QV1-DT0068-240200-085-01 DT0068 Homo sapiens cDNA
42	13158	28049	0.94	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
361	13448	26359	3.23	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
643	13704	26611	2.02	1.0E-102	BE252470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
801	13856	26792	5.9	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (ORA) mRNA
1144	14186	27124	1.58	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1295	14328	27273	2.1	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1295	14328	27274	2.1	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1310	14343	27290	1.83	1.0E-102	4826977	NT	Homo sapiens reelin (RELN) mRNA
1441	14472	27429	74.96	1.0E-102	BE408447.1	EST_HUMAN	601299882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628901 5'
2330	15338	28342	1.52	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
2330	15338	28343	1.52	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
3070	16122		0.67	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3113	16164	29059	1.64	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3178	16228	29121	4.33	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3178	16228	29122	4.33	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4332	17346	30211	1.76	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4520	17529	30393	3.3	1.0E-102	BE251310.1	EST_HUMAN	601107849F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5263	18249	31089	1.61	1.0E-102	R66488.1	EST_HUMAN	Y32c04.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
5556	18634	31514	1.68	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5955	19022		5.11	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 64, complete cds
5995	19060	32187	3.44	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5995	19060	32188	3.44	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
6002	19068	32193	0.66	1.0E-102	11433046	NT	Homo sapiens heat domain and RLD 2 (HERC2), mRNA
6546	19589	32776	2.63	1.0E-102	AI459825.1	EST_HUMAN	ar2f09.x1 Barstead cobin HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52 ;
7436	20133	33373	0.48	1.0E-102	AW451643.1	EST_HUMAN	UIH-B13-ajf-d-10-0-UI.st1 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736835 3'
7495	20435	33716	0.68	1.0E-102	BE728323.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7527	20465	33754	0.84	1.0E-102	BE386106.1	EST_HUMAN	60127215F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818243 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7655	20589	33886	0.44	1.0E-102	AB023177.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
7744	20675	33973	8.39	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
8072	20985	34301	2.71	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Ou Homo sapiens cDNA clone CuaAKD03 5'
8378	21282	34813	0.46	1.0E-102	11420841	NT	Homo sapiens GIL-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA
8801	21731	35080	4.44	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA
8877	21807	35160	1.06	1.0E-102	BE910555.1	EST_HUMAN	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3803145 5'
9165	22093	35451	0.92	1.0E-102	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9489	22414	35778	0.71	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9486	22414	35777	0.71	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9793	22757	36142	0.66	1.0E-102	AI762859.1	EST_HUMAN	w63b06 x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2397971 3' similar to contains MER4.11
9821	22727	36110	0.93	1.0E-102	AV755842.1	EST_HUMAN	MER4 MER4 repetitive element ;
9861	22776	36162	2.23	1.0E-102	T70393.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD06 5'
9861	22776	36163	2.23	1.0E-102	T70393.1	EST_HUMAN	Yd13d07.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:67021 5'
9945	22850	36238	3.57	1.0E-102	AU124629.1	EST_HUMAN	Yd13d07.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:67021 5'
10870	23756		0.63	1.0E-102	AF163716.1	NT	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM400308 5'
10948	23832	37258	3.21	1.0E-102	AI905037.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10948	23832	37259	3.21	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
11009	23893	37327	1.07	1.0E-102	AA970786.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
11493	24405	37857	4.33	1.0E-102	AB040928.1	NT	on57r04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to
11507	24417	37871	3.12	1.0E-102	BE897468.1	EST_HUMAN	SW-CAV2_HUMAN P51636 CAVEOLIN-2, [1];
11511	24421	37878	24.95	1.0E-102	4507822	NT	Homo sapiens mRNA for KIAA1495 protein, partial cds
11511	24421	37877	24.95	1.0E-102	4507822	NT	601433392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924168 5'
11764	24685	38151	1.55	1.0E-102	AA688875.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11841	24692	38181	2.84	1.0E-102	BF369243.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
12132	24973	38477	2.25	1.0E-102	U41302.1	NT	ak49h10.s1 Soares_testis NIH_MGC_70 Homo sapiens cDNA clone IMAGE:1408347 3'
12269	25086		10.98	1.0E-102	AL163280.2	NT	RC8-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
12783	25412	31786	8.06	1.0E-102	AW300882.1	EST_HUMAN	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
13049	25681		2.07	1.0E-102	J05235.1	NT	Homo sapiens chromosome 21 segment HS21C080
72	13187	26095	3.09	1.0E-103	BE908158.1	EST_HUMAN	x407c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
72	13187	26098	3.09	1.0E-103	BE908158.1	EST_HUMAN	Human gamma-glutamyl transpeptidase mRNA, complete cds
							601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
							601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
103	13216	26128	7.79	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
221	13320	26236	1.16	1.0E-103	5483793	NT	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA
1008	14057	26999	0.8	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1271	14305	27256	6.95	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1619	14649	27612	2.27	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1891	15009	27997	0.97	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1991	15009	27998	0.97	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2325	15333	28337	0.99	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000965 5'
2475	15477	28478	1.86	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2636	15633	28629	0.9	1.0E-103	BF529378.1	EST_HUMAN	602041882F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4179429 5'
2636	15633	28630	0.9	1.0E-103	BF529379.1	EST_HUMAN	602041882F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4179429 5'
2665	15661	28660	1.01	1.0E-103	N32770.1	EST_HUMAN	yw91d08.s1 Soares placenta_8loc8weeks_2NbhP8to9W Homo sapiens cDNA clone IMAGE:259599 3'
3117	16168		2.65	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834316 5'
3437	16478	28384	3.89	1.0E-103	AW298245.1	EST_HUMAN	U1-H-BW0-aj1-h-11-0-J1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'
3501	16539	29437	1.45	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3818	16948		1.87	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3858	16987	29772	1.33	1.0E-103	AA485663.1	EST_HUMAN	af10d12.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element
3903	16932	29811	1.42	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4069	17114	29992	2.92	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
6159	19217	32356	0.81	1.0E-103	BF696627.1	EST_HUMAN	602186023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
6167	19224	32368	1.69	1.0E-103	AF179995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6519	19563	32744	0.67	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6519	19563	32745	0.57	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6731	19766	32973	0.8	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6731	19766	32974	0.8	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6775	19809	33020	0.41	1.0E-103	10947051	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 1, mRNA
6878	25657	33124	1.33	1.0E-103	AA781442.1	EST_HUMAN	aj26e03.s1 Soares testis_NHT Homo sapiens cDNA clone 1391452 3'
6922	19952	33171	1	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
7018	20044	33279	1.74	1.0E-103	AI590071.1	EST_HUMAN	tr55b05.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
7018	20044	33280	1.74	1.0E-103	AI590071.1	EST_HUMAN	tr55b05.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769

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Table 4
Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7165	18437	31338	1.9	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS184, DXS208, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7165	18437	31339	1.9	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS184, DXS208, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7306	18476	31296	1.19	1.0E-103	11431100	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7384	20377	33846	1.05	1.0E-103	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
7568	20532	33823	1.37	1.0E-103	AW965776.1	EST_HUMAN	EST1377849 IMAGE resequences, MAGI Homo sapiens cDNA
7719	20651	33945	3.71	1.0E-103	BE748188.1	EST_HUMAN	601571637F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838645 5'
8244	21149	34482	4.16	1.0E-103	AI590071.1	EST_HUMAN	trf58505.x1 NCL CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
8244	21149	34483	4.16	1.0E-103	AI590071.1	EST_HUMAN	trf58505.x1 NCL CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
9181	22109	35467	1.07	1.0E-103	AU140344.1	EST_HUMAN	Q13769 ANONYMOUS.;
9181	22109	35468	1.07	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
9261	22189	35546	1.25	1.0E-103	BF109244.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
9852	22578	35949	3.52	1.0E-103	6005921	NT	7160403.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525984 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1;
9852	22578	35950	3.52	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9891	22617	35992	0.8	1.0E-103	AA581086.1	EST_HUMAN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9731	22656	36038	3.28	1.0E-103	AJ774980.1	EST_HUMAN	nd13c02.s1 NCL CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:L02426 26S
10560	23446	36858	1.79	1.0E-103	Z37976.1	NT	PROTEASE SUBUNIT 4 (HUMAN);
10601	23487	36916	2.33	1.0E-103	AW963676.1	EST_HUMAN	ae84d12.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970871 3' similar to gb:X03747 cds1 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);
10732	23618	37046	11.24	1.0E-103	AI878958.1	EST_HUMAN	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
11174	24101	37547	4.8	1.0E-103	AI792759.1	EST_HUMAN	EST1375749 IMAGE resequences, MAGI Homo sapiens cDNA
11273	24195	37647	1.76	1.0E-103	11424061	NT	eu571g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2618326 5' similar to TR:Q15046 KIAA0338;
11273	24195	37648	1.76	1.0E-103	11424061	NT	ai02d06.y6 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1922283 5' similar to TR:Q62084 Q62084
11813	24734	38225	9.93	1.0E-103	AU136283.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING;
11879	23979	37417	3.52	1.0E-103	L43610.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
							Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
							AU136283 PLACE1 Homo sapiens cDNA clone IMAGE:1003923 5'
							Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12096	24937		1.43	1.0E-103	AB024759.1	NT	Homo sapiens TSA305 gene, exon 18
12167	25003	38505	2.65	1.0E-103	BE644811.1	EST_HUMAN	7689a10.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.k3 MER29 repetitive element;
12264	25082		2.32	1.0E-103	AF224688.1	NT	Homo sapiens mannitolase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12295	25105		1.59	1.0E-103	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12473	25219	31855	2.92	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
262	13350	26263	4.51	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
252	13350	26264	4.51	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1908	14928	27806	1.72	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2209	15220	28223	3.87	1.0E-104	AA193976.1	EST_HUMAN	z022c06.s1 Strata gene cdon (#937204) Homo sapiens cDNA clone IMAGE:587623 3' similar to g5:Z14116 .rna1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2219	15229	28235	2.03	1.0E-104	BE744628.1	EST_HUMAN	601577480F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2392	15397	28400	1.98	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2392	15397	28401	1.98	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2460	15464	28461	1.66	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2527	15528	28529	1.11	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2827	15528	28630	1.11	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2914	15987	28866	11.86	1.0E-104	M34671.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
2959	16011		2.91	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3308	16355	29267	1.31	1.0E-104	AL133926.1	EST_HUMAN	AU133926 OVARC1 Homo sapiens cDNA clone OVARC1000336 5'
3450	16491		2.35	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3663	16697	28593	0.85	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3663	16697	28594	0.85	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4020	17047	28936	1.19	1.0E-104	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4228	17242	30110	0.75	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4484	17495	30355	8.96	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4719	17724	30586	0.93	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4719	17724	30587	0.93	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5295	18280	31130	1.26	1.0E-104	4502192	NT	Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB) mRNA
5339	18322	31171	1.08	1.0E-104	7657038	NT	Homo sapiens death receptor 8 (DR8), mRNA
6165	18222	32364	0.92	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6165	19222	32365	0.92	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6217	19272	32426	1.03	1.0E-104	AB017332.1	NT	Homo sapiens alk3 mRNA for Aurora/pl1-related kinase 3, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6740	19774	32985	7.79	1.0E-104	A1768797.1	EST_HUMAN	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
6740	19774	32986	7.79	1.0E-104	A1768797.1	EST_HUMAN	KIAA0132 PROTEIN. ; contains element LTR7 repetitive element ;
6940	19889	33192	0.81	1.0E-104	7706512	NT	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
7114	20318	33581	9.38	1.0E-104	BE314182.1	EST_HUMAN	KIAA0132 PROTEIN. ; contains element LTR7 repetitive element ;
7114	20318	33582	9.38	1.0E-104	BE314182.1	EST_HUMAN	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
7594	20530	33821	2.1	1.0E-104	11425572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
9159	22087	35446	1	1.0E-104	BF609244.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
9710	22835	36018	2.7	1.0E-104	BF448230.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9824	22730	36166	1.24	1.0E-104	T74219.1	EST_HUMAN	UHH-B14-acw-b-09-Q-U1st1 NCI_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3086176 3'
9865	22770	36166	5.42	1.0E-104	AF091395.1	NT	ned16g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9855	22770	36166	5.42	1.0E-104	AF091395.1	NT	y83f02.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:22440 5'
9974	21332	34665	5.18	1.0E-104	BF352841.1	EST_HUMAN	Homo sapiens Trio isoform mRNA, complete cds
8974	21332	34665	5.18	1.0E-104	BF352841.1	EST_HUMAN	Homo sapiens Trio isoform mRNA, complete cds
10274	23164	36576	0.85	1.0E-104	AW103848.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
10274	23164	36577	0.85	1.0E-104	AW103848.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
10595	23481	36909	3.71	1.0E-104	BE791713.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
10595	23481	36910	3.71	1.0E-104	BE791713.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
10885	23770	37195	1.53	1.0E-104	AV728070.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10822	23807	37235	4.14	1.0E-104	AU130765.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
11029	23913	37355	5.19	1.0E-104	U66535.1	NT	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
11040	23924	37355	0.77	1.0E-104	11427757	NT	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
11743	24645	38124	2.36	1.0E-104	BE720181.1	EST_HUMAN	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
11743	24645	38124	2.36	1.0E-104	BE720181.1	EST_HUMAN	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11743	24845	38125	2.36	1.0E-104	BE720181.1	EST_HUMAN	RCD-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11771	24871	38159	2.65	1.0E-104	BF684288.1	EST_HUMAN	RCD-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
13013	25560		1.5	1.0E-104	BE393892.1	EST_HUMAN	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
298	15842	26310	2.94	1.0E-105	4502166	NT	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688676 5'
448	13116	26001	10.72	1.0E-105	4505150	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
615	13680	26582	2.87	1.0E-105	AF032897.1	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
615	13680	26583	2.87	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1708	14735		2.14	1.0E-105	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1734	14761	27731	1.25	1.0E-105	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1844	14887	27849	2.79	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1841	14962	27840	6.41	1.0E-105	D80918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2205	15216	28220	1.81	1.0E-105	AA318368.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' end similar to autoantigen antigen Ku, p70/p80 subunit
2768	15760		1.01	1.0E-105	AA584808.1	EST_HUMAN	no10d05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
3050	16102		3.87	1.0E-105	AJ228041.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
3373	16417	29318	1.07	1.0E-105	BF347753.1	EST_HUMAN	602022595F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158143 5'
3373	16417	29319	1.07	1.0E-105	BF347753.1	EST_HUMAN	602022595F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4158143 5'
3400	16442	29348	0.8	1.0E-105		NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3400	16442	29349	0.8	1.0E-105		NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3712	16744		1	1.0E-105	11425532	NT	Homo sapiens dermatopontin (DPT), mRNA
4188	17208	30074	2.19	1.0E-105	AW961698.1	EST_HUMAN	EST373761 IMAGE sequences, MAGG Homo sapiens cDNA
4857	17859	30723	0.8	1.0E-105	BE868881.1	EST_HUMAN	601448823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850166 5'
4857	17859	30724	0.8	1.0E-105	BE868881.1	EST_HUMAN	601448823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850166 5'
4873	17872	30738	0.68	1.0E-105	AA698335.1	EST_HUMAN	z44g02.s1 Scars_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:433682 3'
5051	18048		6.19	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5248	18235	31085	1.09	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0798 protein, partial cds
5332	18316	31164	1.35	1.0E-105	7659566	NT	Homo sapiens calpain-like protease (CANPX), mRNA
5513	18592	31440	1.14	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5582	18659		1	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7233	20142	33380	1.28	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7233	20142	33381	1.28	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7322	18480	31282	3.68	1.0E-105	11418196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7322	18490	31283	3.68	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7373	20387	33636	0.62	1.0E-105	AW951634.1	EST_HUMAN	EST363689 IMAGE sequences, MAGB Homo sapiens cDNA
7663	20597	33896	0.98	1.0E-105	BE902816.1	EST_HUMAN	601677279F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3860019 5'
8415	21317	34649	0.43	1.0E-105	L07627.1	NT	Homo sapiens protein-tyrosine phosphatase mRNA, complete cds
8441	21373	34714	1.14	1.0E-105	X12556.1	NT	Human mRNA for dbi proto-oncogene
8606	21537	34878	7.42	1.0E-105	T05087.1	EST_HUMAN	EST02975 Fetal brain, Striatum (cadd9636206) Homo sapiens cDNA clone HFBCR32
8968	21898	35254	1.16	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2500826 3' similar to
9483	22411	35772	0.77	1.0E-105	AW840817.1	EST_HUMAN	SW-ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE
9603	22529	35898	3.15	1.0E-105	AW016878.1	EST_HUMAN	RC1-CN0008-070100-011-405 CN0008 Homo sapiens cDNA
							UIH-B10p-ab1-b-12-0-UJ.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9745	22689	36051	1.05	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9745	22689	36052	1.05	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
10098	22946	36333	0.68	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
10098	22946	36334	0.68	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11370	24287	37732	5.44	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11679	24583	38060	1.95	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for $\alpha 6$ (IV) collagen, exon 31
11727	24629	38109	1.98	1.0E-105	7705936	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
12018	24860	38360	2.59	1.0E-105	AW027554.1	EST_HUMAN	w74707.x1 Soares_thymus_NHFT Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
12220	25054	38553	1.41	1.0E-105	BE314293.1	EST_HUMAN	P87892 PROTEASE:
161	13262		1.45	1.0E-106	AW503208.1	EST_HUMAN	601152196F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508463 5'
218	13317	20234	1.68	1.0E-106	AI565065.1	EST_HUMAN	UJ-HF-BND-akt-g-07-QJL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
565	13634	26544	2.1	1.0E-106	AW965356.1	EST_HUMAN	ig78601.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2215008 3'
628	13691	26595	0.94	1.0E-106	J00146.1	NT	EST377628 MAGE resequences, MAGI Homo sapiens cDNA
629	13691	26595	1.7	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1547	14578	27538	3.05	1.0E-106	AF145712.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1728	14755	27725	5.29	1.0E-106	U48724.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1748	14775	27744	2.26	1.0E-106	U04510.1	NT	Homo sapiens epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1825	14848	27824	4.19	1.0E-106	AA527446.1	EST_HUMAN	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1825	14848	27825	4.19	1.0E-106	AA527446.1	EST_HUMAN	Homo sapiens LTR3 repetitive element;
2136	15149	28150	2.12	1.0E-106	BE144288.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element
2338	15346	28350	4.28	1.0E-106	4504184	NT	LTR3 repetitive element;
2529	15530	28532	3.15	1.0E-106	AF003528.1	NT	MRQ-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2643	15639	28638	1.87	1.0E-106	U64675.2	NT	LTR3 repetitive element;
2645	15641	28640	2.08	1.0E-106	BE260201.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
2807	15796	28786	5.86	1.0E-106	AI276526.1	EST_HUMAN	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2873	14483	27443	3.38	1.0E-106	4504184	NT	601140783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2873	14483	27444	3.38	1.0E-106	4504184	NT	q176h10.x1 Soares_Nhl-HMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2963	16034	28936	7.13	1.0E-106	AB037747.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2983	16034	28937	7.13	1.0E-106	AB037747.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
3223	16271	29170	2.57	1.0E-106	8022965	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3223	16271	29171	2.57	1.0E-106	8922966	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3432	16473	29380	0.74	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3502	16540	29438	0.96	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3502	16540	29439	0.96	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4122	17145	30018	7.5	1.0E-106	AW974650.1	EST_HUMAN	EST386875 IMAGE resequences, MAGN Homo sapiens cDNA
4122	17145	30019	7.5	1.0E-106	AW974650.1	EST_HUMAN	EST386875 IMAGE resequences, MAGN Homo sapiens cDNA
4143	17164	30038	0.96	1.0E-106	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4711	17716	30578	1.62	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5409	18360	31229	1.13	1.0E-106	S97478.1	NT	(GC)S=Vitamin D-binding protein/group specific component [human, peripheral blood leukocytes, Genomio, 2126 nt, segment 5 of 9]
5554	18632	31511	3.07	1.0E-106	AA781155.1	EST_HUMAN	aj24509.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN
6068	19129	32261	0.72	1.0E-106	AU130113.1	EST_HUMAN	PHPS1-2 (HUMAN);
6068	19129	32262	0.72	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6124	19183	32318	0.48	1.0E-106	AA434168.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6225	19280	32434	0.76	1.0E-106	AU143428.1	EST_HUMAN	zw28412.s1 Soares ovary tumor NbhOT Homo sapiens cDNA clone IMAGE:770615 3'
6225	19280	32435	0.76	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6339	19389	32558	19.74	1.0E-106	BF679574.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6451	19497	32672	0.71	1.0E-106	BE897112.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285067 5'
6581	19497	32672	0.57	1.0E-106	BE897112.1	EST_HUMAN	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6686	19722	32922	17.61	1.0E-106	11545913	NT	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6686	19722	32923	17.61	1.0E-106	11545913	NT	Homo sapiens xylotransferase II (XT2), mRNA
7763	20693	33992	5.57	1.0E-106	AA663779.1	EST_HUMAN	Homo sapiens xylotransferase II (XT2), mRNA
7825	20754	34057	4.64	1.0E-106	11429617	NT	ae72e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873
7926	20848	34163	1.43	1.0E-106	BE292722.1	EST_HUMAN	KINESIN HEAVY CHAIN (HUMAN);
8055	20968	34283	9.4	1.0E-106	11425503	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
8055	20968	34284	9.4	1.0E-106	11425503	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
8310	21214	34551	0.48	1.0E-106	AW163047.1	EST_HUMAN	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2888345 5'
8336	21241	34573	0.44	1.0E-106	AU118850.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
8594	21495	34837	4.69	1.0E-106	BE741408.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
8594	21495	34838	4.69	1.0E-106	BE741408.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
							au81f05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783649 5' similar to TR:O75834
							O75834 CULLIN-4A;
							AU116850 HEMBA1 Homo sapiens cDNA clone HEMBA1000129 5'
							601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
							601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8753	21883	35028	1.77	1.0E-106	AI523068.1	EST_HUMAN	ar88a07.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233 CALGRANULIN B (HUMAN);
9264	22192	35550	3.96	1.0E-106	AI654123.1	EST_HUMAN	ly62a05.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN Q05084 69 KD ISLET CELL AUTOANTIGEN;
9269	22187	35554	0.56	1.0E-106	AI991109.1	EST_HUMAN	wu38c03.x1 Soares_Diethgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522308 3' similar to TR:O70273 O70273 ETS HOMOLOGOUS FACTOR;
9690	22816	35990	2.87	1.0E-106	AA825307.1	EST_HUMAN	cc87a08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
9690	22816	35991	2.87	1.0E-106	AA825307.1	EST_HUMAN	cc87a08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
9826	22732	36114	1.12	1.0E-106	AI750447.1	EST_HUMAN	cr03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTEC_cr03a04 random lrr41f02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13
9863	22868	36257	1.99	1.0E-106	AI479569.1	EST_HUMAN	TAR1 PTR5 repetitive element;
9863	22868	36258	1.99	1.0E-106	AI479569.1	EST_HUMAN	lrr41f02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13 TAR1 PTR5 repetitive element;
10507	23394	36806	0.87	1.0E-106	BE389234.1	EST_HUMAN	601282387F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604217 5'
10586	23472	36898	1.43	1.0E-106	BF027310.1	EST_HUMAN	601871874F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10586	23472	36899	1.43	1.0E-106	BF027310.1	EST_HUMAN	601871874F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10735	23621	37051	6.89	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10735	23621	37052	6.89	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10771	23663	37091	0.92	1.0E-106	AW363289.1	EST_HUMAN	RC9-CT0318-201189-031-a11 CT0318 Homo sapiens cDNA
10940	23825	37252	0.84	1.0E-106	AL039886.1	EST_HUMAN	DKFZp434F0712_r1_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434F0712 6'
11052	23936	37375	2.43	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11334	24253	37690	5.36	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
11334	24253	37691	5.36	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
11502	24412	37866	1.85	1.0E-106	J05200.1	NT	Human tyrosine receptor mRNA, complete cds
11502	24412	37867	1.85	1.0E-106	J05200.1	NT	Human tyrosine receptor mRNA, complete cds
11976	24819	38311	1.77	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
11976	24819	38312	1.77	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
12336	25760		4.63	1.0E-106	AW410405.1	EST_HUMAN	h05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861644 5'
12536	25259	31833	3.18	1.0E-106	BE694488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12536	25259	31834	3.18	1.0E-106	BE694488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12741	25381		4.58	1.0E-106	BE695905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
253	13351		4.7	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
284	13378		1.37	1.0E-107	X60458.1	NT	Human IFNAR gene for Interferon alpha/beta receptor

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
654	13715	26625	1.8	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
838	13883	26830	1.15	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
911	13983	26910	1.42	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
995	14045	26988	10	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1304	14337	27285	1.19	1.0E-107	AB032283.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1989	14620	27592	3.09	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1777	14803	27771	2.87	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
1864	14886	27866	0.91	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1884	14886	27887	0.91	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2223	15233	28240	1.25	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2385	16390	28393	1.89	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2385	16390	28394	1.89	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2562	16561	28562	1.52	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842309 5'
2562	16561	28563	1.52	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3842309 5'
3051	16103	29006	3.08	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3051	16103	29007	3.08	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3147	16197	29090	2.44	1.0E-107	AF020671.1	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3900	16929	29807	6.55	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
3976	17004	29891	2.52	1.0E-107	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
3976	17004	29892	2.52	1.0E-107	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
6819	18891	32004	0.86	1.0E-107	AW669038.1	EST_HUMAN	EST381115 IMAGE resequences, MAGK Homo sapiens cDNA
6080	19141	32277	3.32	1.0E-107	BE867469.1	EST_HUMAN	601442558F1 NIH_MGC 85 Homo sapiens cDNA clone IMAGE:3846494 5'
7251	20160	33399	0.5	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1), mRNA
7251	20160	33400	0.5	1.0E-107	11431469	NT	Homo sapiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD) (GTF3C1), mRNA
7755	20685	33984	1.54	1.0E-107	AW503913.1	EST_HUMAN	U1HF-BND-alf-c-08-Q-U1.1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3079310 5'
7755	20685	33985	1.54	1.0E-107	AW503913.1	EST_HUMAN	U1HF-BND-alf-c-08-Q-U1.1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3079310 5'
7934	20878	34187	1.13	1.0E-107	A1765076.1	EST_HUMAN	W6804.1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2384791 3'
8195	21102	34432	0.87	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH8 gene)
8195	21102	34433	0.87	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH8 gene)
8277	21182	34520	0.81	1.0E-107	AW410961.1	EST_HUMAN	h09d11 x2 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:2984524 5'
9924	22812	36301	0.88	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone IMAGE:1002433 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11147	24076	37524	3.33	1.0E-107	A1392850.1	EST_HUMAN	t910406.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_D10DI
11386	24302	37749	1.75	1.0E-107	L49141.1	NT	P05095 ALPHA-ACTININ 3, NON MUSCULAR ;
11397	24313	37759	1.98	1.0E-107	BF66511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11766	24667	38163	7.76	1.0E-107	BE540550.1	EST_HUMAN	602123953F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4281039 5'
11831	23988	37401	5.29	1.0E-107	11419701	NT	60106868F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11831	23988	37402	5.29	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
12103	24944	38447	6.27	1.0E-107	AV712898.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
12152	24981	38491	5.88	1.0E-107	4507822	NT	AV712898 DCA Homo sapiens cDNA clone DCAAWC01 5'
12218	25052	38551	3.36	1.0E-107	4506870	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
12218	25052	38552	3.36	1.0E-107	4506870	NT	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA
12395	25883		7.77	1.0E-107	AA001416.1	EST_HUMAN	Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (SLC10A1) mRNA
188	13287		2.06	1.0E-108	AA341934.1	EST_HUMAN	z945601.s1 Scores refseq N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
981	14032	26975	2.26	1.0E-108	BE286042.1	EST_HUMAN	THR repetitive element ;
1292	14325	27270	3.1	1.0E-108	Y18000.1	NT	EST47363 Fetal muscle Homo sapiens cDNA 5' end
2352	15360	28362	3.13	1.0E-108	A1686040.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
2352	15360	28363	3.13	1.0E-108	A1686040.1	EST_HUMAN	Homo sapiens NF2 gene
2452	15456	28453	13.94	1.0E-108	BE208894.1	EST_HUMAN	t691e10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
3001	16053	28957	0.74	1.0E-108	6005979	NT	PROTEOGLYCAN II PRECURSOR (HUMAN);
3398	16440	29344	0.75	1.0E-108	AF032897.1	NT	t691e10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
3398	16440	29345	0.75	1.0E-108	AF032897.1	NT	PROTEOGLYCAN II PRECURSOR (HUMAN);
3883	16912	29791	1.16	1.0E-108	5453865	NT	t691e10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
4254	17270	30138	1.19	1.0E-108	AW684438.1	EST_HUMAN	PROTEOGLYCAN II PRECURSOR (HUMAN);
4919	17918	30783	2.78	1.0E-108	7661979	NT	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863899 3' similar to gb:X53777 60S
5028	18025	30884	0.74	1.0E-108	AW504799.1	EST_HUMAN	RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
5064	18061	30912	2.22	1.0E-108	AJ008005.1	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens pericentriolar material 1 (PCM1) mRNA
							h12a11.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE
							P55194 SH3-BINDING PROTEIN 3BP-1 ;
							Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
							U1HF-BND-alm-e-04-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080168 5'
							Homo sapiens PSN1 gene, alternative transcript

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5331	18315	31163	1.18	1.0E-108	8400716	NT	Homo sapiens nebulin (NEB), mRNA
5364	18346	31189	0.96	1.0E-108	HT7233.1	EST_HUMAN	Yn42604.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:50868 5'
5667	18741	31650	1.71	1.0E-108	AW384094.1	EST_HUMAN	RCO-H10372-241189-031-d03 HT0372 Homo sapiens cDNA
5717	18790	31722	2.46	1.0E-108	BE889016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848960 5'
5717	18790	31723	2.46	1.0E-108	BE889016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848960 5'
6151	18210		0.85	1.0E-108	AF012623.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6234	19288	32447	0.74	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6379	19428	32595	5.92	1.0E-108	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6379	19428	32596	5.92	1.0E-108	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6513	19557	32738	1.27	1.0E-108	AJ133289.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6618	19288	32447	1.08	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6806	19936	33153	0.74	1.0E-108	AF016706.1	NT	Homo sapiens EG-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6806	19936	33154	0.74	1.0E-108	AF016706.1	NT	Homo sapiens EG-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7519	20458	33744	4.97	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
7843	20770	34073	4.09	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA
7897	20823	34128	1.36	1.0E-108	BE252607.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354064 5'
7928	20850	34156	1.05	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn07 Homo sapiens cDNA clone IMAGE:4181037 5'
7928	20850	34157	1.05	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn07 Homo sapiens cDNA clone IMAGE:4181037 5'
8382	21286	34617	0.48	1.0E-108	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, A TP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8641	21572		1.74	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8692	21623	34965	0.66	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BM0-ads-e-12-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8692	21623	34966	0.66	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BM0-ads-e-12-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
9600	22526	36891	0.69	1.0E-108	AF203977.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
11111	21217	34553	1.94	1.0E-108	BE536227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
11267	18434	31356	2.13	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Gdgl-associated microtubule-binding protein (GMAP-210)
11503	24413	37868	1.96	1.0E-108	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11718	24620	38098	4.03	1.0E-108	AW956186.1	EST_HUMAN	EST1378258 IMAGE resequences, MAGI Homo sapiens cDNA
11767	24668	38154	1.47	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11767	24668	38155	1.47	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11809	24730		1.62	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11860	24750	38243	2.17	1.0E-108	D83539.1	NT	Homo sapiens COL4A6 gene for $\alpha 6$ (IV) collagen, exon 23
12860	25268	31837	4.23	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12910	25493		7.79	1.0E-108	BF345356.1	EST_HUMAN	G02D18571F1 NCI CGAP_Birn07 Homo sapiens cDNA clone IMAGE:4164287 5'
46	13161	26062	0.88	1.0E-109	AW803116.1	EST_HUMAN	IL2-JM0077-260400-078-D06 UM0077 Homo sapiens cDNA
68	13183	26091	1.01	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
234	13332	26246	1.47	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
246	13342	26264	2.7	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
489	13560	26475	3.8	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2), mRNA
619	13684	26587	14.29	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
619	13684	26588	14.29	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
1230	14267	27210	8.63	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1), complete cds
1231	14267	27210	5.33	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1), complete cds
1897	14918	27897	5.83	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2256	15266	28274	5.22	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2266	15276	28282	1.81	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2668	15864	28684	3.56	1.0E-109	A022328.1	EST_HUMAN	ow85a01.x1 Soares fetal liver spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;
2668	15864	28685	3.56	1.0E-109	A022328.1	EST_HUMAN	ow85a01.x1 Soares fetal liver spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN.;
2669	15865	28686	3.18	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3106	16157	29052	1.1	1.0E-109	N85180.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3447	16488	29395	1.32	1.0E-109	AW893182.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3447	16488	29396	1.32	1.0E-109	AW893182.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3578	16615	29518	0.9	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3619	16655	29555	1.17	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3619	16655	29556	1.17	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
4244	17260	30128	4.36	1.0E-109	AB55417.1	EST_HUMAN	ts98a06.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE16100;
4510	17520	30386	2.61	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4710	17715	30577	1.41	1.0E-109	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5031	18028	30886	0.99	1.0E-109	R16400.1	EST_HUMAN	ys48a06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53057 5'
5427	18509	31286	0.84	1.0E-109	AU137282.1	EST_HUMAN	AU137282 PLACE1 Homo sapiens cDNA clone PLACE1006159 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5441	18523	31248	1.05	1.0E-109	BF673718.1	EST_HUMAN	602138446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
5498	18575	31421	2.65	1.0E-109	5174622	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
5801	18873	31421	1.68	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6152	25641	32348	1	1.0E-109	BF379688.1	EST_HUMAN	GMI-UT0038-060900-399-h07 UT0038 Homo sapiens cDNA
6228	18873		1.41	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6608	19849	32832	0.73	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
6608	19849	32833	0.73	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
6873	19804	33119	0.61	1.0E-109	A1221385.1	EST_HUMAN	q88h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
7074	20280	33535	0.4	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7074	20280	33536	0.4	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7289	18458	31328	0.41	1.0E-109	BE074888.1	EST_HUMAN	RC5-BT0580-170300-021-F08 BT0580 Homo sapiens cDNA
7610	20545	33837	0.89	1.0E-109	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7671	20798	34101	0.44	1.0E-109	AE000297.1	NT	Escherichia coli K-12 MG1655 section 187 of 400 of the complete genome
7988	20918	34232	3.86	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8000	20918	34234	4.87	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8000	20918	34235	4.87	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8247	21152	34487	0.6	1.0E-109	BE263297.1	EST_HUMAN	601145017F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160228 5'
8761	21681	35024	1.41	1.0E-109	AL049784.1	NT	Novel human gene mapping to chromosome 13
8882	21792	35144	1.13	1.0E-109	AW749130.1	EST_HUMAN	PMO-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
9215	22143		2.76	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
9293	22221	36578	7.11	1.0E-109	BE787540.1	EST_HUMAN	601478417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9293	22221	36579	7.11	1.0E-109	BE787540.1	EST_HUMAN	601478417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
							ys90g08.11 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP-A63481
9780	22704	36088	1.32	1.0E-109	H84880.1	EST_HUMAN	A63481 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPIN1
9888	22803	36190	0.8	1.0E-109	BE397068.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9888	22803	36191	0.8	1.0E-109	BE397068.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
10017	22917	36306	1.13	1.0E-109	F06804.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
11213	24139	37560	2.24	1.0E-109	BE540908.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11213	24139	37591	2.24	1.0E-109	BE540908.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11247	24171	37618	15	1.0E-109	BF694831.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
11406	24322	37771	1.43	1.0E-109	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
11406	24322	37772	1.43	1.0E-109	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
11585	24474	37841	1.67	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002680 5'
11808	24729	38221	3.03	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11843	24894	38184	4.7	1.0E-108	W16510.1	EST_HUMAN	zb08b12.r1 Soares_fetal_jung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43069 S43069 p54-beta stress-activated protein kinases - rat;
12110	24951	38454	1.48	1.0E-108	11418618	NT	Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA
12459	15276	28282	2.1	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12666	15276	28282	1.81	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12774	25403	31811	8.38	1.0E-109	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
3	13119	26005	1	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
39	13155	26045	4.44	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
39	13155	26046	4.44	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
113	13119	26005	0.73	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
314	13406	26324	1.07	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
550	13619	26527	0.9	1.0E-110	U84550.1	NT	Human dyctobrevin (DTN) gene, exon 20
1208	14247	27188	0.98	1.0E-110	5031820	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1305	14338	27286	0.9	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1936	14957	27935	1.14	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3009883 5'
2071	15088		1.51	1.0E-110	BF508596.1	EST_HUMAN	U1-H-B14-ecb-b-05-0-U1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2886	15940		0.84	1.0E-110	4603098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3077	14338	27286	0.87	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3138	16186		2.19	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3238	16286	29189	1.91	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3238	16286	29189	1.91	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4138	17159	30035	0.96	1.0E-110	BE018556.1	EST_HUMAN	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR.O60312 O60312 KIAA0566 PROTEIN ;
4747	17752	30610	2	1.0E-110	A017213.1	EST_HUMAN	oj32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627883 3' similar to SW:N121_RAT_P62561 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4764	17769	30634	2.95	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5094	18091	31165	2.34	1.0E-110	7652441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5333	18317	31165	3.47	1.0E-110	M36430.1	NT	Human transducin beta-1 subunit mRNA, 3' end
5401	18383	31223	2.55	1.0E-110	M31651.1	NT	Homo sapiens sex hormone-binding globulin (SHBG) gene, complete cds
5477	18558	31400	2.2	1.0E-110	BE299406.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5927	18594	32113	0.72	1.0E-110	BE621066.1	EST_HUMAN	601493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'
5947	19014	32132	6.27	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5947	19014	32134	6.27	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7017	26661	33278	4.3	1.0E-110	M55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7385	20378	33647	0.86	1.0E-110	BE261496.1	EST_HUMAN	60110388F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
7461	20401	33675	0.86	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7461	20401	33676	0.86	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7708	20640	33838	0.84	1.0E-110	AI560288.1	EST_HUMAN	h12d08.x1 NCI_OGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN
7826	20755	34058	17.77	1.0E-110	AV714276.1	EST_HUMAN	P50549 ETS TRANSLOCATION VARIANT 1;
7826	20755	34059	17.77	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCEG01 5'
7859	20786	34089	2.92	1.0E-110	AB020675.1	NT	AV714276 DCB Homo sapiens cDNA clone DCBCEG01 5'
8003	20921	34237	0.85	1.0E-110	AU137923.1	EST_HUMAN	Homo sapiens mRNA for KIAA0868 protein, partial cds
8411	21314	34846	1.01	1.0E-110	9961261	NT	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007811 5'
9874	22789	36180	0.79	1.0E-110	BE302594.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant C, mRNA
10108	22987	36982	2.85	1.0E-110	AW838394.1	EST_HUMAN	bc8801.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905561 5' similar to TR:O77258 O77258
10812	23698	37125	3.75	1.0E-110	11432732	NT	EG:114D9.2 PROTEIN.;
11188	24114	37682	3.42	1.0E-110	Y12337.1	NT	QV2-L1 T0053-020400-119-04 L10053 Homo sapiens cDNA
11404	24320	37768	4.24	1.0E-110	BE734357.1	EST_HUMAN	Homo sapiens galactokinase 2 (GALK2), mRNA
11404	24320	37769	4.24	1.0E-110	BE734357.1	EST_HUMAN	H. sapiens mRNA for myotonic dystrophy protein kinase like protein
11876	23676	37414	2.24	1.0E-110	AA446529.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
12297	25107		2.46	1.0E-110	BE807218.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
12411	25180		6.47	1.0E-110	AW062258.1	EST_HUMAN	zw07g02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816
12631	25313		2.74	1.0E-110	AB011399.1	NT	G1145816 FKBP54;
12762	25893		4.57	1.0E-110	BF364546.1	EST_HUMAN	801439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
185	13284		12.38	1.0E-111	U43701.1	NT	IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
209	13308	26226	1.02	1.0E-111		NT	Homo sapiens gene for AF-6, complete cds
758	13815		1.78	1.0E-111	BF035327.1	EST_HUMAN	PM3-NN1082-140900-008-f12 NN1082 Homo sapiens cDNA
767	13824	26754	3.57	1.0E-111	8393092	NT	Human ribosomal protein L23a mRNA, complete cds
955	14009	26951	2.71	1.0E-111	M25142.1	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4437	17448	30308	5.56	1.0E-111	K02268.1	NT	601456531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
5405	18386	31226	1.18	1.0E-111		NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
5684	18738	31946	0.7	1.0E-111	AA151017.1	EST_HUMAN	Human cardiac alpha-myosin heavy chain (MYH6) gene, exon 32 to 34
						NT	Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds
						NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
						EST_HUMAN	247b07.r1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:606045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9694	18738	31847	0.7	1.0E-111	AA151017.1	EST_HUMAN	z147b07.r1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5827	18898	32012	0.73	1.0E-111	BE867909.1	EST_HUMAN	601443680.F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847656 5'
5950	19017	32137	0.44	1.0E-111	U19969.1	NT	Human two-handed zinc finger protein ZEB mRNA, partial cds
6265	19316	32481	1.77	1.0E-111	A344679.1	EST_HUMAN	qp09g12.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29863 RAS-RELATED PROTEIN RAL-A (HUMAN);
6976	20003	33235	1.07	1.0E-111	AL040782.1	EST_HUMAN	DKFZp434C1815_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1815 5'
7117	20321	33588	1.18	1.0E-111	AW294848.1	EST_HUMAN	U1-HBW0-ait-4-03-0-J1.e1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729525 3'
7563	20500	33788	0.6	1.0E-111	AW693165.1	EST_HUMAN	RC2-BN0033-160200-013-b05 BN0033 Homo sapiens cDNA
7851	20778	34079	2.73	1.0E-111	BF368228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
7963	20876	34186	0.94	1.0E-111	0961253	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant A, mRNA
7961	20883	34194	12.98	1.0E-111	AI761228.1	EST_HUMAN	w68401.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIIA5 (HUMAN);
8059	20972	34288	0.8	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nalp) and survival motor neuron protein (smn) genes, complete cds
8260	21165	34500	0.49	1.0E-111	AA133914.1	EST_HUMAN	zn62c12.r1 Stratiogene muscle 637209 Homo sapiens cDNA clone IMAGE:362774 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8673	21604	34945	0.9	1.0E-111	AA278868.1	EST_HUMAN	zs78g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
8673	21604	34946	0.9	1.0E-111	AA278868.1	EST_HUMAN	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.;
8817	21747	35095	3.93	1.0E-111	U66533.1	NT	zs78g03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
9237	22165	35518	0.89	1.0E-111	11420516	NT	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.;
9335	22293	35627	0.84	1.0E-111	AK024453.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
9386	22294		0.53	1.0E-111	AF177987.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
9367	22295		12.82	1.0E-111	BF214902.1	EST_HUMAN	Homo sapiens mRNA for FLJ00045 protein, partial cds
9441	22369	35731	16.48	1.0E-111	X17033.1	NT	Homo sapiens cone sodium-calcium potassium exchanger splice variant (NCKX) mRNA, complete cds
9441	22369	35732	16.48	1.0E-111	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
9633	22559	35928	3.42	1.0E-111	AF091395.1	NT	Human mRNA for Integrin alpha-2 subunit
9657	22772	36159	0.68	1.0E-111	BF333210.1	EST_HUMAN	Homo sapiens Trio isoform mRNA, complete cds
10649	23535	36888	2.74	1.0E-111	AA504160.1	EST_HUMAN	QV2-BT0817-270900-398-e06 BT0817 Homo sapiens cDNA
							aa58g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:U09235 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);

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10676	23662		1.44	1.0E-111	D10833.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10766	23661	37084	5.85	1.0E-111	AA131248.1	EST_HUMAN	z31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
11480	24393	37843	7.89	1.0E-111	U68159.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
12254	25074	38568	5.81	1.0E-111	11417801	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNI1), mRNA
12758	25392	31805	1.83	1.0E-111	AV708482.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAOB08 5'
12861	25714	31864	4.06	1.0E-111	W22562.1	EST_HUMAN	72C9 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
631	13892	26598	4.74	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
633	13894	26598	5.57	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
633	13894	26599	5.57	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
655	13716	26828	1.23	1.0E-112	BF509039.1	EST_HUMAN	UHH-B14-act-g-04-0-JL1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
655	13716	26827	1.23	1.0E-112	BF509039.1	EST_HUMAN	UHH-B14-act-g-04-0-JL1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1029	14078	27018	11.16	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1089	14133	27069	1	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1709	14737	27704	3.74	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1709	14737	27705	3.74	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1842	14865	27846	4.83	1.0E-112	AF248540.1	NT	Homo sapiens Intersectin 2 (SH-2D1B) mRNA, complete cds
2533	15534	28534	1.96	1.0E-112	BE866859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3127	16178		0.66	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
							wk45b12.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81650_ma1
3415	16457	29383	0.71	1.0E-112	A182651.1	EST_HUMAN	SEMNDELIN 1 PROTEIN PRECURSOR (HUMAN);
3963	16981	29886	0.68	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-080300-113-409 BT0590 Homo sapiens cDNA
4714	17719	30581	1	1.0E-112	4604116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4865	17866	30729	8.93	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4865	17866	30730	8.93	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5387	18369	31207	1.13	1.0E-112	AB020710.1	NT	Homo sapiens mRNA for KIAA0603 protein, partial cds
5387	18369	31208	1.13	1.0E-112	AB020710.1	NT	Homo sapiens mRNA for KIAA0603 protein, partial cds
6864	18936	32054	40.67	1.0E-112	N46046.1	EST_HUMAN	y85d07.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273228 5'
6313	19363	32553	1.07	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6385	19434	32601	0.76	1.0E-112	AW502437.1	EST_HUMAN	UHF-BR0p-els-g-06-0-JL1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6385	19434	32602	0.76	1.0E-112	AW502437.1	EST_HUMAN	UHF-BR0p-els-g-06-0-JL1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6498	19542	32718	2.18	1.0E-112	BE741656.1	EST_HUMAN	601594717F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6732	19767	32975	0.51	1.0E-112	BF672815.1	EST_HUMAN	602152849F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283420 5'
6927	19858	33178	0.8	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6927	19858	33177	0.8	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'

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7157	20265	33519	1.24	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7516	20453	33741	0.44	1.0E-112	AL043299.1	EST_HUMAN	DKFZp434M0523_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M0523 5'
7722	20654	33950	1.71	1.0E-112	11416777	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7722	20654	33951	1.71	1.0E-112	11416777	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8771	21701	35047	3.62	1.0E-112	AU118091.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
9512	22439	35803	2.51	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9512	22439	35804	2.51	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
10405	23294	36714	2.16	1.0E-112	BF111413.1	EST_HUMAN	730907.X1 Scanes_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR-09VW35 09VW35 CG8743 PROTEIN ;
11217	24143	37595	2.98	1.0E-112	AW863327.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
11388	24304	37751	2.87	1.0E-112	AJ249800.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11541	24451	37914	1.94	1.0E-112	BE280478.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
11629	24535	38005	4.32	1.0E-112	AW377670.1	EST_HUMAN	PVO-CT0237-141099-001-h02 CT0237 Homo sapiens cDNA
766	13823	26752	3.52	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
766	13823	26753	3.52	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
970	14021	26885	4.95	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1564	14595	27555	3.71	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1954	16854	27956	1.14	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2107	16121	28124	1.22	1.0E-113	BF515218.1	EST_HUMAN	UI-H-BW1-aml4.03-0-JJ1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3062876 3'
3175	16225	29119	1.02	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5425	25748	31676	3.46	1.0E-113	BE760658.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5981	18755	31676	5.8	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
6029	19091	32217	0.47	1.0E-113	BE789172.1	EST_HUMAN	601476296F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879406 5'
6029	19091	32218	0.47	1.0E-113	BE789172.1	EST_HUMAN	601476296F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879406 5'
6146	19205	32343	3.62	1.0E-113	AU140261.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
6176	19223	32380	2.48	1.0E-113	AF016335.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6305	19359	32527	2.38	1.0E-113	11925737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
6397	19445	32615	2.44	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDRTAP), member 4 (ABCB4), transcript variant B, mRNA
6397	19445	32618	2.44	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDRTAP), member 4 (ABCB4), transcript variant B, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6571	19612	32797	0.76	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6571	19612	32798	0.76	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7705	20637	33934	0.95	1.0E-113	BE262161.1	EST_HUMAN	601162078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
7705	20637	33935	0.95	1.0E-113	BE262161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
8128	21036	34365	0.5	1.0E-113	AW958960.1	EST_HUMAN	EST371030 MAGE sequences, MAGE Homo sapiens cDNA
8449	22377	35740	0.57	1.0E-113	8922818	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9640	22566	35935	3.14	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9640	22566	35936	3.14	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9837	22842	37639	0.67	1.0E-113	BE772967.1	EST_HUMAN	RC1-FT0134-280600-021-d02 FT0134 Homo sapiens cDNA
10346	23236	36653	1.22	1.0E-113	11429387	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10440	23329	36747	0.52	1.0E-113	M21635.1	NT	Human erg protein (erg-related gene) mRNA, complete cds
10553	23439	36860	0.97	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10553	23439	36861	0.97	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11563	24472	37639	1.96	1.0E-113	AW500519.1	EST_HUMAN	UJ-HF-BNO-ek4-b-12-O-JUL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
11571	24480	37946	1.57	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN ;
11571	24480	37947	1.57	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN ;
11667	19612	32797	2.94	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11667	19612	32798	2.94	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11708	24610	38087	3.18	1.0E-113	BE262068.1	EST_HUMAN	601105528F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988366 5'
61	13177	26078	6.19	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	13177	26080	6.19	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	13177	26081	6.19	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
688	13730	26642	19.22	1.0E-114	T70551.1	EST_HUMAN	y016c01.at Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1098	14141	27078	1.53	1.0E-114	8623087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1339	14372	27324	3.06	1.0E-114	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1668	14698	27658	1.17	1.0E-114	8831094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1698	14728	27692	2.15	1.0E-114	6578073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2272	15282	28289	1.13	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2851	13163	26055	1.03	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2851	13163	26058	1.03	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3176	16228	29120	2.37	1.0E-114	X04086.1	NT	Human gene for celtase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3214	16262	29161	0.82	1.0E-114	BF206374.1	EST_HUMAN	601869832F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4102	17127	30002	1.24	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4498	17508	30374	1.44	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Roe) mRNA, complete cds
5239	18226		4.08	1.0E-114	11435940	NT	Homo sapiens keratocan (KERA), mRNA
5287	18273	31121	0.69	1.0E-114	BE275324.1	EST_HUMAN	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346099 5'
5585	18682	31537	1.39	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5585	18682	31538	1.39	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5789	18861	31989	1.17	1.0E-114	9257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
6473	19518	32694	0.57	1.0E-114	Z26298.1	NT	H. sapiens isoform 1 gene for L-type calcium channel, exon 20
7339	18507	31283	0.44	1.0E-114	4759163	NT	Homo sapiens sparc/osteonectin, cwev and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
7432	20130		0.61	1.0E-114	AB041533.1	NT	Homo sapiens HCMOBT-1 mRNA for sperm antigen, complete cds
7609	20544	33835	1.21	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7609	20544	33836	1.21	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7661	20595	33893	7.34	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7661	20595	33894	7.34	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
8471	21402	34741	2.09	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8745	21675	35017	1.48	1.0E-114	AI363139.1	EST_HUMAN	qy88d06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'
8745	21675	35018	1.48	1.0E-114	AI363139.1	EST_HUMAN	qy88d06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'
9259	22187	35544	3.17	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
9328	22254	35619	6.67	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9326	22254	35620	6.67	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9648	22853		2.35	1.0E-114	AW327485.1	EST_HUMAN	dq03f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9895	23152	34890	2.69	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
10077	23992		1.24	1.0E-114	M13538.1	NT	Human centropalmin mRNA
10638	23624	36959	1.18	1.0E-114	BE870004.1	EST_HUMAN	601449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10657	23543	36977	1.68	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
11019	23903	37342	0.97	1.0E-114	BE171994.1	EST_HUMAN	MFG-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
							bat73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
11227	24153		5.73	1.0E-114	BE302696.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11635	24541	38014	2.78	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11635	24541	38015	2.78	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
12671	25556		6.36	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12608	25491	31768	3.26	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12608	25491	31767	3.26	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
23	13139	26027	3.97	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
134	13236	26154	1.33	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
138	13240		12.97	1.0E-115	4557687	NT	Homo sapiens keratin 18 (KRT18) mRNA
312	13404	26321	2.79	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
559	13628	26536	0.9	1.0E-115	A1339206.1	EST_HUMAN	q06701.x1 NCI_CGAP_G04 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00538 O00536
559	13628	26537	0.9	1.0E-115	A1339206.1	EST_HUMAN	TTF-1 INTERACTING PEPTIDE 5;
813	13638	26804	0.73	1.0E-115	5174702	NT	TTF-1 INTERACTING PEPTIDE 5;
813	13638	26805	0.73	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
815	13670	26807	1.01	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1580	14810	27571	3.2	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1580	14810	27572	3.2	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1580	14872	27654	1.77	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1665	14887	27888	1.1	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3532	16570	29474	2.01	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4126	17149	30024	4.78	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4366	17380	30244	3.13	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4507	17517	30383	3.07	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4542	17551	30411	3.2	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4789	17793	30659	3.39	1.0E-115	AL066857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4789	17793	30660	3.39	1.0E-115	AL066857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5014	18012	30670	3.01	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5014	18012	30671	3.01	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5531	18610	31459	1.71	1.0E-115	AW970335.1	EST_HUMAN	EST382410 IMAGE:4276738 5'
6009	18685	31564	1	1.0E-115	BF665387.1	EST_HUMAN	602119346F1 NIH_JMGC_96 Homo sapiens cDNA clone IMAGE:4276738 5'
5732	18805	31989	2.09	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5732	18805	31900	2.09	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5889	18958	32078	1.2	1.0E-115	AI928799.1	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
5889	18958	32077	1.2	1.0E-115	AI928799.1	EST_HUMAN	au64g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
6512	19556	32736	0.61	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6512	19556	32737	0.61	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6659	19698	32894	19.45	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63436), mRNA
6807	19840	33050	1.84	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6807	19840	33051	1.84	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7264	20173	33414	0.8	1.0E-115	T86774.1	EST_HUMAN	yd86608.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP-DPOG, YEAST P15801 DNA POLYMERASE GAMMA ;
7654	20598	33684	1.31	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1676914 3'
7654	20598	33685	1.31	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1676914 3'
7807	20736	34039	7.13	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
8738	21688	35013	11.28	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8738	21688	35014	11.28	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
9371	22299	35681	3.27	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
10294	23184	36595	0.77	1.0E-115	BF382029.1	EST_HUMAN	601816352F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050108 5'
10504	23392	36803	2.11	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10504	23392	36804	2.11	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
11001	23885	37317	1.07	1.0E-115	AI221878.1	EST_HUMAN	qg99e09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
11001	23885	37318	1.07	1.0E-115	AI221878.1	EST_HUMAN	qg99e09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
11007	23891	37325	0.76	1.0E-115	AI524687.1	EST_HUMAN	th12a07.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2118036 3' similar to TR:O16129 O16129 PHENYLALANYL TRNA SYNTHETASE ;
11159	24087	37534	3.71	1.0E-115	AW571544.1	EST_HUMAN	xx32708.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA P10463 CALYCYPHOSINE ;
11707	24609	38085	1.55	1.0E-115	BE045890.1	EST_HUMAN	hq54c10.x1 NCL CGAP_Par3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG ;
11707	24609	38086	1.55	1.0E-115	BE045890.1	EST_HUMAN	hq54c10.x1 NCL CGAP_Par3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG ;
11835	24988	38175	2.27	1.0E-115	4502528	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12185	25030	39531	8.31	1.0E-115	BF361964.1	EST_HUMAN	QV2-NN0044-210800-308-810 NN0044 Homo sapiens cDNA
12278	25092		1.62	1.0E-115	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
594	13661	26564	1.3	1.0E-116	BE275602.1	EST_HUMAN	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988875 5'
827	13682	26819	1.28	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
884	13937		0.88	1.0E-116	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2013	15031	28024	1.93	1.0E-116	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
2013	15031	28025	1.93	1.0E-116	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
2039	15056	28058	0.95	1.0E-116	AU133080.1	EST_HUMAN	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2109	15916	28125	10.85	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2109	15916	28126	10.85	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2328	15336	28340	1.79	1.0E-116	6453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2364	16370		3.68	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
2490	15492	28483	2.87	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2783	15808	28769	1.56	1.0E-116	BE889256.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3217	16265	29163	5.91	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3217	16265	29164	5.91	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4485	17496	30356	2.48	1.0E-116	6031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4985	17863	30821	1.32	1.0E-116	A1807086.1	EST_HUMAN	PV-BT135-070499-016 BT135 Homo sapiens cDNA
5481	18542	31383	0.83	1.0E-116	A1302062.1	EST_HUMAN	q19d04.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896895 3' similar to contains element MER25 repetitive element ;
6207	19262	32412	4	1.0E-116	W42822.1	EST_HUMAN	zc24d07.r1 Soares, senescent, fibroblasts NBH5F Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
6455	19500	32674	1.79	1.0E-116	AB046866.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6455	19500	32675	1.79	1.0E-116	AB046866.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6629	19573	32755	0.99	1.0E-116	BE408097.1	EST_HUMAN	601302281F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638784 5'
6660	19699	32895	9.55	1.0E-116	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6777	19811	33021	0.67	1.0E-116	5729887	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
6777	19811	33022	0.67	1.0E-116	5729887	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
6792	19825		2.62	1.0E-116	BE158133.1	EST_HUMAN	MR2-HIT0379-210200-102-b04 HIT0379 Homo sapiens cDNA
7274	20227	33475	1.93	1.0E-116	C02944.1	EST_HUMAN	C02944 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHQ0567
7563	20505	33793	19.36	1.0E-116	AV716314.1	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCBBCC06 5'
8941	21871	35230	2.27	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8941	21871	35231	2.27	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
9049	21878	35334	0.66	1.0E-116	A1904151.1	EST_HUMAN	ON-BT043-090298-075 BT043 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9494	22422	35785	1.34	1.0E-116	BE566507.1	EST_HUMAN	601338298F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680680 5'
9844	22570	35941	4.33	1.0E-116	A1216352.1	EST_HUMAN	q09c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gb:X63741.maf1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
10169	23090	36491	1.53	1.0E-116	11418646	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA
10763	23649	37082	0.93	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10763	23649	37083	0.93	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10835	23721	37144	0.92	1.0E-116	BE158913.1	EST_HUMAN	QV4-HT0401-281289-063-c09 HT0401 Homo sapiens cDNA
11129	24059	37505	2.98	1.0E-116	BF335849.1	EST_HUMAN	CM2-CT0482-300800-349-e06 CT0482 Homo sapiens cDNA
11574	24483	37951	3.2	1.0E-116	A1367140.1	EST_HUMAN	q041e04.x1 Soares_NHMP_u_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:80495.7 CE01765;
11622	24520	37988	14.28	1.0E-116	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
12948	26826		1.62	1.0E-116	AL134889.1	EST_HUMAN	DKFZp762L1110_r1 782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762L1110 5'
580	13648	26554	1.13	1.0E-117	AF124393.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1105	15892	27087	0.97	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1253	14289	27232	1	1.0E-117	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1778	14804	27772	1.24	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1855	14877	27857	11.96	1.0E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2226	16236	28243	1.56	1.0E-117	AW957699.1	EST_HUMAN	EST369769 IMAGE resequences, IMAGE Homo sapiens cDNA
3312	16359	28260	1.51	1.0E-117	AA978114.1	EST_HUMAN	op32ct11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
4076	17102	29082	2.89	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4453	17459	30320	2.02	1.0E-117	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4692	17697	30563	2.1	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4837	17836	30707	1.45	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPOR16 protein
4837	17838	30708	1.45	1.0E-117	X89670.1	NT	H. sapiens mRNA for TPOR16 protein
4925	17924	30788	7.05	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4926	17924	30789	7.05	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5052	18049	30802	4.08	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5532	18611	31460	4.14	1.0E-117	BE730508.1	EST_HUMAN	601682657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
7292	18461	31332	0.97	1.0E-117	AA323348.1	EST_HUMAN	EST26111 Cerebellum II Homo sapiens cDNA 5' end similar to zinc finger domain
7840	20575	33859	0.62	1.0E-117	4826877	NT	Homo sapiens reelin (RELN) mRNA
7854	20781	34083	7.19	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7854	20781	34084	7.19	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7978	20899	34213	3.63	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7978	20899	34214	3.63	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
8557	21488	34828	1.21	1.0E-117	AI950145.1	EST_HUMAN	wp8607.x1 NCI_CGAP_Brn26 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75065
8886	21816	35167	0.87	1.0E-117	10834989	NT	O75065 KIAA0477 PROTEIN.;
8886	21816	35168	0.87	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8882	21812	35267	0.7	1.0E-117	AI904151.1	EST_HUMAN	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8882	21812	35268	0.7	1.0E-117	AI904151.1	EST_HUMAN	CV-BT043-090299-075 BT043 Homo sapiens cDNA
9839	22744	36126	1.48	1.0E-117	D16524.1	NT	CV-BT043-090299-075 BT043 Homo sapiens cDNA
10305	23195	36605	2.36	1.0E-117	BE733922.1	EST_HUMAN	Human gene for very low density lipoprotein receptor, exon 11
10454	25694	36760	0.71	1.0E-117	AF090033.1	NT	601569317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
11042	23926	37367	0.83	1.0E-117	11420222	NT	Homo sapiens gamma-aminobutyric acid type B receptor 2 (GABABR2), mRNA, complete cds
11292	24212	37661	2.48	1.0E-117	D83776.1	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
11461	24376	37825	2.58	1.0E-117	W50905.1	EST_HUMAN	Human mRNA for KIAA0191 gene, partial cds
11720	24622	38101	2.74	1.0E-117	AB011541.1	NT	z483b11.1 Score: fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:347229 5' similar to
11720	24622	38102	2.74	1.0E-117	AB011541.1	NT	gb:MI4219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11832	24683		9.51	1.0E-117	BE268956.1	EST_HUMAN	Homo sapiens mRNA for MEGF8, partial cds
12024	24866	38367	1.45	1.0E-117	4501848	NT	Homo sapiens mRNA for MEGF8, partial cds
12024	24866	38368	1.45	1.0E-117	4501848	NT	Homo sapiens mRNA for MEGF8, partial cds
12488	25892		2.07	1.0E-117	AF224669.1	NT	601186203F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3544296 5'
73	13188	26097	6.96	1.0E-118	AF161600.1	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
98	13211	26123	0.85	1.0E-118	AL046854.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
540	13809	26519	13.57	1.0E-118	7657016	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
939	16888	26933	1.3	1.0E-118	5714680	NT	(UBE2D3) genes, complete cds
2248	15258	28264	2.64	1.0E-118	BE389705.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
2248	15258	28265	2.64	1.0E-118	BE389705.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
2248	15258	28266	2.64	1.0E-118	BE389705.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
2351	15359		1.72	1.0E-118	AW951729.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
2789	15779	28775	1.77	1.0E-118	U07000.1	NT	Homo sapiens HSPC151 mRNA, complete cds
2789	15779	28776	1.77	1.0E-118	U07000.1	NT	Homo sapiens HSPC151 mRNA, complete cds
3151	16201		5.71	1.0E-118	Y13932.1	NT	Homo sapiens HSPC151 mRNA, complete cds
3239	16237	29180	6.63	1.0E-118	A1347694.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
3239	16237	29191	6.63	1.0E-118	A1347694.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	17055	29844	1.4	1.0E-118	AB024469.1	NT	Pongo pygmaeus DNA, similar to pol gene of HERV-W and MSRV, isolate ORW3-3
4176	17196	30066	1.11	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
5608	18684	31562	2.1	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5608	18684	31563	2.1	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5826	18897	32010	0.62	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5826	18897	32011	0.62	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5913	18982	32100	0.63	1.0E-118	U08892.1	NT	Human GS2 gene, exon 8
5913	18982	32101	0.63	1.0E-118	U08892.1	NT	Human GS2 gene, exon 8
5979	19044	32167	1.12	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
6077	19138	32273	0.95	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6077	19138	32274	0.95	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6169	19225	32369	1.48	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6988	20015	33246	1.56	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6988	20015	33247	1.56	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7456	20396	33687	1.1	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O0127.5'
7456	20396	33688	1.1	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O0127.5'
8043	20857	34272	5.21	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
8058	20971	34287	0.66	1.0E-118	L46650.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
8550	21481	34822	1.99	1.0E-118	BE761223.1	EST_HUMAN	601469159F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3872247 5'
8954	21894	35242	7.95	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8954	21894	35243	7.95	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8960	21890	35248	1.32	1.0E-118	AA443024.1	EST_HUMAN	z888d07.1 Soares_NihMpu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8960	21890	35249	1.32	1.0E-118	AA443024.1	EST_HUMAN	z888d07.1 Soares_NihMpu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
9231	22159	35513	0.56	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
9231	22159	35514	0.56	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
9280	22208	35565	1.68	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9280	22208	35566	1.68	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9587	22513	35676	3.65	1.0E-118	BE263194.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
9618	22544	35915	0.68	1.0E-118	AL048474.2	EST_HUMAN	DKFZp596K1824.1 596 (synonym: huter1) Homo sapiens cDNA clone DKFZp596K1824
10121	23012	36409	1.2	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ5285.9.C1.1), mRNA
10492	23380	36703	0.65	1.0E-118	AL138321.1	EST_HUMAN	DKFZp547O017.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547O017.5'
10863	23749	37174	1.72	1.0E-118	BF195407.1	EST_HUMAN	7n17e06.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW_ZP3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10946	23831	37257	1.09	1.0E-118	AW271289.1	EST_HUMAN	xe46a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2772668 3' similar to
11013	23897	37332	0.6	1.0E-118	AW296351.1	EST_HUMAN	SW:BODG_HUMAN_075936 GAMMA-BUTYROBETAINE_2-OXOGLUTARATE DIOXYGENASE ;
11715	24617	38093	1.43	1.0E-118	11055968	NT	UIH-BW0-elo-a-07-0-J1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729772 3'
11723	24625	38106	1.53	1.0E-118	AA315007.1	EST_HUMAN	Homo sapiens protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum protein (ERPROT213-21), mRNA
11994	24636	38334	1.59	1.0E-118	BF093687.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11994	24636	38335	1.59	1.0E-118	BF093687.1	EST_HUMAN	QV0-JM0091-120900-385-b12 UM0091 Homo sapiens cDNA
782	13838	26773	1.35	1.0E-119	AF170492.1	NT	QV0-JM0091-120900-385-b12 UM0091 Homo sapiens cDNA
1063	15891	27044	2.19	1.0E-119	7705607	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1948	14988	27946	2.47	1.0E-119	AB023147.1	NT	Homo sapiens GGI-105 protein (LOC51011), mRNA
3149	16169	29091	1.15	1.0E-119	892205	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3286	16333		1.14	1.0E-119	AA916780.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
4034	17061	29950	1.03	1.0E-119	4504116	NT	qnl0505.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:EO4F6.2
5521	18600	31449	3.02	1.0E-119	AU133399.1	EST_HUMAN	CE01214 ;
5534	18613	31462	17	1.0E-119	M89914.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5539	18618	31469	2.95	1.0E-119	BE936121.1	EST_HUMAN	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001691 5'
5819	18695	31591	1.15	1.0E-119	AV693731.1	EST_HUMAN	Human neurofibromin (NF1) gene, complete cds
5784	18656	31963	0.75	1.0E-119	AL134903.1	EST_HUMAN	RCT-NN0073-250900-018-g08 NN0073 Homo sapiens cDNA
5784	18656	31964	0.75	1.0E-119	AL134903.1	EST_HUMAN	AV693731 GK Homo sapiens cDNA clone GKODHB03 5'
6367	19416	32561	6.59	1.0E-119	AU150703.1	EST_HUMAN	DKFZp762M0710_J1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6536	19560	32762	0.58	1.0E-119	AF315683.1	NT	DKFZp762M0710_J1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6536	19580	32763	0.58	1.0E-119	AF315683.1	NT	qbt7709.x1 Soares_fetal_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to
6588	19629	32811	1.35	1.0E-119	AI476732.1	EST_HUMAN	SW:K1CJ_MOUSE_P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
6733	19768	32978	2.86	1.0E-119	X06292.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6745	18779	32982	4.46	1.0E-119	AW974193.1	EST_HUMAN	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
7809	20738	34041	1.09	1.0E-119	BE786814.1	EST_HUMAN	trn23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2167451 3'
8021	20937	34252	0.51	1.0E-119	AJ277657.1	NT	Human c-fos/prob-oncogene
9220	22148	35501	1.1	1.0E-119	BE615150.1	EST_HUMAN	EST13862936 MAGE resequences, MAGM Homo sapiens cDNA
10418	23307	36727	1.24	1.0E-119	11036643	NT	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3046081 5'
							Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
							601280564F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3822528 5'
							Homo sapiens KIAA0477 gene product (KIAA0477), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10607	23493	36923	0.53	1.0E-119	A1149796.1	EST_HUMAN	q143a11.1 Sceres testis_NHT Homo sapiens cDNA clone IMAGE:1752764 3' similar to TR:Q13458
10740	23626	37056	2.97	1.0E-119	AA465124.1	EST_HUMAN	Q13458 NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO. ;
10982	23896	37293	0.76	1.0E-119	AJ297701.1	NT	aa32f05.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:314977 5'
11022	23906	37345	0.9	1.0E-119		NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11022	23906	37346	0.9	1.0E-119		NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
11492	24404	37855	1.59	1.0E-119	AJ297701.1	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
11492	24404	37856	1.59	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11849	24535		2.24	1.0E-119	BF669571.1	EST_HUMAN	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
12542	28881		5.11	1.0E-119	AW847519.1	EST_HUMAN	RC3-CT0212-240898-011-03 CT0212 Homo sapiens cDNA
12833	25711		1.48	1.0E-119	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
256	13353	26289	0.64	1.0E-120	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
321	13413	26330	1.09	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1067	14111	27050	2.02	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B), mRNA, complete cds
1087	14111	27051	2.02	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B), mRNA, complete cds
1447	14478	27437	1.51	1.0E-120	N44873.1	EST_HUMAN	yy40g12.1 Sceres melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:273766 5'
1624	14654	27618	3.59	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1828	14851	27829	1.21	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10), mRNA
2119	15132	28138	1.62	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2119	15132	28139	1.62	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2556	15558	28554	1.04	1.0E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
3353	19418	28330	0.96	1.0E-120	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4467	17478	30337	2.42	1.0E-120	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A), mRNA, partial cds
4467	17478	30338	2.42	1.0E-120	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A), mRNA, partial cds
4774	17779	30648	1.72	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4774	17779	30649	1.72	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5128	18124	30966	0.98	1.0E-120	AF054821.1	NT	Homo sapiens cytochrome P-450 mRNA, complete cds
5323	18307	31157	1.14	1.0E-120	AJ04161.1	EST_HUMAN	CN-BT043-090299-075 BT043 Homo sapiens cDNA
5936	19005	32124	13.82	1.0E-120	BF669222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5938	19005	32125	13.82	1.0E-120	BF669222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
8006	20023	34239	1.66	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
8383	21287	34618	0.53	1.0E-120	BE785942.1	EST_HUMAN	501475178F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878155 5'
8383	21287	34619	0.53	1.0E-120	BE785942.1	EST_HUMAN	501475178F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878155 5'
8396	21298	34629	0.46	1.0E-120	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8474	21405	34743	1.76	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8474	21405	34744	1.76	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8907	21837	35193	4.04	1.0E-120	BF337599.1	EST_HUMAN	602036352F1 NCJ_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183333 5'
8975	21905	35261	1.02	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8976	21906	35262	1.02	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8979	21909	35264	2.05	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8979	21909	35265	2.05	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
9021	21960	35306	1.21	1.0E-120	AB007934.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
10033	22933	36320	4.84	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
10033	22933	36321	4.84	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
10265	23155	36565	3.95	1.0E-120	BF306541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
10280	23170	36583	5.12	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
10296	23186	36598	0.8	1.0E-120	AL049807.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10404	23293		0.58	1.0E-120	A1904151.1	EST_HUMAN	CM-BT043-090293-075 BT043 Homo sapiens cDNA
10578	23464	36888	3.24	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11566	24475	37942	2.16	1.0E-120	BE296387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632015 5'
11784	24706	38197	1.42	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3847281 5'
11784	24706	38198	1.42	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3847281 5'
76	13190	26101	0.98	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
389	13481	26401	0.74	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
747	15882	26729	1.44	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1596	14627	27587	0.93	1.0E-121	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
1981	14999	27984	0.94	1.0E-121	4755139	NT	Homo sapiens Inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
1981	14999	27985	0.94	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
2114	15127	28132	1.02	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
3130	16180	29074	3.61	1.0E-121	Y19208.1	NT	Homo sapiens hrb3 gene for hair keratin, exons 1 to 9
3130	16180	29075	3.61	1.0E-121	Y19208.1	NT	Homo sapiens hrb3 gene for hair keratin, exons 1 to 9
3598	16635	29540	1.25	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1937 protein, partial cds
3598	16635	29541	1.25	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1937 protein, partial cds
3745	16777	29668	9.91	1.0E-121	AF155158.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4438	17449	30309	2.03	1.0E-121	A1263294.1	EST_HUMAN	qk57601 x1 NCJ_CGAP_Far1 Homo sapiens cDNA clone IMAGE:2005417 3'
5097	18094	30941	4.29	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5350	18333	31181	1.01	1.0E-121	AB032481.1	NT	Homo sapiens HOXD13 gene for homeobox transcription factor, complete cds
5450	18531	31257	0.8	1.0E-121	BE22250.1	EST_HUMAN	hu09f08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168119 3'
5753	18826	31925	0.53	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6910	19940	33159	0.46	1.0E-121	M91463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
7215	20215		0.91	1.0E-121	AJ271736.1	NT	Homo sapiens Xa pseudautosomal region; segment 2/2
7299	18468	31289	0.77	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
7299	18468	31280	0.77	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-402 NN0066 Homo sapiens cDNA
8516	21447	34789	1.38	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8520	21451	34793	2.37	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8520	21451	34794	2.37	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
10372	23261	36682	1.19	1.0E-121	AW583868.1	EST_HUMAN	PHOSPHOLIPASE A2-GAMMA. ;
10372	23261	36683	1.19	1.0E-121	AW583868.1	EST_HUMAN	PHOSPHOLIPASE A2-GAMMA. ;
11215	24141	37593	2.35	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
11222	24148	37599	13.65	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
11407	24328	37773	2.62	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11433	24349	37795	1.51	1.0E-121	N59624.1	EST_HUMAN	W74c01.st Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'
287	13381	26295	1.5	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
356	13443	26355	2.98	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
378	13463	26380	1.99	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
907	13959	26907	3.23	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1248	14284	27227	5.68	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1719	14747	27715	1.63	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S92 precursor, mRNA, complete cds
1741	14768	27739	2.09	1.0E-122	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
1741	14768	27740	2.09	1.0E-122	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
1836	14859	27841	6.18	1.0E-122	BE96024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899358 5'
2514	15515	28518	5.05	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'
2514	15515	28519	5.05	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126234 5'
4958	17956	30814	1.1	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5111	18108		1.52	1.0E-122	AW504645.1	EST_HUMAN	UI-HF-BND-ell-a-03-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'

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5755	18828	31928	1.22	1.0E-122	BE266039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7061	18828	31928	6.36	1.0E-122	BE266039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7581	20517	33805	0.47	1.0E-122	AA668671.1	EST_HUMAN	ek49r06.at Scarsa_testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'
8358	21263	34597	0.48	1.0E-122	AA224259.1	EST_HUMAN	zr15a03.11 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:663436 5' similar to TR:G940370 G940370 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE;
8358	21263	34598	0.48	1.0E-122	AA224259.1	EST_HUMAN	zr15a03.11 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:663436 5' similar to TR:G940370 G940370 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE;
9354	22282	35643	0.63	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
9579	22506	35870	1.42	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9863	22778	36166	1.07	1.0E-122	AJ359618.1	EST_HUMAN	qy92r07.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1;
9863	22778	36167	1.07	1.0E-122	AJ359618.1	EST_HUMAN	qy92r07.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1;
10633	23519	36953	0.87	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dbl (proto-oncogene)
11425	24341	37786	1.53	1.0E-122	AW956834.1	EST_HUMAN	EST367904 MAGE sequences, MAGD Homo sapiens cDNA
12314	25119		6.21	1.0E-122	11418187	NT	Homo sapiens phosphonannomutase 1 (PNM1), mRNA
201	13300	28215	19.2	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxykinase (PCK1) gene, promoter region and partial cds
794	13849	26783	2.17	1.0E-123	BF345274.1	EST_HUMAN	602018038F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
794	13849	26784	2.17	1.0E-123	BF345274.1	EST_HUMAN	602018038F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
1040	14086	27025	6.09	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1049	14093	27032	3.01	1.0E-123	5603114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1266	14300	27247	4.34	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1266	14300	27248	4.34	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1474	14505	27467	5.94	1.0E-123	AJ388641.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02
2111	15124	28128	2.36	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2111	15124	28129	2.36	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2111	15124	28130	2.36	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2336	15344		3.14	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
5632	18708	31607	1.64	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5632	18708	31608	1.64	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5773	18846	31949	1.42	1.0E-123	BE769746.1	EST_HUMAN	601691108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6742	19776	32989	1.88	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7347	20343	33609	0.94	1.0E-123	H53198.1	EST_HUMAN	Y848403.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14680 PROTEIN KINASE YAK1;
7360	20355	33624	1.36	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7558	20495	33785	0.57	1.0E-123	U55258.1	NT	Human hBRAVO/NI-CAM precursor (hBRAVO/NI-CAM) gene, complete cds
7801	20730	34032	0.88	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HSSST2), mRNA
8091	21003	34326	1.32	1.0E-123	11499439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
8100	21012	34338	1.94	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
8108	21020	34346	0.57	1.0E-123	11437202	NT	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA
8282	21187	34524	0.48	1.0E-123	N35841.1	EST_HUMAN	Y88411.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611
8282	21187	34525	0.48	1.0E-123	N35841.1	EST_HUMAN	Y88411 protein kinase Pkca - Phycomyces blakesleeanus;
8368	21270	34604	0.42	1.0E-123	AA308629.1	EST_HUMAN	Y88411.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611
8098	22028		1.08	1.0E-123	AW371924.1	EST_HUMAN	S49611 protein kinase Pkca - Phycomyces blakesleeanus;
9908	22896	36283	1.46	1.0E-123	AB007623.1	NT	EST177573 Jurkat T-cells VI Homo sapiens cDNA 5' and similar to similar to multiple drug resistance-associated protein
10036	22936	36325	41.79	1.0E-123	U09823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
12142	24982	38482	4.85	1.0E-123	BF677292.1	EST_HUMAN	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabellaz) mRNA, complete cds
12142	24982	38483	4.85	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
288	13392	26296	1.1	1.0E-124	4607600	NT	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
288	13392	26297	1.1	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
294	13382		1.29	1.0E-124	D87675.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
508	13579	26495	2.61	1.0E-124	AL163246.2	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
715	13773	26692	4.04	1.0E-124	AA397551.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
715	13773	26693	4.04	1.0E-124	AA397551.1	EST_HUMAN	Z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
783	13839	26774	4.54	1.0E-124	AF156054.1	EST_HUMAN	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
834	13889	26826	1.15	1.0E-124	4507500	NT	Z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
829	13881	26928	1.77	1.0E-124	7705446	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
1341	14374	27327	0.65	1.0E-124	11418092	NT	Human putative ribosomal protein S1 mRNA
1375	14407	27360	4.07	1.0E-124	AF274892.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
							Homo sapiens hypothetical protein (HSPC0068), mRNA
							Homo sapiens ring finger protein (RNF), mRNA
							Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds

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1375	14407	27361	4.07	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1837	14860	27842	3.1	1.0E-124	AJ191712.1	NT	Homo sapiens mRNA for nuclear RNA-helicase (nclh81 gene)
2075	15089	28088	1.48	1.0E-124	BE879824.1	EST_HUMAN	601461716F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3883954 5'
2481	15483	28484	1.35	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
3420	16462	29369	0.65	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3549	16587	29492	1.15	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3549	16587	29493	1.15	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3970	16998	29884	0.87	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4162	17183	30056	1.13	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4858	17858	30722	1.09	1.0E-124	BE220437.1	EST_HUMAN	h039c07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175788 3'
4858	17860	30725	2.75	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
5047	18044		1.23	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5480	18561	31405	11.08	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5869	18940	32056	0.83	1.0E-124	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6104	19185	32298	6.68	1.0E-124	BF698135.1	EST_HUMAN	602124644F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:4281635 5'
6410	19458	32632	0.65	1.0E-124	AV711263.1	EST_HUMAN	AV711263 Cu Homo sapiens cDNA clone CuAADF07 5'
6701	19737	32939	1.24	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7356	20351	33919	2.92	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene
7497	20437	33717	1.02	1.0E-124	BE271285.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'
7497	20437	33718	1.02	1.0E-124	BE271285.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'
7984	20905	34221	0.96	1.0E-124	AA630331.1	EST_HUMAN	ac08h05.s1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:655897 3'
8834	21764	35111	9.53	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
9031	21980	36319	2.2	1.0E-124	AW612105.1	EST_HUMAN	hg94a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O85162
9031	21980	36320	2.2	1.0E-124	AW612105.1	EST_HUMAN	Q95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9705	22630	36008	0.57	1.0E-124	A1799884.1	EST_HUMAN	hg94a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2963240 3' similar to TR:O95162
9705	22630	36009	0.57	1.0E-124	A1799884.1	EST_HUMAN	Q95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
10023	22923	36311	2.8	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
10023	22923	36312	2.8	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
10107	22998	36393	0.86	1.0E-124	AF022855.1	NT	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
10107	22998	36394	0.86	1.0E-124	AF022855.1	NT	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
10135	23028	36422	7.36	1.0E-124	A1767133.1	EST_HUMAN	Homo sapiens cap280 centrosome associated protein mRNA, complete cds
							Homo sapiens cap280 centrosome associated protein mRNA, complete cds
							wi63f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10135	23028	36423	7.36	1.0E-124	A1767133.1	EST_HUMAN	wf9302.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
10383	23272	36895	1.67	1.0E-124	AW503755.1	EST_HUMAN	U1-HF-BNO-ekz-b-04-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'
11483	24396	37846	1.49	1.0E-124	U94776.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
11777	24676	38165	3.54	1.0E-124	AW665663.1	EST_HUMAN	h05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'
11904	24004	37444	2.19	1.0E-124	AI446455.1	EST_HUMAN	h19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
11904	24004	37445	2.19	1.0E-124	AI446455.1	EST_HUMAN	h19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN.;
12073	24914	38417	4.69	1.0E-124	AB032857.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
12383	13773	26592	5.81	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
12383	13773	26593	5.81	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
339	13429	26002	7.35	1.0E-125	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
449	13116	26002	4.78	1.0E-125	BE743922.1	EST_HUMAN	801577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
667	13729	26840	22.97	1.0E-125	AI110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
667	13729	26841	22.97	1.0E-125	AI110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
751	13808	26733	1.65	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
885	13938	26885	3.65	1.0E-125	AA042813.1	EST_HUMAN	z163c07.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1026	14075	27015	1.06	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1181	14221	27168	1.2	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product, histone deacetylase 7 (KIAA0744), mRNA
1899	15907	27693	2.01	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1833	14856	27837	3.08	1.0E-125	AF015450.1	NT	Homo sapiens Usurin-alpha mRNA, complete cds
1833	14856	27838	3.08	1.0E-125	AF015450.1	NT	Homo sapiens Usurin-alpha mRNA, complete cds
2381	15386	28397	1.18	1.0E-125	AA011278.1	EST_HUMAN	z101g09.r1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:429668 5'
2528	15529	28531	1.42	1.0E-125	AA042813.1	EST_HUMAN	z163c07.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2638	15635	28632	2.35	1.0E-125	4504696	NT	Homo sapiens inhibitor, alpha (INH) mRNA
2638	15635	28633	2.35	1.0E-125	4504696	NT	Homo sapiens inhibitor, alpha (INH) mRNA
3053	18398	29010	1.02	1.0E-125	BE018009.1	EST_HUMAN	bb74f06.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:O95604 O95604 ZINC FINGER PROTEIN.;
3925	16983	29837	1.32	1.0E-125	AA042813.1	EST_HUMAN	z163c07.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4666	17671	30541	2.3	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4666	17671	30542	2.3	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4730	17735	30597	0.84	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5'
5163	13261	26179	1.13	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN IA;
5163	13261	26180	1.13	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN IA;
5965	19032	32153	0.65	1.0E-125	BF683645.1	EST_HUMAN	602139874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'
6088	19149	32285	1.3	1.0E-125	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6109	19169	32301	0.98	1.0E-125	BE175169.1	EST_HUMAN	QV2-HT0577-010600-185-b08 HT0577 Homo sapiens cDNA
6156	19214	32354	3.77	1.0E-125	BE892690.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6203	19259	32406	0.85	1.0E-125	AI675904.1	EST_HUMAN	tu87c07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP:C45G9.2
6334	19578	32760	0.49	1.0E-125	BE739055.1	EST_HUMAN	CE01854;
6863	19895	33109	2.04	1.0E-125	BE562526.1	EST_HUMAN	601305670F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640097 5'
6863	19895	33110	2.04	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7415	20114	33349	8.45	1.0E-125	XQ3427.1	NT	Homo sapiens IGF-II gene, exon 5
7415	20114	33350	8.45	1.0E-125	XQ3427.1	NT	Homo sapiens IGF-II gene, exon 5
7956	20878	34189	0.87	1.0E-125	BE278823.1	EST_HUMAN	601159076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
8223	21128	34459	0.4	1.0E-125	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8319	21224	34558	0.57	1.0E-125	BE515100.1	EST_HUMAN	601236183F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608084 5'
9110	22038	35393	1.21	1.0E-125	U50288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9110	22038	35394	1.21	1.0E-125	U50288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9662	22568	35959	8.85	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
9662	22568	35960	8.85	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
9919	22807	36286	1.16	1.0E-125	AI665996.1	EST_HUMAN	h52603.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089 HYPOTHETICAL PROTEIN;
10972	23656	37283	0.85	1.0E-125	AB002298.1	NT	Human mRNA for KIAA0300 gene, partial cds
11125	24055	37502	2.88	1.0E-125	AF043458.1	NT	Homo sapiens IREL gene, exon 5
11210	24136	37685	1.54	1.0E-125	AW131202.1	EST_HUMAN	x59902.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 LAMBDA/OTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11210	24136	37586	1.54	1.0E-125	AW131202.1	EST_HUMAN	xf5902.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284
11575	24484	37952	3.89	1.0E-125	AB014567.1	NT	LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
11734	24636	38117	1.95	1.0E-125	769505	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
11741	24643	38123	3.42	1.0E-125	AF026028.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11838	24689	38178	2.18	1.0E-125	AW812899.1	EST_HUMAN	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11935	24779	38274	5.43	1.0E-125	BE074267.1	EST_HUMAN	RC3-ST0186-250200-078-c11 ST0186 Homo sapiens cDNA
11935	24779	38274	5.43	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
11935	24779	38274	5.43	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
800	13855	28791	1.71	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
803	13858	28794	0.8	1.0E-126	M81936.1	NT	Human laminin B1 chain gene, exon 20
844	13955	28936	824.88	1.0E-126	X68735.1	NT	H. sapiens gene for alpha1-antichymotrypsin, exon 3
2639	15936	28934	3.51	1.0E-126	6392078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3120	16171	29066	10.77	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3120	16171	29067	10.77	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3121	16172	29068	0.73	1.0E-126	BF510408.1	EST_HUMAN	UI-H-B14-acc-b-05-0-U1.st NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084608 3'
3121	16172	29069	0.73	1.0E-126	BF510408.1	EST_HUMAN	UI-H-B14-acc-b-05-0-U1.st NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084608 3'
3697	16728	29620	1.63	1.0E-126	X63941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3723	16755	29643	2.64	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4899	17898	30763	1.05	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4899	17898	30764	1.05	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4949	17948	30806	1.72	1.0E-126	N84078.1	EST_HUMAN	y78c08.r1 Scores melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:267850 5'
5901	18970	32088	0.69	1.0E-126	T66988.1	EST_HUMAN	y452b12.e1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:36527 3'
6480	19525	32703	3.4	1.0E-126	AA460075.1	EST_HUMAN	z080c03.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:36527 3'
6543	19566	32771	3.81	1.0E-126	AB040988.1	NT	TR:G1145980 G1145980 TITIN ;
6543	19566	32771	3.81	1.0E-126	AB040988.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6543	19566	32772	3.81	1.0E-126	AB040988.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7921	20844	34148	0.89	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7921	20844	34149	0.89	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8158	21085	34395	0.65	1.0E-126	AU136463.1	EST_HUMAN	AU136463 PLACE1 Homo sapiens cDNA clone PLACE1004325 5'
8222	21127	34458	0.5	1.0E-126	AB06483.1	EST_HUMAN	wf0501.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350009 3' similar to
8458	21389	34728	0.73	1.0E-126	AB037715.1	NT	SW:MPP2_HUMAN Q14168 MAGUK P55 SUBFAMILY MEMBER 2 ;
8458	21389	34729	0.73	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8567	21498	34841	2.54	1.0E-126	X10609.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
							Human mRNA for ankryrin (variant 2.1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8761	21691	36034	0.69	1.0E-126	AA483888.1	EST_HUMAN	ne74b12.s1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909983 similar to SW:TSG6_HUMAN
10312	23201	36610	0.51	1.0E-126	4505424	NT	P98086 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR ;
11233	24159	37608	1.45	1.0E-126	M93196.1	NT	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
11293	24213	37662	2.12	1.0E-126	BF683175.1	EST_HUMAN	Human macrophage mannose receptor (MRC1) gene, exon 5
11948	24792	38290	1.99	1.0E-126	BE261680.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298240 5'
12816	18433	31355	6.47	1.0E-126	BE743922.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
182	13282	26198	1.94	1.0E-127	AB024597.1	NT	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926686 6'
182	13282	26199	1.94	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
183	13282	26198	1.37	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
183	13282	26199	1.37	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
183	13282	26199	1.37	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
293	13387	26304	1.53	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
293	13387	26305	1.53	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
906	13958	26906	1.54	1.0E-127	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
941	13982	26935	0.84	1.0E-127	U72821.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1717	14745	27713	0.96	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2079	15093	28091	2.05	1.0E-127	5803085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2079	15093	28092	2.05	1.0E-127	5803085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2216	15226	28230	7.33	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2365	16371	28374	3.83	1.0E-127	AF245505.1	NT	Homo sapiens adiccin mRNA, complete cds
2652	15847	28847	7.24	1.0E-127	X12881.1	NT	Human mRNA for cyokeratin 18
2666	15862	28861	1.03	1.0E-127	AA450131.1	EST_HUMAN	zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789088 5'
2668	15862	28862	1.03	1.0E-127	AA450131.1	EST_HUMAN	zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789088 5'
3755	16787	29876	0.84	1.0E-127	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3879	16908	29789	0.9	1.0E-127	AW161297.1	EST_HUMAN	au80a08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ; contains element MER22 repetitive element ;
4209	17228	30094	0.94	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4318	17332	30195	0.75	1.0E-127	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21T0047
4352	17366	30229	32.28	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4352	17366	30230	32.28	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4616	17624	30488	0.94	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds
4713	17718	30580	5.66	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4744	17749		2.87	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4783	17788	30657	1.18	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5905	18974	32092	2.27	1.0E-127	W03547.1	EST_HUMAN	zad1a10.1 Scores melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:291258 5' similar to SW-PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5939	19006	32126	0.64	1.0E-127	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
6013	19076	32202	4.6	1.0E-127	X85764.1	NT	H. sapiens NOS2 gene, exon 6
6403	19451	32822	2.14	1.0E-127	X84060.1	NT	H. sapiens TCF11 gene, exon 3-6
6576	19617	32802	6.11	1.0E-127	4504778	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
6952	19981	33206	0.96	1.0E-127	11421606	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7410	20115	33351	0.81	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
8259	21164	34498	1.34	1.0E-127	11421914	NT	Homo sapiens Perlecan (PDS), mRNA
8269	21164	34498	1.34	1.0E-127	11421914	NT	Homo sapiens Perlecan (PDS), mRNA
8275	21180	34518	0.59	1.0E-127	BF871355.1	EST_HUMAN	602151232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'
8278	21183	34521	0.58	1.0E-127	AW996282.1	EST_HUMAN	QV3-BN0046-150300-121-h11 BN0046 Homo sapiens cDNA
9444	22372	35738	0.93	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9444	22372	35737	0.93	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
10166	23057	36456	4.34	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10166	23057	36457	4.34	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10385	23274	36696	0.87	1.0E-127	AI298932.1	EST_HUMAN	qm94h09.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896448 3'
10831	23717	37142	1.74	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11598	24507	37973	7.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (martalin-2) (H. sapiens) (LOC63184), mRNA
11598	24507	37974	7.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (martalin-2) (H. sapiens) (LOC63184), mRNA
12053	24894	38397	1.63	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
12053	24894	38398	1.63	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
12584	13282	26198	1.57	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12584	13282	26199	1.57	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12775	25404	31812	1.93	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13078	25840		2.03	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
482	13553	26470	1.88	1.0E-128	BC395617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618922 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2084	15098	28096	8.75	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2084	15098	28097	8.75	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2224	15234	28241	24.03	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2469	15472		1.68	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3453	16484	29398	1.14	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4778	17781	30851	5.39	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5736	18809	31903	14.94	1.0E-128	X68539.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6865	19721	32921	1.7	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7260	20169	33409	6.72	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3'
7631	20760	34064	0.45	1.0E-128	BE614105.1	EST_HUMAN	601503646F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905794 5'
8175	21082	34412	0.58	1.0E-128	BF529931.1	EST_HUMAN	602042322F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4179988 5'
8175	21082	34413	0.58	1.0E-128	BF529931.1	EST_HUMAN	602042322F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4179988 5'
8176	21082	34414	0.58	1.0E-128	BF529931.1	EST_HUMAN	602042322F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4179988 5'
8279	21184	34522	0.67	1.0E-128	11545923	NT	Homo sapiens putative ABC transporter (WHITE2), mRNA
9112	22040	35396	0.63	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9112	22040	35397	0.63	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10638	23522	36957	0.77	1.0E-128	AA639188.1	EST_HUMAN	ns04a11.1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS.;
11162	24081	37528	3.21	1.0E-128	11425254	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
11160	24088	37535	3.77	1.0E-128	AA929359.1	EST_HUMAN	om68r08.s1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
11405	24321	37770	4.36	1.0E-128	BE687554.1	EST_HUMAN	601611912F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913371 5'
12464	25211		3.61	1.0E-128	AW955290.1	EST_HUMAN	EST367360 MAGE resequences, MAGE Homo sapiens cDNA
126	13507	26433	8.32	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
436	13607	26433	10.42	1.0E-129	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1747	14774	27743	2.72	1.0E-129	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1752	14779	27748	1.49	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1752	14779	27749	1.49	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1871	14892	27873	2.39	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
2828	15817	28811	1.03	1.0E-129	4505882	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2828	15817	28812	1.03	1.0E-129	4505882	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3173	16223	29114	0.96	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3173	16223	29115	0.96	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3173	16223	29116	0.96	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4229	17245	30113	1.08	1.0E-129	5032230	NT	Homo sapiens A kinase (PRKA) anchor protein 9 (AKAP9), mRNA
4229	17245	30114	1.08	1.0E-129	5032230	NT	Homo sapiens A kinase (PRKA) anchor protein 9 (AKAP9), mRNA
4261	17277	30146	2.06	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4379	17393	30257	2.26	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
4379	17393	30258	2.26	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
6328	19378	32545	4.83	1.0E-129	AJ005345.1	NT	Cardiomyopathy associated gene 5
6803	19836	33047	0.44	1.0E-129	BE868934.1	EST_HUMAN	Homo sapiens KVLQT1 gene
7244	20153	33392	0.41	1.0E-129	BE868933.1	EST_HUMAN	601513861F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915350 5'
7244	20153	33393	0.41	1.0E-129	BE868933.1	EST_HUMAN	601449740F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853688 5'
7487	20427	33707	4.11	1.0E-129	AJ006345.1	NT	601449740F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853688 5'
7554	20491	33780	16.7	1.0E-129	11420850	NT	Homo sapiens KVLQT1 gene
7852	20874	34184	0.8	1.0E-129	AF041056.1	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
7852	20874	34185	0.8	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8893	21823		4.44	1.0E-129	AB014534.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
10581	23467	36892	0.96	1.0E-129	11437282	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10581	23467	36893	0.96	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10980	23874	37302	0.6	1.0E-129	AI99117.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10980	23874	37303	0.6	1.0E-129	AI99117.1	EST_HUMAN	q140d08.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840
11672	24576	38052	3.2	1.0E-129	AA625526.1	EST_HUMAN	q140d08.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840
11744	20491	33780	3.74	1.0E-129	11420850	NT	MITOGEN INDUCIBLE GENE MIG-2;
12452	25202		3.06	1.0E-129	H83155.1	EST_HUMAN	q140d08.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1047589 5'
12809	25431		1.81	1.0E-129	AL120739.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIG-2;
79	13183	26105	1.26	1.0E-130	7705530	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
1198	14237	27177	0.79	1.0E-130	AB037835.1	EST_HUMAN	SP-B48150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ;
1693	14723	27687	6.94	1.0E-130	BE275192.1	EST_HUMAN	DKFZp762K171.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5'
1693	14723	27688	6.94	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens hypothetical protein (HSPC242), mRNA
							Homo sapiens mRNA for KIAA1414 protein, partial cds
							601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
							601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'

Single Exon Probes Expressed In Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2000	15018		2.8	1.0E-130	X04092.1	NT	Human gene for catalase (EC 1.11.1.6) exon 8 mapping to chromosome 11, band p13
2821	15810		7.65	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2921	15974	28871	1.39	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
2921	15974	28872	1.39	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3638	16674	28572	0.87	1.0E-130	AF240696.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3832	15974	28871	6.64	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3832	15974	28872	6.64	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4012	17039	29928	1.92	1.0E-130	AW503580.1	EST_HUMAN	UHF-BNO-aky-g-08-q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 6'
4654	17660	30527	10.78	1.0E-130	AW843983.1	EST_HUMAN	GM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
5233	18221	31069	1.32	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
5233	18221	31070	1.32	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
7031	20057	33290	0.58	1.0E-130	X57825.1	NT	Human germline immunoglobulin lambda light chain pseudogene (VII.1)
7133	20241	33491	0.85	1.0E-130	AW843876.1	EST_HUMAN	GM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
7133	20241	33492	0.85	1.0E-130	AW843876.1	EST_HUMAN	GM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
7149	20257	33510	0.76	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7625	20560	33853	1.78	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7739	20670	33987	0.57	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7739	20670	33988	0.57	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
9240	22168		0.61	1.0E-130	AF008651.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
9378	22306	35667	2.77	1.0E-130	AW958242.1	EST_HUMAN	EST368312 MAGE resequences, MAGD Homo sapiens cDNA
9766	22679	36084	1.62	1.0E-130	AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
10442	23331		0.72	1.0E-130	AW103454.1	EST_HUMAN	x330600.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595874 3'
11719	24821	38099	1.77	1.0E-130	8923197	NT	Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA
11719	24821	38100	1.77	1.0E-130	8923197	NT	Homo sapiens hypothetical protein FLJ20208 (FLJ20208), mRNA
12127	24968	38472	1.7	1.0E-130	4504142	NT	Homo sapiens glutamate receptor, metabotropic 5 (GRM5) mRNA
4	13120	26006	1.82	0.0E+00	AA228126.1	EST_HUMAN	zr56c04.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	13120	26007	1.82	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	13123	26011	1.44	0.0E+00	4885136	NT	zr56c04.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
16	13131	26017	3.89	0.0E+00	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
16	13131	26018	3.89	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
22	13138	26025	2.95	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
							Homo sapiens DCRR1 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
22	13138	26026	2.96	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
28	13144	26031	15.23	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
36	13152	26041	0.91	0.0E+00	5802397	NT	Homo sapiens Cdc42 effector protein 2 (GEP2), mRNA
38	13154	26044	15.3	0.0E+00	M58500.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
41	13157	26048	4.2	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
43	13159	26050	1.94	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
60	13176	26077	18.82	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
62	13178	26082	1.16	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
62	13178	26083	1.16	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFUJ1wara) Homo sapiens cDNA clone GEN-516H08 5'
63	13179	26084	10.74	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
65	13181	26087	9.6	0.0E+00	AW069834.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
65	13181	26088	9.6	0.0E+00	AW069834.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
69	13184	26092	0.8	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
70	13185	26103	0.67	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
78	13192	26103	5.5	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	13192	26104	5.5	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
81	13192	26103	3.7	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
81	13192	26104	3.7	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
84	13197	26110	1.49	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amilin oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
85	13198	26110	6.01	0.0E+00	4504444	NT	Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
94	13207	26119	27.76	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
97	13210	26122	14.89	0.0E+00	U89277.1	NT	Human polyhomocytic 1 homolog (H1PH1) mRNA, partial cds
104	13217	26129	2.13	0.0E+00	A1114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
105	13218	26130	0.82	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
111	13221	26134	0.69	0.0E+00	X91213.1	NT	H. sapiens nex1 gene (exon 2)
120	13228	26140	1.42	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
121	13228	26140	1.54	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
122	15841	26141	2.41	0.0E+00	N36040.1	EST_HUMAN	YY01h09.r1 Scores melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270017 5'
122	15841	26142	2.41	0.0E+00	N36040.1	EST_HUMAN	YY01h09.r1 Scores melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270017 5'
125	13231	26147	0.76	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
135	13237	26155	3.59	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
135	13237	26156	3.59	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
143	13495	26417	0.65	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP mRNA
145	13245	26163	1.04	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:38310 5'
145	13245	26164	1.04	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:38310 5'
163	13284		6.67	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
167	13268	26185	1.19	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
169	13270		15.62	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
172	13273	26188	0.99	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
174	13275	26189	1.36	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
175	13275	26189	0.98	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
176	13276	26190	2.39	0.0E+00	W73973.1	EST_HUMAN	z62805.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346201 5' similar to
177	13277	26191	1.25	0.0E+00	BE162832.1	EST_HUMAN	gbX16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
177	13277	26192	1.25	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
178	13278	26193	1.88	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
181	13281	26196	8.26	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
181	13281	26197	8.26	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
182	13290	26204	2.89	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP.Y57A10A.Z
192	13290	26205	2.89	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP.Y57A10A.Z
197	13295	26208	2.25	0.0E+00	AB018327.1	NT	CE22631
197	13295	26209	2.25	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
198	13296	26210	1.42	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
198	13296	26211	1.42	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
207	13306	26223	68.46	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
212	13311	26228	2.96	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set4-3 mRNA, complete cds
212	13311	26229	2.96	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set4-3 mRNA, complete cds
214	13313	26231	4.87	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
214	13313	26232	4.87	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
224	15869	26239	20.86	0.0E+00	AI687308.1	EST_HUMAN	tg04f08.x1 NCI_CGAP_L33 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
224	15869	26240	20.98	0.0E+00	AI587308.1	EST_HUMAN	U04008.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gbJ03191 PROFILIN1 (HUMAN);
226	13324	26242	1.61	0.0E+00	AF106558.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
230	13328		20.4	0.0E+00	4606822	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
231	13329		6.66	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
238	13336	26250	1.92	0.0E+00	AB018294.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
239	13336	26250	1.46	0.0E+00	AB018294.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
240	13337	26251	2.47	0.0E+00	6878444	NT	Mus musculus testis-specific protein, Y-encoded-like (TespY), mRNA
254	13352	26265	0.93	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
254	13352	26266	0.93	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
257	13354	26270	7.47	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
259	13356		3.05	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21G001
266	13361	26276	3.24	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
268	13363	26279	1.55	0.0E+00	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
276	13371		6.8	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
288	13383	26298	1.29	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
289	13383	26299	1.29	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
291	13385	26301	2.17	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC81260), mRNA
302	13395		1.41	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
303	13396	26314	2.24	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
303	13398	26315	2.24	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
304	13397		1.1	0.0E+00	AW1845283.1	EST_HUMAN	IL2-CT0031-181199-020-303 GT0031 Homo sapiens cDNA
313	13405	26322	5.67	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
313	13405	26323	5.67	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
324	13416	26333	3.1	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
328	13417	26334	3.07	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
326	15872		13.21	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S6 (RPS6) mRNA
327	13418	26335	0.76	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
328	13419		1.82	0.0E+00	AA480002.1	EST_HUMAN	phosphoribosylaminimidazole synthetase (GART) mRNA
328	13420	26336	12.99	0.0E+00	4507152	NT	zV1Bc06.r1 Soares, NHMPu, S1 Homo sapiens cDNA clone IMAGE:753994 5'
330	13420	26336	10.02	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
334	13424	26340	2.68	0.0E+00	AF114488.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
347	13436	26349	0.7	0.0E+00	O14867	SWISSPROT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
							TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
347	13436	26350	0.7	0.0E+00	O14897	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
348	13437	26351	3.25	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
349	13437	26351	2.08	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
364	13451	26363	3.4	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4), mRNA
365	13452	26364	0.71	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
368	13455	26368	24.99	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1), mRNA
371	13458	26373	1.18	0.0E+00	U71600.1	NT	Human zinc finger protein Zfp31 (Zf31), mRNA, partial cds
376	13462	26377	2.49	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
376	13462	26378	2.49	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
377	15873	26379	2.61	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
378	13464	26381	0.88	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
382	13467	26385	1.32	0.0E+00	4503954	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
383	13468	26386	1.36	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
384	13468	26386	1.04	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
386	13470	26388	0.73	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
397	13478	26398	1.4	0.0E+00	AU134983.1	EST_HUMAN	AU134983 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
408	13521	26443	5.23	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
409	13522	26444	1.49	0.0E+00	A1363014.1	EST_HUMAN	qy81h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb.X64189
414	13487	26406	1.89	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);
417	13489	26409	1.34	0.0E+00	4503680	NT	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA
418	13490	26410	2.22	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
418	13490	26411	2.22	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
419	13491	26412	1.39	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
420	13492	26413	1.41	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
420	13492	26414	1.41	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
421	13493	26415	0.71	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
422	13494	26416	2.6	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
423	13495	26417	1.12	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP), mRNA
424	13496	26418	1.35	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pd I largest subunit, exons 23-29
424	13496	26419	1.36	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pd II largest subunit, exons 23-29
425	13496	26418	1.14	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pd I largest subunit, exons 23-29
425	13496	26419	1.14	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pd II largest subunit, exons 23-29

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
429	13500		36.83	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
443	13110	25996	1.01	0.0E+00	R17795.1	EST_HUMAN	yg08a02.r1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:31652 5'
451	13523	26445	0.85	0.0E+00			Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
452	13524		8.84	0.0E+00	4503914	NT	phosphoribosylmethionine synthetase (GART) mRNA
453	13525	26446	2.7	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
454	13526	26447	3.19	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
454	13526	26448	3.19	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
455	13527	26449	2.23	0.0E+00	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
468	13539	26462	3.81	0.0E+00	4557879	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
473	13544		0.91	0.0E+00	AA324262.1	EST_HUMAN	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
474	13545		1.1	0.0E+00	BE264447.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' and
490	13561	26476	4.19	0.0E+00	4504532	NT	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
490	13561	26477	4.19	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
496	13566	26485	14.93	0.0E+00	4557887	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
496	13566	26486	14.93	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
506	13577	26492	2.13	0.0E+00	AL163246.2	NT	Homo sapiens keratin 18 (KRT18) mRNA
507	13578	26493	5.89	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
507	13578	26494	5.89	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
516	13586	26499	5.84	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
518	13589	26501	1.62	0.0E+00	AU132898.1	EST_HUMAN	AL132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
528	13596	26507	3.08	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
527	13578	26508	1.99	0.0E+00	AW938825.1	EST_HUMAN	PMO-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
530	13599	26510	1.36	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
531	13600	26511	1.18	0.0E+00	8923855	NT	Homo sapiens PC326 protein (PC326), mRNA
535	13604		0.81	0.0E+00	BF373403.1	EST_HUMAN	IL2-F10169-070800-120-F07 F10159 Homo sapiens cDNA
542	13611	26521	5.84	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
549	13677	26525	1.01	0.0E+00	BE081627.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
554	13623	26531	1.5	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996998 5'
560	13629	26538	0.94	0.0E+00	AB049008.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
563	13632	26541	7.91	0.0E+00	6005030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
564	13633	26542	3.95	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
564	13633	26543	3.95	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
570	13638		3.94	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
578	13646	26553	1.36	0.0E+00	AW135324.1	EST_HUMAN	U1-H-B11-ecb-h-04-0-U1.s1 NCI_OGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
598	13656		5.37	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
607	13673	26577	4.13	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
620	13685		8.03	0.0E+00	J04088.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
623	13688	26591	1.5	0.0E+00	BF104898.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
625	13690	26593	3.67	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
625	13690	26594	3.67	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
626	13690	26593	2.83	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
626	13690	26594	2.83	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
627	13690	26593	3.96	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
627	13690	26594	3.96	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
632	13693	26597	4.64	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
637	13698	26603	0.85	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-Interacting zinc finger protein mRNA, partial cds
637	13698	26604	0.85	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-Interacting zinc finger protein mRNA, partial cds
648	13707	26614	2.89	0.0E+00	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
648	13709	26617	0.72	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
650	13711	26618	1.16	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
651	13712	26619	1.89	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
651	13712	26620	1.89	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
652	13713	26621	1.74	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
652	13713	26622	1.74	0.0E+00	8808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
656	13720	26631	1.1	0.0E+00	AA399486.1	EST_HUMAN	z80c07.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
662	13724	26635	6.75	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
666	13728	26638	35.2	0.0E+00	W7881.1	EST_HUMAN	zh51504.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
666	13728	26639	35.2	0.0E+00	W7881.1	EST_HUMAN	zh51504.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
669	13731		3.56	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
676	13738	26651	3.64	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
678	13740	26654	1.36	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
681	13743	26658	1.56	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
685	13747	26661	0.82	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
685	13747	26662	0.82	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
691	13752	26687	3.52	0.0E+00	4828947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
691	13752	26668	3.52	0.0E+00	4828947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
697	15380		1.1	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
708	13765	26682	6.52	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HM/G1) mRNA
711	13770	26686	6.56	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
721	13779	26701	3.22	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA np49d01.s1 NCI_OGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1126533 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
732	13790	26714	87.75	0.0E+00	AA614637.1	EST_HUMAN	
736	13794	26718	3.54	0.0E+00	M60676.1	NT	Human von Willebrand factor gene, exons 23 through 34
736	13794	26719	3.54	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
746	13804	26728	1.36	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
752	13809	26734	3.52	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
752	13809	26735	3.52	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
754	13811	26738	9.98	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA TCAAP-ID0778 Pediatric acute myelogenous leukemia cell (FAB M1) BAYor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
760	13917	26746	1.42	0.0E+00	BE241577.1	EST_HUMAN	
780	13835	26770	1.03	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
780	13836	26771	1.03	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
781	13837	26772	0.66	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
784	13840	26775	2.01	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
784	13840	26776	2.01	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
787	13843	26777	1.3	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1939 protein, partial cds
788	13844	26778	1.11	0.0E+00	6891249	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
780	15884	26780	1.54	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
791	13846	26781	2.2	0.0E+00	BE889735.1	EST_HUMAN	601445647-1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
795	13850	26785	3.57	0.0E+00	R48915.1	EST_HUMAN	y59g08.r1 Scarsa breast 2NBbBst Homo sapiens cDNA clone IMAGE:154046 5'
796	13851	26786	2.88	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120KD (SF3A1), mRNA
805	13860	26795	1.35	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
808	13864	26799	2.28	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
819	13874	26811	1.06	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
819	13874	26812	1.06	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
824	13878	26816	1.89	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
828	13883	26820	2.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
828	13883	26821	2.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
832	13887	26825	7.59	0.0E+00	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
833	13888	26849	8.25	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
849	13904	26846	1.55	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	13905	26847	2.23	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
852	13907	26849	3.59	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNK1) mRNA
858	13912	26855	1.09	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
858	13912	26856	1.09	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
859	13913	26857	0.95	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
864	13918	26862	1.53	0.0E+00	4503864	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
866	13921	26867	2.13	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
866	13921	26868	2.13	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
875	13928	26868	1.31	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC3A3) gene, complete cds
879	13932	26879	3.49	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
879	13932	26880	3.49	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
880	13933	26881	8.07	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
881	13934	26882	2.29	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
882	13935	26883	6.27	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
886	13939	26886	1.07	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
886	13939	26887	1.07	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
887	13940	26888	1.53	0.0E+00	AA533272.1	EST_HUMAN	h66307 at NCI CGAP P10 Homo sapiens cDNA clone IMAGE:997463
887	13940	26889	1.53	0.0E+00	AA533272.1	EST_HUMAN	h66307 at NCI CGAP P10 Homo sapiens cDNA clone IMAGE:997463
888	13941	26890	5.97	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249916 5'
892	13945	26890	1.59	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
892	13945	26891	1.59	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
893	13946	26892	2.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
893	13946	26893	2.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
916	13968	26916	0.99	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
923	13975	26921	1.9	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
923	13975	26922	1.9	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
933	13985	26931	3.75	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
943	13994	26939	19.56	0.0E+00	4504968	NT	Homo sapiens laminiin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
948	13997	26939	3.17	0.0E+00	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
948	13997	26940	3.17	0.0E+00	U35484.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
949	13994	26942	8.03	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67KD, ribosomal protein SA) (LAIR1), mRNA
949	13989	26942	729.35	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
950	14000	26943	6.71	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
950	14000	26944	6.71	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
950	14000	26945	6.71	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
951	14001	26946	8.7	0.0E+00	Z8101.1	NT	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds
951	14004	26949	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
954	14004	26950	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
978	14029	26971	0.91	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
979	14030	26972	6.24	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
980	14031	26973	9.08	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
980	14031	26974	9.08	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
988	15889	26981	3	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NC1 CGAP GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
988	15889	26982	3	0.0E+00	A1001948.1	EST_HUMAN	os98e03.s1 NC1 CGAP GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
990	14040	26984	4.79	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1001	14050	26994	2.53	0.0E+00	AB030568.1	NT	Homo sapiens mRNA for PSP24, complete cds
1010	14059	27001	1.4	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
1010	14059	27002	1.4	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
1010	14059	27003	1.4	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-402 GN0014 Homo sapiens cDNA
1011	14060	27004	1.79	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1011	14060	27005	1.79	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1020	14069	27012	1.4	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1032	14080	27020	1.15	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1033	14081	27021	13.88	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1034	14081	27021	6.54	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1037	14084		5.05	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1038	14084		6.98	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1041	14087	27026	1.14	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1042	14087	27026	1.28	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1043	14087	27026	1.25	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1044	14088	27027	2.02	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1047	14091	27030	2.12	0.0E+00	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1051	14085	27034	2.35	0.0E+00	6803114	NT	Homo sapiens Inner membrane protein, mitochondrial (IMMT), mRNA
1052	14086		3.07	0.0E+00	AA458880.1	EST_HUMAN	aa8607.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PR38_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8;
1055	14089	27038	1.8	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1055	14089	27039	1.8	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1056	14100	27040	1.73	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1056	14100	27041	1.73	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1059	14103		3.42	0.0E+00	8922833	NT	Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA
1073	14117	27055	7.87	0.0E+00	4758569	NT	Homo sapiens heat shock 70kD protein 98 (HSP90B) mRNA
1092	14135	27071	1.66	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1092	14135	27072	1.66	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1098	14139	27076	2.58	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1098	14139	27077	2.58	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1097	14140	27078	12.79	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1099	14142		0.9	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1101	14144	27082	2.61	0.0E+00	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1109	14151	27092	3.51	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1123	14165	27102	2.29	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-H08 BN0115 Homo sapiens cDNA
1146	14188	27128	4.2	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1146	14188	27127	4.2	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1159	14200	27137	0.86	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1159	14200	27138	0.86	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1160	14201	27139	11.99	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1162	14203	27141	1	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1165	14208	27144	2.97	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1167	14208	27145	7.45	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1168	14209	27146	3.4	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1168	14209	27147	3.4	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1172	14212	27150	1.24	0.0E+00	7706500	NT	Homo sapiens Npr38-binding protein NprBP (LOC51729), mRNA
1173	14213	27151	1.71	0.0E+00	X55826.1	NT	H sapiens ART4 gene
1173	14213	27152	1.71	0.0E+00	X55826.1	NT	H sapiens ART4 gene
1174	14214	27153	1.46	0.0E+00	AI147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1176	14216	27155	1.28	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1183	14223	27161	1.51	0.0E+00	9966944	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1196	14235	27174	1.16	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1196	14235	27175	1.16	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD26, mRNA
1199	14239	27178	1.15	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1208	14245	27187	13.55	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18), mRNA
1237	14273		1.09	0.0E+00	7657336	NT	Homo sapiens muLL (E. coli) homolog 3 (MLH3), mRNA
1254	14280	27233	0.98	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1254	14280	27234	0.98	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1255	14291	27235	1.37	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1258	15895	27238	0.86	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1274	14308	27259	4.51	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1275	14309	27260	1.01	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1293	14328		1.72	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1301	14334	27260	60.39	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1307	14340	27268	2.7	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9), mRNA, complete cds
1314	14347	27283	1.54	0.0E+00	AB040840.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1314	14347	27284	1.54	0.0E+00	AB040840.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1328	14360	27307	2.76	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS), mRNA
1326	14360	27308	2.76	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS), mRNA
1328	14360	27309	2.76	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS), mRNA
1327	14361		2.24	0.0E+00	AF096156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1337	15897	27321	1.32	0.0E+00	7657528	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1337	15897	27322	1.32	0.0E+00	7657528	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1343	15861	27328	0.89	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1344	14376	27329	1.84	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1345	14377	27330	2.23	0.0E+00	4608004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1347	14379	27331	0.9	0.0E+00	5803146	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1348	14380	27332	1.83	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1350	14382	27334	3.86	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1351	14383	27335	2.89	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1352	14384	27336	5.09	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1353	14385	27337	3.86	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1353	14385	27338	3.86	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA

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1365	14396	27351	1.34	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1437	14468	27424	1.35	0.0E+00	AJ277802.1	NT	Homo sapiens partial TTN gene for titin
1440	14471	27428	4.16	0.0E+00	8042208	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1449	14480	27440	2.85	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1449	14480	27441	2.85	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1451	14482	27442	7.52	0.0E+00	AJ238083.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1459	14491	27452	2.71	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1468	14499	27460	1.21	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1468	14499	27481	1.21	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1472	14503	27484	5.87	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1472	14503	27486	5.87	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1481	14512	27472	2.75	0.0E+00	AL132989.1	NT	Novel human gene on chromosome 20
1482	14513	27473	1.4	0.0E+00	AL137794.1	NT	Novel human gene mapping to chromosome 1
1486	14517	27478	2.41	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1489	14520	27481	4.34	0.0E+00	6912467	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1491	14522	27483	1.18	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1491	14522	27484	1.18	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1496	14527	27489	1.61	0.0E+00	M60878.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1498	14527	27490	1.61	0.0E+00	M60878.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1532	14562	27522	1.96	0.0E+00	7706434	NT	Homo sapiens h-IDG for homolog of Drosophila headcase (LOC51696), mRNA
1548	14578	27539	1.93	0.0E+00	A4481172.1	EST_HUMAN	aa34a03.f1 NCL_CGAP_GC31 Homo sapiens cDNA clone IMAGE:816116 5'
1555	14586	27543	17.47	0.0E+00	AF023860.1	NT	Carcipithecus aethiops cyclophilin A mRNA, complete cds
1555	14588	27544	17.47	0.0E+00	AF023860.1	NT	Carcipithecus aethiops cyclophilin A mRNA, complete cds
1557	14588	27547	1.04	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1557	14588	27548	1.04	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1558	14589	27549	0.95	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1560	14591		5.14	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1561	14592	27552	1.98	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1561	14592	27553	1.98	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1562	14593	27564	2.89	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1563	14594		10.66	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1567	14598	27558	3.58	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1570	14801	27580	1.96	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1570	14801	27581	1.96	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1571	15004		11.95	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1572	14802	27582	11.4	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1583	14814	27578	10.2	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1591	14822		1.58	0.0E+00	D90333.1	NT	human c-yes-2 gene
1602	14833	27593	2.68	0.0E+00	263738.1	NT	H. sapiens hH2B/e gene
1603	14834	27594	1.9	0.0E+00	5921480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1603	14834	27595	1.9	0.0E+00	5921480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1604	14835	27596	13.79	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCB0F02 5'
1604	14835	27597	13.79	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCB0F02 5'
1607	15905	27600	2.29	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1611	14841	27601	1.28	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1613	14843	27604	3.18	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1613	14843	27605	3.18	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1615	14845	27608	18.93	0.0E+00	5729878	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1615	14845	27607	18.93	0.0E+00	5729878	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1617	14847	27609	2.33	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1631	14681	27624	3.83	0.0E+00	H26973.1	EST_HUMAN	y978c05.a1 Soares adult brain N2b4HB5Y Homo sapiens cDNA clone IMAGE:183848 3'
1641	14672	27636	1.57	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1641	14672	27637	1.57	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1664	14694	27654	1.11	0.0E+00	AW444637.1	EST_HUMAN	U1H-B18-gw-c-04-U1.a1 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1691	14721	27684	1	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0168-191189-004-b11 HT0168 Homo sapiens cDNA
1691	14721	27685	1	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0168-191189-004-b11 HT0168 Homo sapiens cDNA
1695	14725	27689	1.1	0.0E+00	AF788104.1	EST_HUMAN	wg81b07.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to
1698	14726	27690	2.36	0.0E+00	AF057177.1	NT	TR-Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. ;
1700	14729	27694	1.17	0.0E+00	M29580.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1700	14729	27695	1.17	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1702	14731	27697	12.36	0.0E+00	4557887	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1703	14732	27698	1.47	0.0E+00	7657065	NT	Homo sapiens keratin 18 (KRT18) mRNA
1707	14738	27701	1.31	0.0E+00	BE222374.1	EST_HUMAN	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA hu11405.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168281 3' similar to TR:Q95147 O85147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1707	14738	27702	1.31	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168281 3' similar to TR:095147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1710	14738	27706	3.74	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1710	14738	27707	3.74	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1712	14740		1.21	0.0E+00	A114980.1	EST_HUMAN	qf43f09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
1713	14741	27709	2.19	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
1713	14741	27710	2.19	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
1716	14744		9.49	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1726	14753	27723	4.63	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1729	14766	27728	3.03	0.0E+00	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1736	14763	27734	1.22	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1742	14769	27741	4.43	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1744	14771		2.22	0.0E+00	S94400.1	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1753	14780	27750	0.93	0.0E+00	4557638	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
1761	15909	27758	0.92	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1772	14798	27768	2.15	0.0E+00	AF273841.1	NT	Homo sapiens SMGY (SMGY) gene, complete cds
1809	15910		20.59	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1812	14837	27808	2.18	0.0E+00	4557559	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1812	14837	27809	2.18	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1816	14839	27813	1.64	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1818	14842		0.99	0.0E+00	W76571.1	EST_HUMAN	z668g09.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345664 5'
1819	15911	27817	3.07	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1829	14852	27830	10.54	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1831	14854	27833	3.31	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1832	14855	27834	6	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1832	14855	27835	6	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1832	14855	27836	6	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1846	14869	27851	1	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1846	14869	27852	1	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1858	14880	27859	7.22	0.0E+00	60056855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1858	14880	27860	7.22	0.0E+00	60056855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1859	14891	27871	1.43	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1859	14891	27872	1.43	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1872	14893	27874	4.78	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1872	14893	27875	4.78	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1873	14894	27876	5.07	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1873	14894	27877	5.07	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1876	14897	27880	2.49	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B1-afn-407-0-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1876	14897	27881	2.49	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B1-afn-407-0-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1898	14919	27898	2.39	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3547239 5'
1898	14919	27899	2.39	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3547239 5'
1912	14933	27910	1.05	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-b04 BN0126 Homo sapiens cDNA
1935	14956	27933	1.42	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1935	14956	27934	1.42	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1938	14959	27936	1.78	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1938	14959	27937	1.78	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1946	14967	27948	1.61	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1947	15913	27948	3.26	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1947	15913	27947	3.26	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1952	14972	27954	1.7	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1952	14972	27955	1.7	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1955	14974	27957	1.04	0.0E+00	7637038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1957	14976		4.64	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1962	14981		1.89	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1963	15914	27964	1.86	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1970	14988	27970	2.93	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1970	14988	27971	2.93	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1982	15000		1.09	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
1984	15002	27987	2.88	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1984	15002	27988	2.88	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1985	15003	27989	3.9	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1985	15003	27990	3.9	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1997	15015	28005	1.39	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1997	15015	28006	1.39	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2003	15021	28010	1.5	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2003	15021	28011	1.5	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2005	15023	28012	1.71	0.0E+00	AW193024.1	EST_HUMAN	X69501.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
2005	15023	28013	1.71	0.0E+00	AW193024.1	EST_HUMAN	X69501.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
2006	15024	28014	3.87	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2008	15024	28015	3.87	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2008	15028	28017	1.11	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2009	15027	28018	1.13	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2009	15027	28019	1.13	0.0E+00	Z47556.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2016	15034	28028	3	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2034	15051	28049	0.9	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2034	15051	28049	0.9	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2070	15085	28084	4.95	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2070	15085	28085	4.95	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2072	15087	28088	2.93	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2073	15088	28087	5.21	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE400321 5'
2074	14480	27440	1.84	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2074	14480	27441	1.84	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2076	15090	28089	1.91	0.0E+00	AA077599.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2076	15090	28090	1.91	0.0E+00	AA077599.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2078	15092		7.31	0.0E+00	7687468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2080	15094		1.52	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2081	15095	28093	0.91	0.0E+00	Z42399.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02
2083	15097		1.37	0.0E+00	A1244247.1	EST_HUMAN	q96088.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988971 3' similar to contains Alu repetitive element
2088	15102	28102	1.9	0.0E+00	BE977225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2090	15104	28104	1.76	0.0E+00	BF315325.1	EST_HUMAN	601602604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2090	15104	28105	1.76	0.0E+00	BF315325.1	EST_HUMAN	601602604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2093	15107	28108	3.38	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2093	15107	28109	3.38	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2099	15113	28117	2.99	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2099	15113	28118	2.99	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2104	15118	28122	0.92	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2128	15139		3.8	0.0E+00	BE767884.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2127	15140		1.41	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLRIS1) gene, exon 6 and complete cds
2128	15142	28145	3.73	0.0E+00	BF027562.1	EST_HUMAN	601872086F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2130	15143	28146	1.57	0.0E+00	BE072824.1	EST_HUMAN	PM0-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2132	15145	28147	1.29	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2135	15148	28149	2.59	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2137	15150	28151	2.51	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2137	15150	28152	2.51	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2171	15183		1	0.0E+00	7657252	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA
2193	15204		1.04	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2201	15212	28214	0.98	0.0E+00	BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346888 5'
2203	15214	28217	1.01	0.0E+00	D67685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2204	15215	28218	6.93	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2204	15216	28218	6.93	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2208	15217	28221	1.34	0.0E+00	AA931691.1	EST_HUMAN	cc32a01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2208	15219		29.79	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
2210	15221	28224	15.41	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150734 5'
2211	15222	28225	17.81	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2214	15226	28228	11.4	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2214	15225	28229	11.4	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2218	15919	28234	3.1	0.0E+00	BF313617.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129822 5'
2221	15231	28237	1.27	0.0E+00	BE018750.1	EST_HUMAN	b684e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN:
2222	15232	28238	1.89	0.0E+00	AA042813.1	EST_HUMAN	z633c07.s1 Soares pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:U65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2222	15232	28239	1.89	0.0E+00	AA042813.1	EST_HUMAN	z633c07.s1 Soares pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:U65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2230	15240	28247	2.52	0.0E+00	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004

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2230	15240	28248	2.52	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2235	15245		1.68	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2241	15251		11.93	0.0E+00	M20903.1	NT	Human apolipoprotein C-I pseudogene, complete cds
2255	15265	28273	5.6	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2261	15271	28277	1.23	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2269	15279	28286	1.89	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918607 5'
2273	15283	28280	1.27	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3897457 5'
2273	15283	28291	1.27	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3897457 5'
2276	15285	28293	1.03	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2319	15327	28328	1.05	0.0E+00	BF344766.1	EST_HUMAN	602014009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149770 5'
2319	15327	28328	1.05	0.0E+00	BF344766.1	EST_HUMAN	602014009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149770 5'
2320	15328	28330	4.27	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2320	15328	28331	4.27	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2321	15329	28332	2.52	0.0E+00	A1076404.1	EST_HUMAN	o203c07.x1 Soares fetal liver spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2324	15332	28335	1.85	0.0E+00	AA429001.1	EST_HUMAN	zv78a11.1 Soares total_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2324	15332	28336	1.85	0.0E+00	AA429001.1	EST_HUMAN	zv78a11.1 Soares total_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2326	15334	28338	5.26	0.0E+00	AA690367.1	EST_HUMAN	zi11612.s1 Soares fetal_liver_spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:430510 3'
2327	15335	28339	1.16	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5'
2332	15340	28345	2.72	0.0E+00	L02840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2333	15341	28346	7.01	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2340	15348	28352	2.25	0.0E+00	BE676095.1	EST_HUMAN	7f22a02.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3285370 3' similar to TR:O94939 O94939
2343	15351	28354	5.72	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHKA2) gene, exon 32
2344	15352	28355	2.4	0.0E+00	AB25542.1	EST_HUMAN	v67c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2345	15353	28356	1.36	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
2360	15358	28360	2.44	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2360	15358	28361	2.44	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2357	15364	28366	1.59	0.0E+00	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2357	15364	28367	1.59	0.0E+00	7662007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2362	15368		1.69	0.0E+00	4557521	NT	Homo sapiens delatidase, isobutyranine, type 1 (DIO1) mRNA
2371	15377	28378	3.14	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2375	15380	28382	2.68	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2376	15381		7.46	0.0E+00	BE794026.1	EST_HUMAN	601596843F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3941003 5'
2377	15382	28383	1.09	0.0E+00	AW867078.1	EST_HUMAN	MR1-SN0033-120400-002-e04 SN0033 Homo sapiens cDNA

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2378	15383	28384	3.83	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2379	15384	28385	2.37	0.0E+00	4758497	NT	Homo sapiens hexose-8-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2379	15384	28386	2.37	0.0E+00	4758497	NT	Homo sapiens hexose-8-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2380	15385		8.43	0.0E+00	AF280407.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2382	15387	28388	7.6	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2382	15387	28389	7.6	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2382	15387	28390	7.6	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2383	15388	28391	0.98	0.0E+00	8923089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2439	15443	28443	1.62	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2441	15445		4.5	0.0E+00	AJ042035.1	EST_HUMAN	ox80b02x1 Scarses_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1680683 3' similar to TR:O08862
2442	15446	28445	0.91	0.0E+00	8923020	NT	O08662 230kDA PHOSPHATIDYLINOSITOL 4-KINASE
2445	15449		1.23	0.0E+00	BE95605.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2448	15452	28448	1.76	0.0E+00	BE957632.1	EST_HUMAN	801432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2457	15461		2.94	0.0E+00	AB005622.1	EST_HUMAN	NR1-TN0021-280800-001-h06 TN0021 Homo sapiens cDNA
2459	15463	28460	5.79	0.0E+00	6006002	NT	AB005622 HeLa cDNA (T Nome) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2463	15465	28464	1.83	0.0E+00	D85606.1	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2463	15466	28465	1.83	0.0E+00	D85606.1	NT	Homo sapiens gene for cholestylinin type-A receptor, complete cds
2472	15475	28475	2.34	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2477	15479	28480	1.46	0.0E+00	BF345274.1	EST_HUMAN	602018058F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
2483	15485	28487	4.12	0.0E+00	5729777	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
2491	15493	28493	12.96	0.0E+00	BF569144.1	EST_HUMAN	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4900383 3'
2500	15502	28503	2.95	0.0E+00	AW468922.1	EST_HUMAN	ha04h04.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2502	15504	28504	3.27	0.0E+00	AW501010.1	EST_HUMAN	UJ-HF-BPop-als-c-07-0-UJr1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2530	15531		2.28	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2535	15536	28536	15.31	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2536	14974	27957	1.39	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2537	15537	28537	1.76	0.0E+00	BF509482.1	EST_HUMAN	UJ-H-BI4-a02-b-08-0-UJr1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2540	15540	28539	2.44	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2542	15542		5.02	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2545	15545	28543	0.91	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2548	15548	28544	8.62	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA

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2547	15547	28545	1.21	0.0E+00	BE150865.1	EST_HUMAN	RC4-HT0276-160200-013-005 HT0276 Homo sapiens cDNA
2548	15548	28546	1.79	0.0E+00	B923340	NT	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
2549	15549	28547	4.11	0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2555	15555	28553	1.54	0.0E+00	BE886490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2560	15559	28559	6.48	0.0E+00	BE876511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2560	15559	28560	6.48	0.0E+00	BE876511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2561	15560	28561	1.09	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF6
2563	15562	28564	1.46	0.0E+00	AF245605.1	NT	Homo sapiens adiccan mRNA, complete cds
2583	15582	28574	1.53	0.0E+00	BE536921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2591	15599	28583	16.77	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2591	15599	28584	16.77	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2592	15590	28585	1.25	0.0E+00	BE292896.1	EST_HUMAN	601108312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2592	15590	28586	1.25	0.0E+00	BE292896.1	EST_HUMAN	601108312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2593	15591	28587	1.21	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE: 3' similar to TR:O00246 O00246
2596	15594	28589	9.36	0.0E+00	AF245605.1	NT	HYPOTHETICAL 9.3 KD PROTEIN ;
2622	15620	28613	1.31	0.0E+00	BE296813.1	EST_HUMAN	Homo sapiens adiccan mRNA, complete cds
2640	15661	28636	1.98	0.0E+00	AB037836.1	NT	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
2640	15661	28638	1.98	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2641	15637		3.24	0.0E+00	BF513835.1	EST_HUMAN	Homo sapiens mRNA for KIAA1415 protein, partial cds
2646	15642	28641	1.69	0.0E+00	BF672818.1	EST_HUMAN	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2655	15650	28649	1.23	0.0E+00	AB037742.1	NT	60215263F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283612 5'
							Homo sapiens mRNA for KIAA1321 protein, partial cds
2658	15651	28650	1.5	0.0E+00	AJ571737.1	EST_HUMAN	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2657	15652	28651	2.87	0.0E+00	5032150	NT	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2660	15656	28656	5.07	0.0E+00	AB037859.1	NT	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2681	15657	28657	1	0.0E+00	BE795445.1	EST_HUMAN	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2681	15657	28658	1	0.0E+00	BE795445.1	EST_HUMAN	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2684	15660	28659	0.92	0.0E+00	BE293328.1	EST_HUMAN	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2672	15668		4.1	0.0E+00	BE792472.1	EST_HUMAN	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2674	15670	28669	1.29	0.0E+00	AB020710.1	NT	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2681	15676	28675	2.44	0.0E+00	4504886	NT	U1H-BW1-amp-1-12-Q-J1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'

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2693	15687		1.12	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2694	15688	28685	5.54	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2698	15692	28686	1.1	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2701	15695	28689	1.37	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2702	15698	28690	1.57	0.0E+00	M69225.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2704	15698	28692	1.02	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2704	15698	28693	1.02	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2706	15700	28695	1.4	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA
2710	15704	28700	0.9	0.0E+00	BF000018.1	EST_HUMAN	7n16h05.x1 NCI_CGAP C016 Homo sapiens cDNA clone IMAGE:3316089 3'
2711	15705	28701	4.81	0.0E+00	BE383165.1	EST_HUMAN	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2712	15706		3.28	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610287 5'
2749	15740	28735	0.92	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2769	15761		6.42	0.0E+00	AA316723.1	EST_HUMAN	EST168414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L28
2770	15762	28754	7.64	0.0E+00	BE794884.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2771	15763	28763	2.99	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2779	15770	28765	1.26	0.0E+00	7689517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA
2780	15771	28766	1.41	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
2787	15777	28773	7.98	0.0E+00	BE795378.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2790	15834	28777	5.97	0.0E+00	BE563433.1	EST_HUMAN	601333485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688564 5'
2791	15780		1.22	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2793	15782	28780	2.43	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2793	15782	28781	2.43	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2794	15783	28782	1.18	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2794	15783	28783	1.18	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2795	15784	28784	2.92	0.0E+00	AF280195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2796	15785		95.03	0.0E+00	AV651088.1	EST_HUMAN	AV651088 GLC Homo sapiens cDNA clone GLCCLD07 3'
2797	15786	28785	10.79	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2797	15786	28786	10.79	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2804	15783	28793	3.97	0.0E+00	BE747193.1	EST_HUMAN	60158903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
							y935h10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773
2805	15784	28784	0.92	0.0E+00	N44974.1	EST_HUMAN	A45773 kelch protein, long form - fruit fly
2808	15797	28797	0.91	0.0E+00	BE176836.1	EST_HUMAN	RC4-HT0587-170300-012-d11 HT0587 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2819	15908		1.67	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2820	15909	28807	3.82	0.0E+00	BF514110.1	EST_HUMAN	U1H-BW1-amy-07-0-U1.st NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2825	15914		1.15	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2832	15921	28816	5.52	0.0E+00	BF677694.1	EST_HUMAN	602085578F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4249815 5'
2836	15925	28822	1.3	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR-T), mRNA
2839	15928	28824	7.64	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2839	15928	28825	7.64	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2841	15930		8.96	0.0E+00	AI879163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2844	15933	28830	2.13	0.0E+00	BF530061.1	EST_HUMAN	502071957F1 NCL CGAP_Brr07 Homo sapiens cDNA clone IMAGE:4214679 5'
2845	15934	28831	8.8	0.0E+00	BE872768.1	EST_HUMAN	501450912F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3854642 5'
2847	15936	28832	1.34	0.0E+00	AU131484.1	EST_HUMAN	AU131484 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2847	15936	28833	1.34	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2848	15937	28834	22.38	0.0E+00	BE300344.1	EST_HUMAN	500844794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860808 5'
2848	15937	28835	22.38	0.0E+00	BE300344.1	EST_HUMAN	500844794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860808 5'
2853	15938	28213	2.74	0.0E+00	S78830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2856	15943		1.76	0.0E+00	AB033281.1	NT	Homo sapiens BTROP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2862	13914	26743	1.68	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2862	13914	26744	1.68	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2867	14109	27047	4.3	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2867	14109	27048	4.3	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2882	15937	28842	3.76	0.0E+00	X35980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2883	15938		1.67	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
2884	15939		1.49	0.0E+00	AB040360.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2890	15944	28845	3.54	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2894	15948	28848	1.82	0.0E+00	M80802.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2897	15951		1.29	0.0E+00	X73428.1	NT	H. sapiens lds gene for HLH type transcription factor
2898	15952		3.26	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C068
2899	15953	28851	1.08	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2899	15953	28852	1.08	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2899	15953	28853	1.08	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2901	15955	28854	1.17	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2905	15958	28858	5.69	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2905	15958	28859	5.69	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2909	15962	28862	2.19	0.0E+00	AL090857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2910	15963		5.24	0.0E+00	Y10693.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2911	15964		1.16	0.0E+00	AF162303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2912	15965	28863	8.41	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2912	15965	28864	8.41	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2922	15976	28873	2.62	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2925	15978	28877	1.1	0.0E+00	AL047599.1	EST_HUMAN	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2926	15979		1.27	0.0E+00	4503098	NT	DKFZP586G0621_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp586G0621
2926	15982	28878	6.43	0.0E+00	BE081896.1	EST_HUMAN	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2929	15982	28880	6.43	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2935	15988	28888	0.8	0.0E+00	6808918	NT	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2935	15988	28889	0.8	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2938	15991	28893	2.14	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2938	15991	28894	2.14	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2939	15992	28895	1.19	0.0E+00	AA215579.1	EST_HUMAN	z68511.st NCJ CGAP GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element
2948	16000		4.1	0.0E+00	Y19210.1	NT	Homo sapiens Hb5 gene for hair keratin, exons 1 to 9
2951	16003	28905	1.27	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPA4) mRNA
2952	16004	28906	4.27	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2954	16006	28908	1.12	0.0E+00	AF162338.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2970	16022	28920	2.13	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2970	16022	28921	2.13	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2971	16023	28922	5.8	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2971	16023	28923	5.8	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2974	16026	28926	2.2	0.0E+00	7661803	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2974	16026	28927	2.2	0.0E+00	7661803	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
							Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (MLLT4) mRNA
2975	16027	28928	3.27	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (MLLT4) mRNA
2975	16027	28929	3.27	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (MLLT4) mRNA
2987	16039	28943	5.51	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2987	16039	28944	5.51	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2995	16047	28950	1.95	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
2998	16050	28953	1.05	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2998	16050	28954	1.05	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
3000	16052	28956	12.2	0.0E+00	AF106273.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3014	16056		1.88	0.0E+00	AF149880.1	EST_HUMAN	q143f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
3022	16074	28976	0.67	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3022	16074	28977	0.67	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3023	16075	28978	1.39	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3024	16076	28979	2.3	0.0E+00	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3035	16087	28988	1.35	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
3036	16088	28989	1.04	0.0E+00	AW612526.1	EST_HUMAN	h103f08.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2954055 3' similar to TR:O60407 O60407
3038	16090	28991	2.25	0.0E+00	6729755	NT	PAC CLONE DJ1168D11 FROM 7P21-P22, COMPLETE SEQUENCE ;
3038	16090	28992	2.25	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3047	16099	29001	1.02	0.0E+00	AF114488.1	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3047	16099	29002	1.02	0.0E+00	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3072	16124	29024	0.81	0.0E+00	AL163246.2	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3074	16126	29024	1.27	0.0E+00	M74099.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3084	16135	29031	0.74	0.0E+00	4506882	NT	Homo sapiens chromosome 21 segment HS21C046
3091	16142	29042	4.21	0.0E+00	AF195953.1	NT	Human displacement protein (CCAAT) mRNA
3094	16145	29042	3.83	0.0E+00	5579469	NT	Homo sapiens semenogelin 1 (SEMG1) mRNA
3094	16145	29043	3.83	0.0E+00	5579469	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3096	16147	29048	7.92	0.0E+00	AL359403.1	NT	Homo sapiens heat shock 70kD protein 1 (HSPA7A), mRNA
3101	16152	29048	2.38	0.0E+00	AF017433.1	NT	Homo sapiens heat shock 70kD protein 1 (HSPA7A), mRNA
							isoform 2 of a novel human mRNA from chromosome 22
							Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JV10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3104	16155		3.12	0.0E+00	AF196778.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (Ig-L-C16.1)
3125	16176	29071	4.46	0.0E+00	X03529.1	NT	Homo sapiens F-box protein FBL5 (FBL5), complete cds
3131	16181		2	0.0E+00	AF169355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3135	16185	29078	1.33	0.0E+00	AF004569.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3153	16203	29094	1.58	0.0E+00	AF265208.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3154	16204	29095	4.51	0.0E+00	AF149773.1	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3158	16208	29098	4.85	0.0E+00	7662139	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3159	16209	29099	1.35	0.0E+00	AF042075.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3185	16234	29129	3.4	0.0E+00	4926783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3193	16241	29136	21.09	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3197	16245	29140	1.13	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3197	16245	29141	1.13	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3203	16251	29147	3.74	0.0E+00	T94870.1	EST_HUMAN	ye32f03 s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:529639
3218	16266	29165	1.35	0.0E+00	BF243336.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3220	16268	29166	1.42	0.0E+00	A1968086.1	EST_HUMAN	wu12h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516803 3'
3225	16273	29173	5.95	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3225	16273	29174	5.95	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3236	16284	29186	1.46	0.0E+00	4759827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3236	16284	29187	1.46	0.0E+00	4759827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3243	16291	29194	11.35	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3244	16292	29195	1.21	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3244	16292	29196	1.21	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3255	16303	29209	1.2	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
3263	16311	29215	1.21	0.0E+00	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3267	16315	29218	1.14	0.0E+00	4502098	NT	(SLC29A5), nuclear gene encoding mitochondrial protein, mRNA
3273	16321	29226	1.09	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Ruibinstein-Taybi syndrome) (CREBBP) mRNA
3273	16321	29227	1.09	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Ruibinstein-Taybi syndrome) (CREBBP) mRNA
3275	16323	29228	6.85	0.0E+00	AA774783.1	EST_HUMAN	ae87b11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3283	16331	29236	1.91	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3283	16331	29237	1.91	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3293	16340	29242	1.6	0.0E+00	4557590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3298	16345	29249	1.32	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3306	16353		1.73	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
3306	16356	29258	5.06	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3319	16399	29265	1.76	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3319	16399	29267	1.76	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3333	16379	29279	1.77	0.0E+00	AF266208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3334	16380	29280	1.44	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3343	16392	29292	1.43	0.0E+00	AF087925.1	NT	Homo sapiens olfactory receptor 17-93 (OR1E2) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3346	16392	29293	1.43	0.0E+00	AF087925.1	NT	Homo sapiens olfactory receptor 17-53 (OR1E2) gene, complete cds
3359	16403	29304	1.32	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3369	16413	29314	1.14	0.0E+00	AI589294.1	EST_HUMAN	t58608.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222635 3' similar to SW:RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11, contains AU repetitive element;
3372	16416	29317	1.97	0.0E+00	AW955400.1	EST_HUMAN	EST367470 MAGE resequences, MAGD Homo sapiens cDNA
3380	16423	29325	2.6	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3380	16423	29326	2.6	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3381	16424	29327	1.11	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3381	16424	29328	1.11	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3383	16426	29330	1.78	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3383	16426	29331	1.79	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3387	16430	29334	13.95	0.0E+00	AF111163.1	NT	Homo sapiens pyruvate (MEFV) gene, complete cds
3389	16432	29336	1.19	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3396	16438	29342	0.89	0.0E+00	BE778039.1	EST_HUMAN	60148495F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869246 5'
3411	16453	29359	0.73	0.0E+00	AI632589.1	EST_HUMAN	wb10b4.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN.;
3456	16497	29401	2.31	0.0E+00	AU123664.1	EST_HUMAN	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3463	16503	29404	1.08	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3463	16503	29405	1.06	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3466	16506	29407	1.28	0.0E+00	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOGS1694), mRNA
3467	16507	29408	1.13	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
3472	16512		1.17	0.0E+00	AW867015.1	EST_HUMAN	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3485	16524	29423	1.39	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3485	16524	29424	1.39	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3486	16526	29425	1.27	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSF1) mRNA
3489	16528	29427	1.6	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3498	15771	28766	1.56	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3503	16541	29440	2.51	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3506	16544	29444	5.94	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC Incompatibility determinants
3508	16546	29448	1.45	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, I (PTPR1), mRNA
3511	16549	29449	1.18	0.0E+00	4557746	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3515	16553	29453	3.95	0.0E+00	AI935169.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3515	16553	29454	3.95	0.0E+00	AI935169.1	EST_HUMAN	NEURAL CELL ADHESION MOLECULE.;
3519	16557	29459	1.41	0.0E+00	AJ278120.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3520	16558	29460	0.97	0.0E+00	7706378	NT	NEURAL CELL ADHESION MOLECULE.;
3531	16569	29473	1.58	0.0E+00	M14123.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3536	16574	29478	6.96	0.0E+00	U43293.1	NT	Homo sapiens ASB-4 protein (LOC51666), mRNA
3544	16582	29486	2.33	0.0E+00	AF045452.1	NT	Human endogenous retrovirus HERV-K10
3544	16582	29487	2.33	0.0E+00	AF045452.1	NT	Human MDS1A (AML1/MDS1 fusion), mRNA, partial cds
3552	16590	29496	1.3	0.0E+00	AF231922.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3562	16599	29502	2.28	0.0E+00	BE304791.1	EST_HUMAN	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3562	16599	29503	2.28	0.0E+00	BE304791.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3565	16602	29506	3.47	0.0E+00	4503648	NT	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3566	16603	29507	1.28	0.0E+00	4826795	NT	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3568	16606	29510	0.7	0.0E+00	O14887	SWISSPROT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
3574	16611	29514	0.75	0.0E+00	AI384007.1	EST_HUMAN	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3577	16614	29517	1.06	0.0E+00	M10976.1	NT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3594	16631	29535	0.96	0.0E+00	AB032979.1	NT	tc35g12.x1 Scarses_NhiMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3594	16631	29536	0.96	0.0E+00	AB032979.1	NT	O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN;
3601	16638	29542	0.85	0.0E+00	AV701869.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
3602	16639	29543	1.19	0.0E+00	4508884	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3611	16648	29549	1.28	0.0E+00	AL133204.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3615	16651	29552	1.24	0.0E+00	AB040909.1	NT	AV701869 ADB Homo sapiens cDNA clone ADBDAH06 5'
3624	16660	29560	0.88	0.0E+00	8923087	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3635	16671	29568	1.52	0.0E+00	6997248	NT	Novel human gene mapping to chromosome X
3635	16671	29569	1.52	0.0E+00	6997248	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3636	16672		0.84	0.0E+00	AI081807.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3643	16679		5.1	0.0E+00	AW852217.1	EST_HUMAN	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3650	16686		0.85	0.0E+00	AF118946.1	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3651	16687	29681	9.04	0.0E+00	BF076933.1	EST_HUMAN	ox77c11.x1 Scarses_NhiMPu_S1 Homo sapiens cDNA clone IMAGE:1662355 3' similar to WP:1984.4 CE13742;
							QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
							Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
							602084583F1 NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:4248696 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3685	16599	29595	1.42	0.0E+00	AW937977.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3686	16713	29604	0.67	0.0E+00	BF672054.1	EST_HUMAN	602162486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3687	16713	29605	0.67	0.0E+00	BF672054.1	EST_HUMAN	602162486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3688	16714		1.15	0.0E+00	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3689	16716	29607	0.97	0.0E+00	AW694683.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3690	16716	29608	0.97	0.0E+00	AW694683.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3691	16721	29614	0.77	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3692	16748	29635	2.47	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3693	16761		2.78	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3694	16767	29653	2.13	0.0E+00	AB026942.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3695	16770	29655	3.74	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3696	16770	29656	3.74	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3697	16776	29664	1.64	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3698	16776	29665	1.64	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3699	16778	29667	1.19	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3700	16779	29668	1.19	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3701	16783	29672	2.09	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3702	16785	29674	1.76	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3703	16788	29677	0.7	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3704	16798	29678	0.7	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3705	16801	29687	5.07	0.0E+00	AW298134.1	EST_HUMAN	UIH-BW0-ajs-e-12-0-UI.st NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3706	16801	29688	5.07	0.0E+00	AW298134.1	EST_HUMAN	UIH-BW0-ajs-e-12-0-UI.st NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3707	16823	29710	1.38	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen at chain, exon 6
3708	16824	29711	1.18	0.0E+00	AA463659.1	EST_HUMAN	aa08g01.1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW4KRB4 SHEEP P02448 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1]:
3709	16828	29715	0.98	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3710	16831	29717	4.63	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POW121 (POW121L1), mRNA
3711	16840	29727	0.72	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3712	16853	29737	6.99	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3713	16857	29740	6.94	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3714	16863	29745	1	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3715	16863	29746	1	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3637	16866	29749	1.67	0.0E+00	4505564	NT	Homo sapiens plasminogen activator inhibitor, type II (arginine-serpin) (PAI2) mRNA
3668	16897	29781	3.66	0.0E+00	7681867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
3668	16897	29782	3.66	0.0E+00	7681867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
3890	16919	29796	1.05	0.0E+00	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3892	16921		0.66	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3893	16922	29798	2.87	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3897	16926	29803	2.12	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3897	16926	29804	2.12	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3902	16931	29810	1.04	0.0E+00	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3905	16934	29813	1.49	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3905	16934	29814	1.49	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3906	16935	29815	1.05	0.0E+00	AI377698.1	EST_HUMAN	tc6210.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3907	16936	29816	1.23	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
3909	16938	29817	4.06	0.0E+00	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3910	16939	29818	2.43	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3911	16940	29819	1.43	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3916	16944	29823	1.13	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3921	16949	29831	8.56	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3921	16949	29832	8.56	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3923	16951	29835	4.66	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3924	16952	29836	0.98	0.0E+00	AF114468.1	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
3927	16955	29838	1.44	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3930	16958	29841	1.43	0.0E+00	AF012815.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3931	16959	29842	1.76	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3934	16962	29845	0.73	0.0E+00	AF098117.1	NT	Homo sapiens amphiphysin gene, partial cds
3944	16972	29855	2.01	0.0E+00	AI684727.1	EST_HUMAN	wk01601.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340
3945	16973	29856	1.34	0.0E+00	AL163248.2	NT	O43340 R28830_2, contains element PTR7 repetitive element;
3948	16976	29860	3.87	0.0E+00	4506742	NT	Homo sapiens chromosome 21 segment HS21C048
3951	16979	29863	1.68	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S6 (RP58), mRNA
3957	16985	29870	1.19	0.0E+00	6005987	NT	DKFZp434N0413.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0413 5'
3957	16985	29871	1.19	0.0E+00	6005987	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3959	16937	29873	3.54	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3961	16989		2.62	0.0E+00	4506078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3965	16923	29877	0.9	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3982	17010	29898	1.79	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3989	17016	29905	1.4	0.0E+00	BF355295.1	EST_HUMAN	RC3-H10860-170800-011-a12 H10860 Homo sapiens cDNA
3991	17018	29907	1.25	0.0E+00	AW898221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1998726 similar to MXRA5
3991	17018	29908	1.25	0.0E+00	AW898221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1998726 similar to MXRA5
3999	17026	29915	3.2	0.0E+00	AF129833.1	NT	Matrix remodeling associated gene 5
4002	17029	29918	1.12	0.0E+00	AW461306.1	EST_HUMAN	Homo sapiens F-box protein Fb3b (FBL3B) mRNA, partial cds
4003	17030	29919	1	0.0E+00	U86281.1	NT	U1-H-B13-ah-g-07-U1 s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2739949 3'
4003	17030	29920	1	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4007	17034	29924	4.98	0.0E+00	BE37802.1	EST_HUMAN	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4009	17036	29926	0.78	0.0E+00	BE313146.1	EST_HUMAN	60123696F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608900 5'
4017	17044	29934	1.13	0.0E+00	AW580740.1	EST_HUMAN	60116372F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3609743 5'
4053	17080	29964	0.72	0.0E+00	U10991.1	NT	PM3-L10031-100100-003-h09 L10031 Homo sapiens cDNA
4053	17080	29965	0.72	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4053	17080	29966	0.72	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4060	17086	29969	4.9	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4060	17086	29970	4.9	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4071	17097		3.41	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4073	17099		7.21	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4083	17108	29986	3.75	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4091	17116	29994	1.76	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4095	17120	29997	1.18	0.0E+00	S78653.1	NT	intra-mas-related [human, Genomic, 2416 nt]
4104	17129		9.34	0.0E+00	4603470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4111	17134	30009	0.99	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
4130	17152	30029	4.46	0.0E+00	AB015610.1	NT	Chlorococcus aestivus mRNA for ribosomal protein S4X, complete cds
4140	17151		4.72	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
4152	17173	30045	1.14	0.0E+00	AB002314.2	NT	Homo sapiens mRNA for KIAA0316 protein, partial cds
4153	17174	30046	1.43	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4154	17175	30047	1.85	0.0E+00	AJ272726.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4154	17175	30048	1.85	0.0E+00	AJ272726.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4160	17181	30053	8.32	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4160	17181	30054	8.32	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4172	17193	30085	0.7	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylamimidazole synthetase (GART) mRNA
4178	17198	30088	7.7	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21) mRNA
4179	17199	30069	1.38	0.0E+00	AB006825.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4183	17203	30071	7.82	0.0E+00	11419287	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
4184	17204	30072	2.05	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4185	17205		1.07	0.0E+00	AA018976.1	EST_HUMAN	ze55609.r1 Scores retina N2b-4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element;
4193	17213	30080	3.09	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4194	17214		0.98	0.0E+00	AW880878.1	EST_HUMAN	QV0-OT0033-070300-152-g12 OT0033 Homo sapiens cDNA
4201	18404	30085	1.05	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4205	14200	27137	0.92	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4205	14200	27138	0.92	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4211	17228	30085	1.28	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2) mRNA
4213	17230	30098	0.89	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA) mRNA
4213	17230	30099	0.89	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA) mRNA
4216	16639	29543	0.75	0.0E+00	4609884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
4218	17234	30102	1.19	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379) mRNA
4218	17234	30103	1.19	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379) mRNA
4224	17240	30107	0.77	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4232	17248	30116	5.7	0.0E+00	A1982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4232	17248	30117	5.7	0.0E+00	A1982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4234	17250	30119	0.95	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4234	17250	30120	0.95	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4238	17254		2.8	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987690 5'
4246	17262	30128	2.49	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3) mRNA
4253	17269		5.17	0.0E+00	AW675399.1	EST_HUMAN	ba5f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:TH12_BOVIN
4258	17274	30142	1.12	0.0E+00	AW408788.1	EST_HUMAN	Q85108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4259	17275	30143	2	0.0E+00	8922466	NT	UI-HF-BMO-adv-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083147 5'
4259	17275	30144	2	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4267	17283		2.23	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4280	17294	30160	1.26	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4288	17302	30169	13.81	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4288	17302	30169	13.81	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4288	17302	30170	13.81	0.0E+00	AA401438.1	EST_HUMAN	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4291	17305	30174	1.04	0.0E+00	AF157476.1	NT	Homo sapiens titin (TTN) mRNA
4303	17317	30184	1.01	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4303	17317	30185	1.01	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4321	17335	30188	1.12	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4321	17335	30189	1.12	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4330	17344		0.81	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4356	17370	30234	1.47	0.0E+00	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4372	17386	30250	11.78	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4377	17391	30254	1.1	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4377	17391	30255	1.1	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4385	17399	30287	0.72	0.0E+00	AW936689.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4393	16438	26342	0.97	0.0E+00	BE170039.1	EST_HUMAN	601484956F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
4398	17411	30277	5.52	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fb14 (FBL4) mRNA, partial cds
4406	17418	30282	0.88	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4406	17418	30283	0.88	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4407	17419		3.18	0.0E+00	A1189844.1	EST_HUMAN	qtd23106.x1 Soares placenta_8to9weeks_21NbHP8to9W Homo sapiens cDNA clone IMAGE:1724578 3'
4411	17422		5.96	0.0E+00	U14520.1	NT	similar to contains MER20 b2 MER20 repetitive element ;
4415	17426	30288	0.78	0.0E+00	5174574	NT	Human CBFA3 (Cbfa3) gene, partial cds
4425	17436	30296	1.18	0.0E+00	4503548	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
4432	17443	30303	0.67	0.0E+00	6863384	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
4432	17443	30304	0.67	0.0E+00	6863384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4439	17450	30310	1.11	0.0E+00	U10991.1	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4439	17450	30311	1.11	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4439	17450	30311	1.11	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4450	17460	30317	10.93	0.0E+00	8912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4468	17479		1.39	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4477	17488	30347	5.28	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4481	17492	30352	3.62	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4481	17492	30353	3.62	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4482	17493	30354	0.95	0.0E+00	AW166933.1	EST_HUMAN	xc88e10.x1 NCL CGAP Lit4 Homo sapiens cDNA clone IMAGE:2633514 3' similar to TR:P97365 P97365
4488	17499	30380	0.95	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 84;
4488	17499	30381	0.95	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4493	17503	30387	10.13	0.0E+00	7662091	NT	H. sapiens H4/d gene for H4 histone
4493	17503	30388	10.13	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4504	17514	30381	14.29	0.0E+00	4885128	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4505	17515	30382	0.93	0.0E+00	AJ271736.1	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4508	17518	30384	1.2	0.0E+00	AB037781.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4551	17560		6.89	0.0E+00	AF195953.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4558	17567	30425	1.22	0.0E+00	AJ249765.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4558	17567	30426	1.22	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4562	17570	30432	0.68	0.0E+00	W26178.1	EST_HUMAN	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4562	17570	30433	0.68	0.0E+00	W26178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4580	17588		1.97	0.0E+00	AF200629.1	NT	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4600	17608	30465	0.74	0.0E+00	T10233.1	EST_HUMAN	Homo sapiens HPS1 gene, intron 5
4600	17608	30468	0.74	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Co8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4622	17629	30483	3.15	0.0E+00	AW084994.1	EST_HUMAN	seq1329 b4HB3MA Co8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4624	18408		1.38	0.0E+00	8051619	NT	xc88e08.x1 NCL CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN Q08666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNK ;
4628	17632	30486	1.11	0.0E+00	AF016050.1	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4631	17637		11.42	0.0E+00	AL163207.2	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4639	17645	30509	0.97	0.0E+00	4758467	NT	Homo sapiens chromosome 21 segment HS21C007
4640	17646	30510	2.81	0.0E+00	AF108830.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4646	17652	30517	1.03	0.0E+00	AF111163.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4646	17652	30518	1.03	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4655	18407	30528	3.69	0.0E+00	6005973	NT	Homo sapiens pyrin (MEFV) gene, complete cds
							Homo sapiens zinc finger protein 195 (ZNF195), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4860	17695	30533	8.72	0.0E+00	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4865	17670	30540	1.35	0.0E+00	AF152337.1	NT	Homo sapiens probocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4878	17683	30551	4.97	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4886	17691	30558	0.8	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4890	17695	30561	1.31	0.0E+00	4503038	NT	Homo sapiens chondroin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4893	17698	30594	1.24	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4898	17703		3.12	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4700	17705	30597	14.56	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4700	17705	30588	14.56	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4712	17717	30579	1.16	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4715	17720	30582	13.35	0.0E+00	AJ245416.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4715	17720	30583	13.35	0.0E+00	AJ245416.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4737	17742		1.97	0.0E+00	AA174072.1	EST_HUMAN	zP18g08.61 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4739	17744		2.38	0.0E+00	7657410	NT	Homo sapiens cdz (odd Ozfien-m, Drosophila) homolog 1 (ODZ1), mRNA
4741	17746		2.91	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4742	17747	30607	5.13	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4743	17748		2.24	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4746	17760	30608	1.12	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4751	17756	30616	1.08	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4753	17758	30618	4.94	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4753	17758	30619	4.94	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4754	17759	30620	1.01	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4754	17759	30621	1.01	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4763	17768	30632	0.99	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4763	17768	30633	0.99	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4769	17774	30641	23.91	0.0E+00	Y18930.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4777	17782	30652	1	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-180400-142-H05 BT0635 Homo sapiens cDNA
4782	17787		2.09	0.0E+00	AF086841.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4790	17794	30661	2.6	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4790	17794	30662	2.6	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4791	17795	30663	1.81	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4796	17799	30666	2.27	0.0E+00	8453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4796	17799	30667	2.27	0.0E+00	8453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4797	13245	26163	1.04	0.0E+00	T56945.1	EST_HUMAN	ye83g04.r2 Stragene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
4797	13245	26164	1.04	0.0E+00	T56945.1	EST_HUMAN	ye83g04.r2 Stragene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
4804	17805	30671	0.77	0.0E+00	BE900050.1	EST_HUMAN	601285245F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5'
4821	17822	30691	1.11	0.0E+00	U56651.1	NT	Mus musculus neurophilin 1 (Nph1) gene, large exon and 3' end of the intron, and partial cds
4826	17827	30695	9.22	0.0E+00	M80802.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
4829	17830	30698	88.34	0.0E+00	M69197.1	NT	Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
4829	17830	30699	88.34	0.0E+00	M69197.1	NT	Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
4833	17834	30704	1.08	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4836	17837	30706	1.85	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4847	17848	30716	1.06	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4855	17857	30735	1.02	0.0E+00	X58467.1	NT	Human GYP2D7AP pseudogene for cytochrome P450 2D6
4872	17871	30738	1.69	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4875	17874	30738	0.97	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4876	17874	30739	0.97	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4877	17876	30741	0.86	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (ADO13), mRNA
4877	17876	30742	0.86	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (ADO13), mRNA
4898	17897	30762	1.51	0.0E+00	AW444637.1	EST_HUMAN	UJ-H-B13-ajw-o-04-0-UJ.e1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2733294 3'
4904	17903	30772	1.57	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4908	17907		1.84	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4956	17954		4.74	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4959	17957	30815	1.02	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4960	17958	30816	1.94	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4962	17960	30818	3.08	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4964	17962	30820	0.98	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA
4968	17968	30825	1.78	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4972	17970	30829	1.69	0.0E+00	M84081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J81 segments; and Tcr-C-alpha gene, exons 1-4

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4972	17970	30830	1.69	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1- J61 segments; and Tcr-C-alpha gene, exons 1-4
4973	17971	30831	1.67	0.0E+00	X94628.1	NT	H sapiens MeCP-2 gene
4973	17971	30832	1.67	0.0E+00	X94628.1	NT	H sapiens MeCP-2 gene
4976	17974	30835	2.35	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4977	17975	30836	0.88	0.0E+00	7706604	NT	Homo sapiens MAGE-C2 (MAGEC2), mRNA
4995	17894	30851	0.99	0.0E+00	X92841.1	NT	H sapiens MICA gene
4996	17895	30852	0.66	0.0E+00	AB037864.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4997	17896	30853	1.78	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4998	17897	30854	2.41	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
4999	17898	30855	1	0.0E+00	5174560	NT	Homo sapiens meninoma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
5001	18000	30857	1.93	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP), mRNA
5003	18002	30859	1.57	0.0E+00	5174560	NT	Homo sapiens meninoma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
5003	18002	30860	1.57	0.0E+00	5174560	NT	Homo sapiens meninoma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
5004	18003		3.03	0.0E+00	AJ010442.1	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, therad 7
5008	18006	30865	7.51	0.0E+00	AF050066.1	NT	Homo sapiens MHC class 1 region
5010	18008		2.19	0.0E+00	4505508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1), mRNA
5011	18009	30868	3.47	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
5020	18017	30876	0.98	0.0E+00	4507720	NT	Homo sapiens titin (TTN), mRNA
5023	18020	30879	1.15	0.0E+00	D63562.1	NT	Homo sapiens COL4A6 gene for ad(V) collagen, exon 44 and partial cds
5026	18023	30881	1.77	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FPPS), mRNA
5032	18029		1.01	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5046	18043	30889	1.02	0.0E+00	4504082	NT	Homo sapiens glypican 4 (GPC4), mRNA
5046	18043	30890	1.02	0.0E+00	4504082	NT	Homo sapiens glypican 4 (GPC4), mRNA
5068	18065	30915	1.66	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5070	18076	30925	0.77	0.0E+00	AA205437.1	EST_HUMAN	zq66506.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:646547 3'
5085	18082	30931	1.27	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
5085	18082	30932	1.27	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
5093	18090		6.04	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
5104	18101	30949	1.07	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5106	18103		3.93	0.0E+00	BE408863.1	EST_HUMAN	501303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
5109	18108	30953	4.94	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP), mRNA
5116	18113	30957	1.28	0.0E+00	AB028366.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5130	18128	30867	1.98	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5130	18128	30868	1.98	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5149	18143	30988	0.86	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5149	18143	30989	0.86	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5149	18143	30990	0.86	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5168	18160		1.04	0.0E+00	4758228	NT	Homo sapiens E2F transcription factor 2 (E2F2), mRNA
5180	18172	31017	0.71	0.0E+00	U53588.1	NT	Homo sapiens MHC class 1 region
5187	18179		1.6	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5193	18185		1.1	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5208	17317	30184	1.34	0.0E+00	4507720	NT	Homo sapiens titin (TTN), mRNA
5208	17317	30185	1.34	0.0E+00	4507720	NT	Homo sapiens titin (TTN), mRNA
5220	18210	31056	3.95	0.0E+00	X52988.1	NT	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)
5234	18222	31071	0.88	0.0E+00	AF272683.1	NT	Homo sapiens gephyrin mRNA, complete cds
5243	18230	31080	1.01	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP), mRNA
5266	18252	31102	0.97	0.0E+00	7657193	NT	Homo sapiens hypothetical protein (HS747E2A), mRNA
5277	18263	31113	0.7	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5289	18275	31123	0.87	0.0E+00	8923822	NT	Homo sapiens solute carrier family 5 (inositol transporters), member 3 (SLC5A3), mRNA
5305	18289	31141	1.4	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5305	18289	31142	1.4	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5307	18291	31144	0.7	0.0E+00	7708245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5307	18291	31145	0.7	0.0E+00	7708245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5308	18292	31146	1.03	0.0E+00	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5318	18302	31152	5.68	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
5329	18313	31162	6.24	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
5341	18324	31173	1.01	0.0E+00	AE000327.1	NT	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome
5351	18334	31182	5.95	0.0E+00	4502152	NT	Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB), mRNA
5385	18367	31205	0.92	0.0E+00	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSBEC05 6
5386	18367	31206	0.92	0.0E+00	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSBEC05 5
5390	18372	31211	1.09	0.0E+00	AA526781.1	EST_HUMAN	no156107.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980845
5390	18372	31212	1.09	0.0E+00	AA526781.1	EST_HUMAN	no156107.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980845
5422	18419		3.4	0.0E+00	AF093093.1	NT	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15

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5433	18515	31239	2.27	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5433	18515	31240	2.27	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cde
5456	18537	31378	1.49	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCI_OGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
5459	18540	31382	1.04	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDH13), mRNA
5474	18555	31397	3.9	0.0E+00	BE681080.1	EST_HUMAN	RC3-GN0078-310800-013-b03 GN0076 Homo sapiens cDNA
5478	18559	31401	3.28	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5478	18559	31402	3.28	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5486	18586	31411	5.31	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5486	18586	31412	5.31	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5568	18646	31524	5.83	0.0E+00	BE675498.1	EST_HUMAN	7f10c06.x1 NCI_OGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5569	18647	31525	1.55	0.0E+00	BE220753.1	EST_HUMAN	h59a02.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165184 3' similar to SW:Y054_HUMAN
5570	18648	31526	1.4	0.0E+00	BE794412.1	EST_HUMAN	P42894 HYPOTHETICAL PROTEIN KIAA0054. ;
5570	18648	31527	1.4	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
							601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5571	18649	31528	0.88	0.0E+00	AI189142.1	EST_HUMAN	qd04a04.x1 Soares_placenta_86weeks_2NbhP8c9w Homo sapiens cDNA clone IMAGE:1722702 3' similar to SW:T2D3_DROME P49846 TRANSCRIPTION INITIATION FACTOR TFIIID 86 KD SUBUNIT ;
5575	18653	31531	5.19	0.0E+00	M29808.1	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5578	18657	31534	0.48	0.0E+00	AI781363.1	EST_HUMAN	ch68a09.y6 NCI_OGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:IM18512 IG
5589	25630	31542	4.46	0.0E+00	11421038	NT	HEAVY CHAIN PRECURSOR V-J REGION (HUMAN);
5599	18675		2.83	0.0E+00	BF665962.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4), mRNA
5600	18676	31553	0.89	0.0E+00	AU134408.1	EST_HUMAN	602118928F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4276254 5'
5600	18676	31554	0.89	0.0E+00	AU134408.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5608	18682	31561	0.55	0.0E+00	BE538867.1	EST_HUMAN	AU134408 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5615	18691	31586	1.33	0.0E+00	BE262784.1	EST_HUMAN	601081489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5620	18696	31592	1.53	0.0E+00	BF526328.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5'
5620	18696	31593	1.53	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_OGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5639	20167	33406	1.24	0.0E+00	4557364	NT	602071372F1 NCI_OGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5642	18717	31619	0.88	0.0E+00	AB007935.1	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5642	18717	31620	0.88	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5647	18721	31625	4.44	0.0E+00	AF267737.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5647	18721	31626	4.44	0.0E+00	AF267737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5661	18735	31642	1.19	0.0E+00	D26535.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
							Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)

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5661	18735	31643	1.19	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5677	18751	31673	1.94	0.0E+00	11420819	NT	Homo sapiens cDNA clone IMAGE:4179988 5'
5683	18758	31679	0.94	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin
5703	18776	31704	0.91	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5703	18776	31705	0.91	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5708	18779	31709	2.72	0.0E+00	BF529931.1	EST_HUMAN	602042322F1 NCI CGAP_Brn07 Homo sapiens cDNA clone IMAGE:4179988 5'
5706	18779	31710	2.72	0.0E+00	BF529931.1	EST_HUMAN	602042322F1 NCI CGAP_Brn07 Homo sapiens cDNA clone IMAGE:4179988 5'
5711	18784	31714	2.33	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5722	18795	31887	4.47	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5738	18811	31905	0.47	0.0E+00	A928181.1	EST_HUMAN	w095602.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054
5738	18811	31906	0.47	0.0E+00	A928181.1	EST_HUMAN	w095602.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:O75054
5756	18829	31929	1.12	0.0E+00	BE260777.1	EST_HUMAN	O75054 KIAA0466 PROTEIN ;
5765	18838		2.12	0.0E+00	AW867316.1	EST_HUMAN	601150252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502809 5'
5781	18853	31958	3.04	0.0E+00	BE292868.1	EST_HUMAN	MR0-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5781	18853	31959	3.04	0.0E+00	BE292868.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5802	18874	31981	1.75	0.0E+00	11420819	NT	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5802	18874	31982	1.75	0.0E+00	11420819	NT	Homo sapiens cDNA clone IMAGE:2987903 5'
5810	18882	31990	4.45	0.0E+00	AF064254.1	NT	Homo sapiens cDNA clone IMAGE:2987903 5'
5810	18882	31991	4.45	0.0E+00	AF064254.1	NT	Homo sapiens cDNA clone IMAGE:2987903 5'
5817	18889	32001	2.83	0.0E+00	AJ224639.1	NT	Homo sapiens cDNA clone IMAGE:2987903 5'
5817	18889	32002	2.83	0.0E+00	AJ224639.1	NT	Homo sapiens cDNA clone IMAGE:2987903 5'
5849	18920	32034	0.63	0.0E+00	A1198513.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1757730 3'
5853	18924	32040	5.89	0.0E+00	M85719.1	EST_HUMAN	qf04gt10.x1 Sceres placenta_8to9weeks_2NhpHP8to9w Homo sapiens cDNA clone IMAGE:1757730 3'
5860	18931	32049	7.56	0.0E+00	AW405472.1	EST_HUMAN	similar to SW:CADDC_HUMAN P95289 BRAIN-CADHERIN PRECURSOR ;
5873	18943	32059	1.31	0.0E+00	Z28269.1	NT	EST02238 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCM48
5885	18954	32069	1.78	0.0E+00	AW361877.1	EST_HUMAN	U1HF-BLC-ech-4-02-0-U1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5885	18954	32070	1.78	0.0E+00	AW361877.1	EST_HUMAN	H. sapiens isoform 1 gene for L-type calcium channel, exon 14 adnd 15
5885	18954	32071	1.78	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5888	18957	32074	0.58	0.0E+00	AB035268.1	NT	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5888	18957	32074	0.58	0.0E+00	AB035268.1	NT	Homo sapiens mRNA for neurexin II, complete cds

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5988	18957	32075	0.58	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neuroligin II, complete cds
5990	18959	32078	1.97	0.0E+00	U36261.1	NT	Human beta-prime-adeptin (BAM22) gene, exon 13
5924	18991	32110	0.77	0.0E+00	AB040861.1	NT	Homo sapiens mRNA for KIAA1641 protein, partial cds
5946	19013	32133	0.6	0.0E+00	AI114826.1	EST_HUMAN	HA1435 Human fetal liver cDNA library Homo sapiens cDNA
5987	19052	32177	0.47	0.0E+00	AA195805.1	EST_HUMAN	zp95b11.r1 Stratiene muscle 937209 Homo sapiens cDNA clone IMAGE:627833 5' similar to gb:X03740
5988	19053	32178	1.49	0.0E+00	AJ006345.1	NT	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); Homo sapiens KVLQ11 gene
5988	19063	32179	1.49	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQ11 gene
5996	19061	32189	1.24	0.0E+00	AI207616.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
6018	19080	32206	4.16	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
6023	19085	32209	1.24	0.0E+00	BE791173.1	EST_HUMAN	601584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938551 5'
6033	19095	32222	1.27	0.0E+00	9998943	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
6034	19096	32223	7.12	0.0E+00	BE600082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
6035	19097	32224	1.26	0.0E+00	10048478	NT	Mus musculus ezrin (Ac2), mRNA
6036	19098	32225	2.63	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
6036	19098	32226	2.63	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
6056	19118	32247	2.56	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCI CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4184321 5'
6060	19122	32250	1.03	0.0E+00	AF142621.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
6061	19123	32251	3.64	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
6073	19134	32268	0.91	0.0E+00	BE503098.1	EST_HUMAN	h283df11.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q62084 Q62084
6078	19139	32275	2.41	0.0E+00	BF669905.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING;
6083	19144	32279	0.95	0.0E+00	AA454942.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6119	19178	32313	2.44	0.0E+00	AF217289.1	NT	z89406.s1 Soares_NihMPu_ST Homo sapiens cDNA clone IMAGE:811883 3'
6121	19180	32315	2.06	0.0E+00	BE928744.1	EST_HUMAN	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6126	19185	32320	1.12	0.0E+00	BE958636.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
6132	19191	32328	0.5	0.0E+00	AJ289880.1	NT	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
6145	19204	32341	0.45	0.0E+00	BE673986.1	EST_HUMAN	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
6145	19204	32342	0.45	0.0E+00	BE673986.1	EST_HUMAN	7d72et11.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN
6145	19204	32342	0.45	0.0E+00	BE673986.1	EST_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1. [1]; 7d72et11.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6150	19209	32348	0.78	0.0E+00	AW276780.1	EST_HUMAN	xp6503.x1 NCL CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335
6162	19219	32362	2.16	0.0E+00	BF031742.1	EST_HUMAN	GUANYLATE KINASE ASSOCIATED PROTEIN 1 ;
6162	19219	32363	2.16	0.0E+00	BF031742.1	EST_HUMAN	601559060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6174	19231	32378	1.51	0.0E+00	AW470846.1	EST_HUMAN	601559060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6188	19245	32390	1.04	0.0E+00	BF155670.1	EST_HUMAN	ha34d08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q9Z1N3
6188	19245	32391	1.04	0.0E+00	BF155670.1	EST_HUMAN	Q9Z1N3 MYOSIN-RHOGAP PROTEIN, MYR 7 ;
6196	19252	32397	1.35	0.0E+00	W33069.1	EST_HUMAN	QV4-HT0894-290900-399-a10 HT0894 Homo sapiens cDNA
6198	19252	32398	1.35	0.0E+00	W33069.1	EST_HUMAN	QV4-HT0894-290900-399-a10 HT0894 Homo sapiens cDNA
6197	19253	32404	2.23	0.0E+00	AF012618.1	NT	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321765 6'
6201	19257	32404	2.79	0.0E+00	BE280197.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321765 5'
6208	19263	32413	2.4	0.0E+00	BE889610.1	EST_HUMAN	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
6210	19265	32416	0.54	0.0E+00	BE388673.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3503323 5'
6226	19281	32436	0.66	0.0E+00	AW752848.1	EST_HUMAN	601612630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3514238 5'
6229	19283	32438	1.47	0.0E+00	11433071	NT	601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613085 5'
6229	19283	32439	1.47	0.0E+00	11433071	NT	IL3-CT0220-11199-028-E04 CT0220 Homo sapiens cDNA
6230	19284	32440	1.09	0.0E+00	BE901608.1	EST_HUMAN	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6230	19284	32441	1.09	0.0E+00	BE901608.1	EST_HUMAN	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6230	19284	32442	1.09	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6246	25644	32459	10.74	0.0E+00	9789998	NT	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6249	19302	32462	1.3	0.0E+00	AA193506.1	EST_HUMAN	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6249	19302	32463	1.3	0.0E+00	AA193506.1	EST_HUMAN	z40h01.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to
6272	19323	32488	12.56	0.0E+00	U34625.1	NT	SW:YY05 HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5 ;
6272	19323	32489	12.56	0.0E+00	U34625.1	NT	z40h01.r1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to
6274	19325	32491	0.41	0.0E+00	AW853983.1	EST_HUMAN	SW:YY05 HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5 ;
6274	19325	32492	0.41	0.0E+00	AW853983.1	EST_HUMAN	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6316	19365	32535	1.07	0.0E+00	BE258330.1	EST_HUMAN	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6325	19375	32543	4.4	0.0E+00	BE156561.1	EST_HUMAN	RC3-CT0254-110300-027-a09 CT0254 Homo sapiens cDNA
6335	19385	32553	0.49	0.0E+00	M38107.1	NT	RC3-CT0254-110300-027-a09 CT0254 Homo sapiens cDNA
6371	19420	32586	1.44	0.0E+00	BE379007.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355565 5'
							QV0-HT0369-090200-099-e09 HT0369 Homo sapiens cDNA
							Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
							601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6377	19426	32592	1.31	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6399	19447	32618	3.48	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
6428	19475	32650	4.17	0.0E+00	AA204740.1	EST_HUMAN	zq81c03.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648005 5' similar to
6429	19476	32651	3.87	0.0E+00	11545913	NT	TR-6854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6429	19476	32652	3.87	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6450	19498	32671	0.94	0.0E+00	U07223.1	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6468	19513	32688	1.91	0.0E+00	11426367	NT	Human beta2-chimaerin mRNA, complete cds
6472	19517	32693	3.71	0.0E+00	BE287173.1	EST_HUMAN	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6489	19533		0.79	0.0E+00	A1686048.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6493	19537	32714	1.55	0.0E+00	L36830.1	NT	h91f10.x1 NCL_CGAP_P-28 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839
6502	19548	32722	1.07	0.0E+00	BE797365.1	EST_HUMAN	MI-2 PROTEIN ;
6502	19548	32723	1.07	0.0E+00	BE797365.1	EST_HUMAN	Human anion exchanger (AE1) gene, exons 1-20
6514	19558	32739	0.54	0.0E+00	A198025.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6514	19558	32740	0.54	0.0E+00	A198025.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6517	19561	32742	1.21	0.0E+00	BF387123.1	EST_HUMAN	q150b11.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12838
6525	19569	32752	1.81	0.0E+00	11435630	NT	TFIIIC ALPHA SUBUNIT ;
6535	19579	32761	0.75	0.0E+00	D55649.1	NT	TFIIIC ALPHA SUBUNIT ;
6554	19596	32784	1.16	0.0E+00	AW178142.1	EST_HUMAN	MRQ-HT0923-220800-102-b05 HT0923 Homo sapiens cDNA
6575	19615	32801	0.7	0.0E+00	BE674544.1	EST_HUMAN	Homo sapiens peptide transporter 3 (LOC51296), mRNA
6581	19622	32807	1.08	0.0E+00	7682039	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6595	19636		6.88	0.0E+00	AV650020.1	EST_HUMAN	IL3-HT0062-010999-014-A04 HT0062 Homo sapiens cDNA
6604	19645	32828	3.62	0.0E+00	AW575998.1	EST_HUMAN	Q14681 HYPOTHETICAL PROTEIN KIAA0176 ;
6607	19648	32831	5.76	0.0E+00	H01255.1	EST_HUMAN	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6617	19658	32842	0.59	0.0E+00	11426293	NT	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'
6622	19662	32847	1.89	0.0E+00	X15377.1	NT	UHF-BLD-eco-g-12-0-J1.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3056751 3'
6624	19664	32849	0.71	0.0E+00	AA455375.1	EST_HUMAN	UHF-BLD-eco-g-12-0-J1.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3056751 3'
6625	19665	32850	1.09	0.0E+00	A1612841.1	EST_HUMAN	W27003.r1 Soares placenta N121P Homo sapiens cDNA clone IMAGE:148933 5'
6631	19671	32856	4.46	0.0E+00	BE735989.1	EST_HUMAN	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
							Human gene for the light and heavy chains of myeloperoxidase
							aa14e07.r1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:813262 5'
							tz57d08.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292887 3' similar to SW:NTCS_HUMAN
							P53796 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
							601305369F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3639616 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6631	19671	32857	4.46	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639816 5'
6635	19675	32863	0.84	0.0E+00	AW748596.1	EST_HUMAN	MRO-BT0284-221189-002-f11 BT0284 Homo sapiens cDNA
6636	19676	32864	0.84	0.0E+00	AW748596.1	EST_HUMAN	MRO-BT0284-221189-002-f11 BT0284 Homo sapiens cDNA
6638	19678	32866	129.09	0.0E+00	AU119245.1	EST_HUMAN	Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
6638	19678	32867	129.09	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6643	19682	32873	0.69	0.0E+00	BE760483.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6644	19683	32874	1.07	0.0E+00	X92217.1	NT	H. sapiens geminine immunoglobulin heavy chain, variable region, (13-2)
6662	19700	32898	1.94	0.0E+00	AJ989483.1	EST_HUMAN	ws25c07.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2498220 3'
6677	19714	32908	2.55	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887983 5'
6677	19714	32910	2.55	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887983 5'
6711	19747	32950	0.53	0.0E+00	BE867657.1	EST_HUMAN	601443175F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3847291 5'
6717	19753	32959	0.46	0.0E+00	BF057438.1	EST_HUMAN	7k43h05.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3478496 3' similar to TR:O14553 O14553 R31240.1;
6764	19788	33001	1.48	0.0E+00	AW408348.1	EST_HUMAN	UI-HF-BL0-eco-h-02-0-J1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
6754	19788	33002	1.48	0.0E+00	AW408348.1	EST_HUMAN	UI-HF-BL0-eco-h-02-0-J1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
6789	19822	33034	15.78	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLG Homo sapiens cDNA clone GLCEHC06 5'
6798	19831	33041	0.8	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6798	19831	33042	0.8	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6801	19834	33045	2.53	0.0E+00	AF190860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
6804	19837	33048	0.47	0.0E+00	L48548.1	NT	Homo sapiens tuberin (TSC2) gene, exons 38, 39, 40 and 41
6806	19839	33049	1.14	0.0E+00	11420558	NT	Homo sapiens transcription/transcription domain-associated protein (TRRAP), mRNA
6813	19846	33056	4.34	0.0E+00	AW163640.1	EST_HUMAN	TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;
6813	19846	33057	4.34	0.0E+00	AW163640.1	EST_HUMAN	TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;
6817	19850	33060	1.07	0.0E+00	W37163.1	EST_HUMAN	SW_ZN45 HUMAN Q02386 ZINC FINGER PROTEIN 45 ;
6817	19850	33061	1.07	0.0E+00	W37163.1	EST_HUMAN	Zb20e06.r1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to
6835	19857	33081	1.3	0.0E+00	BE794853.1	EST_HUMAN	SW_ZN45 HUMAN Q02386 ZINC FINGER PROTEIN 45 ;
6842	19874	33088	4.78	0.0E+00	BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6843	19875	33089	0.79	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6843	19875	33090	0.79	0.0E+00	BE767955.1	EST_HUMAN	QV1-GN0065-140800-318-H02 GN0065 Homo sapiens cDNA
6847	19879	33093	7.27	0.0E+00	BE889813.1	EST_HUMAN	60151208F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6847	19879	33094	7.27	0.0E+00	BE889813.1	EST_HUMAN	60151208F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6857	19890	33103	3.58	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6862	19894	33107	2.53	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6862	19894	33108	2.53	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6868	19900	33115	3.77	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6872	19903	33118	4.2	0.0E+00	A1638412.1	EST_HUMAN	t31f11.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
6874	19905	33120	1.71	0.0E+00	L32832.1	NT	P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR ;
6887	19917	33133	0.72	0.0E+00	AW505430.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
6889	19919	33134	4.43	0.0E+00	AA434584.1	EST_HUMAN	UI-HF-BN0-ama-c-01-0-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6904	19934	33158	1.1	0.0E+00	BF217200.1	EST_HUMAN	zw52c03.r1 Soares, total, fetus_Nb2-HF8 9w Homo sapiens cDNA clone IMAGE:773668 5'
6909	19939	33159	1.88	0.0E+00	BE925875.1	EST_HUMAN	601865317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
6943	19972	33195	0.76	0.0E+00	11428758	NT	QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA
6943	19972	33196	0.76	0.0E+00	11428758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6944	19973	33198	0.52	0.0E+00	AJ230823.1	EST_HUMAN	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6945	19974	33198	0.51	0.0E+00	AW611984.1	EST_HUMAN	AJ230823 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D7 3'
6965	19993	33221	1.33	0.0E+00	AJ125928.1	EST_HUMAN	hg82e04.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2852126 3'
6967	19995	33223	0.63	0.0E+00	BE701434.1	EST_HUMAN	AL125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6967	19996	33224	0.63	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-H10 NN0174 Homo sapiens cDNA
6980	20017	33249	1.29	0.0E+00	BE142363.1	EST_HUMAN	PM2-NN0174-260700-001-H10 NN0174 Homo sapiens cDNA
7012	20039	33272	0.83	0.0E+00	BE006012.1	EST_HUMAN	GM0-HT0143-270989-062-d08 HT0143 Homo sapiens cDNA
7012	20039	33273	0.83	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
7041	20057	33301	7.63	0.0E+00	BE169131.1	EST_HUMAN	RCO-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
7043	20069	33303	1.48	0.0E+00	BF085667.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7083	20269	33548	3.09	0.0E+00	AA180755.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
7095	20301	33562	1.01	0.0E+00	U39673.1	NT	zp88e03.r1 Strategene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627282 5'
7099	20305	33564	0.77	0.0E+00	BE671987.1	EST_HUMAN	Human salivary peroxidase mRNA, complete cds
7111	20315	33578	6.63	0.0E+00	A1940821.1	EST_HUMAN	7a49b07.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285 TEKTN ;
7111	20315	33579	6.63	0.0E+00	A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
7111	20315	33579	6.63	0.0E+00	A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA

Single Exon Probes Expressed in Adult Liver

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7123	20327	33592	1.99	0.0E+00	11435626	NT	Homo sapiens CD6 antigen (CD6), mRNA
7137	20245	33497	0.91	0.0E+00	AL042443.1	EST_HUMAN	DKFZp434D2021_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2021 5'
7138	20246	33498	4.06	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
7141	20249	33501	0.84	0.0E+00	AI168270.1	EST_HUMAN	001001.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1565761 3' similar to
7146	20254	33506	0.91	0.0E+00	BE734087.1	EST_HUMAN	TRQ28823 Q28823 TEKIN C1.;
7171	18443	31312	1.18	0.0E+00	BE666381.1	EST_HUMAN	601567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
7181	18453	31322	13.52	0.0E+00	BE667889.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3882267 5'
7181	18453	31323	13.52	0.0E+00	BE667889.1	EST_HUMAN	601443687F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
7189	20189	33432	2.33	0.0E+00	BE550162.1	EST_HUMAN	601443687F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
7189	20189	33433	2.33	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
7203	20203	33448	0.55	0.0E+00	BF700780.1	EST_HUMAN	Q08379 GOLGIN-95.;
7217	20217	33464	1.43	0.0E+00	BF088376.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
7224	20223	33471	2.11	0.0E+00	AA195106.1	EST_HUMAN	Q08379 GOLGIN-95.;
7232	20141		11.86	0.0E+00	11034810	NT	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
7234	20143	33382	1.04	0.0E+00	11431474	NT	Q08379 GOLGIN-95.;
7250	20159	33398	2.57	0.0E+00	BF569905.1	EST_HUMAN	60218582F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7258	20167	33406	0.59	0.0E+00	4557364	NT	Homo sapiens Bloem syndrome (BLM) mRNA
7266	20175		1.94	0.0E+00	J03068.1	NT	Homo sapiens Bloem syndrome (BLM) mRNA
7276	20229	33477	2.97	0.0E+00	AF217289.1	NT	Human MYC2 gene, complete cds
7276	20229	33478	2.97	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7277	20230	33479	0.88	0.0E+00	M38113.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7280	18459	31329	3.15	0.0E+00	11420775	NT	Human neurofibromatosis type 1 gene, exon x8
7291	18460	31330	0.58	0.0E+00	AI419889.1	EST_HUMAN	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7291	18460	31331	0.58	0.0E+00	AI419889.1	EST_HUMAN	ig53c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to
7296	18465	31335	0.88	0.0E+00	BE256708.1	EST_HUMAN	SW:OXYB_HUMAN P22069 OXYSTEROL-BINDING PROTEIN.;
7308	18476	31288	0.56	0.0E+00	BE904955.1	EST_HUMAN	ig53c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112490 3' similar to
							SW:OXYB_HUMAN P22069 OXYSTEROL-BINDING PROTEIN.;
							601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3366330 5'
							601498743F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898739 5'

Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7310	18478	31300	0.42	0.0E+00	AI680911.1	EST_HUMAN	wf21c09.x1 Scores: Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74287 HOMEBOX PROTEIN HOX-A4 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element;
7310	18478	31301	0.42	0.0E+00	AI680911.1	EST_HUMAN	wf21c09.x1 Scores: Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74287 HOMEBOX PROTEIN HOX-A4 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element;
7321	18489	31261	1.18	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003679 5'
7324	18492	31265	5.41	0.0E+00	BE262941.1	EST_HUMAN	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'
7325	18493	31266	2.62	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7325	18493	31267	2.62	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7326	18494	31268	2.7	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 8 (DNAH9) mRNA, complete cds
7326	18494	31269	2.7	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7333	18501	31276	1.35	0.0E+00	AF310103.1	NT	Homo sapiens NALP1 mRNA, complete cds
7335	18503	31278	0.71	0.0E+00	BF130916.1	EST_HUMAN	601819722F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4051709 5'
7340	20336	33601	0.64	0.0E+00	BE762770.1	EST_HUMAN	QV3-NT0022-140600-223-01 NT0022 Homo sapiens cDNA
7346	20342	33608	2.33	0.0E+00	BF669005.1	EST_HUMAN	602165832F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7348	20344	33610	0.66	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7348	20344	33611	0.56	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7352	20348	33616	3.51	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7357	20352	33620	0.62	0.0E+00	AW502362.1	EST_HUMAN	UI-HF-BR0p-eka-d-10-Q-UI-1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7357	20352	33621	0.62	0.0E+00	AW502362.1	EST_HUMAN	UI-HF-BR0p-eka-d-10-Q-UI-1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7367	20361	33630	1	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7367	20361	33631	1	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7377	20371	33640	5.86	0.0E+00	BF306966.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7383	20376	33645	2.24	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7427	20126	33365	0.94	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7433	20131	33372	0.47	0.0E+00	AW513068.1	EST_HUMAN	xc40e02.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2706458 3' similar to TR:094895 094895 KIAA0803 PROTEIN;
7467	20407	33683	0.64	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7467	20407	33684	0.64	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7472	20412	33680	0.8	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7472	20412	33681	0.8	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7478	20418	33687	1.4	0.0E+00	AW954806.1	EST_HUMAN	EST366876 IMAGE resequences, MAGC Homo sapiens cDNA

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7479	20419	33698	1.08	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354568 5'
7493	20433	33712	1.27	0.0E+00	LO1973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7501	20440	33722	0.71	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7501	20440	33723	0.71	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7507	20448	33730	2.19	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001558 5'
7524	20463	33751	0.86	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7528	20465	33763	0.42	0.0E+00	AA312125.1	EST_HUMAN	EST182818 Jurkat T-cells VI Homo sapiens cDNA 5' end
7532	20471	33760	2.81	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
7533	20472	33760	0.82	0.0E+00	4758839	NT	Homo sapiens netrin 1 (NTN1), mRNA
7543	20482	33770	1.24	0.0E+00	BE891289.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7543	20482	33771	1.24	0.0E+00	BE891289.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7566	18515	31239	2.46	0.0E+00	AF137285.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7566	18515	31240	2.46	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7578	20514	33801	0.68	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7578	20514	33802	0.66	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7591	20527	33816	4.25	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7591	20527	33817	4.26	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7606	20541	33831	0.52	0.0E+00	AF227744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform ae (CACNA1G) mRNA, complete cds
7628	20553	33856	36.3	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NBHP808W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51889 ARYL SULFATASE D PRECURSOR ;contains element HGR repetitive element;
7628	20553	33856	36.3	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NBHP808W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51889 ARYL SULFATASE D PRECURSOR ;contains element HGR repetitive element;
7628	20563	33857	36.3	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NBHP808W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51889 ARYL SULFATASE D PRECURSOR ;contains element HGR repetitive element;
7631	20566	33860	0.56	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7631	20566	33861	0.56	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7634	20569	33864	3.46	0.0E+00	11428392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7634	20569	33865	3.46	0.0E+00	11428392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7638	20573		13.17	0.0E+00	BF337375.1	EST_HUMAN	602035069F1 NCI_CGAP_Brim4 Homo sapiens cDNA clone IMAGE:4162899 5'
7641	20576	33870	2.93	0.0E+00	AA128463.1	EST_HUMAN	zn60f09.r1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G809582 G809582 NEBULIN ;
7646	20580	33876	2.2	0.0E+00	AL078497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7646	20580	33877	2.2	0.0E+00	AL078497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7657	20591	33989	0.6	0.0E+00	AJ270936.1	NT	Homo sapiens partial mRNA for LTRPC5 protein (LTPC5 gene)
7692	20624	33924	1.16	0.0E+00	BE295499.1	EST_HUMAN	601174578F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794 5'
7694	20626	33925	0.87	0.0E+00	11427965	NT	Homo sapiens hypothetical protein (FLJ20281), mRNA
7697	20629		2.81	0.0E+00	AU118607.1	EST_HUMAN	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003989 5'
7698	20630	33928	2.12	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7698	20630	33928	2.12	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7710	20642	33939	0.83	0.0E+00	AF245505.1	NT	Homo sapiens adiccan mRNA, complete cds
7718	20650	33944	14.21	0.0E+00	X70172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7720	20652	33948	9.51	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7720	20652	33947	9.51	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7734	20665	33963	0.88	0.0E+00	AW956503.1	EST_HUMAN	EST368573 IMAGE resequences, MAGD Homo sapiens cDNA
7736	20668	33965	0.84	0.0E+00	BE072445.1	EST_HUMAN	7a60h08.x1 NCL CGAP GC6 Homo sapiens cDNA clone IMAGE:3223167 3' similar to gb:M54911_mai1 IG
7737	20669	33968	2.27	0.0E+00	AW950516.1	EST_HUMAN	HEAVY CHAIN PRECURSOR V-II REGION (HUMAN);
7766	20698	33995	0.88	0.0E+00	AF001543.1	EST_HUMAN	EST392588 IMAGE resequences, MAGA Homo sapiens cDNA
7766	20698	33996	0.88	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7766	20698	33997	0.88	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7791	20720		0.88	0.0E+00	M80354.1	NT	Human BTF3 protein homologue gene, complete cds
7792	20721	34024	0.59	0.0E+00	BE408293.1	EST_HUMAN	601302679F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7804	20733	34035	0.6	0.0E+00	AW402542.1	EST_HUMAN	UHF-BKO-aas-g-07-0-UJ.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054924 5'
7823	20762		1.04	0.0E+00	R87430.1	EST_HUMAN	ym88h10.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:166051 5'
							x039a06.y1 NCL CGAP Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050
7824	20753	34058	1.68	0.0E+00	AW238328.1	EST_HUMAN	HNF3/FH TRANSCRIPTION FACTOR GENESIS;
7846	20773		1.37	0.0E+00	AU117553.1	EST_HUMAN	UHF-BKO-aas-g-07-0-UJ.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:166051 5'
7848	20775	34076	4.38	0.0E+00	11427135	NT	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7870	20797	34100	0.54	0.0E+00	AA211683.1	EST_HUMAN	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7878	20804	34107	0.83	0.0E+00	BF229235.1	EST_HUMAN	z15602.r1 Stralagene muscle 937208 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740
7883	20809	34115	0.92	0.0E+00	AW405627.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7889	20815	34121	0.88	0.0E+00	AW990499.1	EST_HUMAN	MRO-AN0083-270800-004-007 AN0083 Homo sapiens cDNA
7892	20818	34124	0.71	0.0E+00	L32832.1	NT	UHF-BKO-aas-g-07-0-UJ.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057489 5'
7919	20842	34145	0.79	0.0E+00	BF306998.1	EST_HUMAN	QV3-BN0048-220300-129-e04 BN0048 Homo sapiens cDNA
7919	20842	34146	0.79	0.0E+00	BF306998.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7929	20851	34158	1.35	0.0E+00	AU118767.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
							601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
							AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7884	20886	34187	0.53	0.0E+00	AW499551.1	EST_HUMAN	UI-HF-BRDP-ell-e-10-Q-UL1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074778 5'
7892	20910	34224	0.46	0.0E+00	AB002355.1	NT	Human mRNA for KIAA0357 gene, partial cds
7893	20911	34225	4.12	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7893	20911	34226	4.12	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
8065	20978	34283	0.53	0.0E+00	AA399959.1	EST_HUMAN	zu88b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743125 5'
8065	20978	34294	0.53	0.0E+00	AA399959.1	EST_HUMAN	zu88b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743125 5'
8066	20979	34295	0.68	0.0E+00	AL046347.2	EST_HUMAN	DKFZp434J087.r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434J087 5'
8083	20995	34314	1.14	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
8083	20995	34315	1.14	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
8084	20996	34316	0.42	0.0E+00	AI980099.1	EST_HUMAN	ws28b04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498576 3' similar to gb:M28668 CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR (HUMAN);
8092	21004	34327	1.01	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
8108	21018	34344	0.57	0.0E+00	BE439545.1	EST_HUMAN	HTM1-183F1 HTM1 Homo sapiens cDNA
8107	21019	34345	1.2	0.0E+00	11417942	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8123	21033	34361	0.49	0.0E+00	AW672785.1	EST_HUMAN	ba01e06.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823106 5' similar to SW:P101_PIG O02686 PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT ;
8123	21033	34362	0.49	0.0E+00	AW672785.1	EST_HUMAN	ba01e06.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823106 5' similar to SW:P101_PIG O02686 PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT ;
8139	21048	34378	0.68	0.0E+00	AI825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305978 3' similar to TR:O75363 O75363 AIBC1.;
8139	21048	34379	0.68	0.0E+00	AI825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305978 3' similar to TR:O75363 O75363 AIBC1.;
8148	21057	34380	2.62	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
8154	21061	34392	1.06	0.0E+00	N78126.1	EST_HUMAN	za86a05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289456 3'
8163	21070	34399	5.4	0.0E+00	BF217905.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
8168	21075	34405	0.46	0.0E+00	BF569862.1	EST_HUMAN	602185808F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310256 5'
8173	21080	34410	4.39	0.0E+00	AU129622.1	EST_HUMAN	AU128622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
8197	25685	34434	0.86	0.0E+00	AW068274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
8197	25685	34435	0.86	0.0E+00	AW068274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8201	21107	34437	6.76	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8208	21114	34444	0.97	0.0E+00	AV758467.1	EST_HUMAN	AV758467 BM Homo sapiens cDNA clone BMFBGG05 5'
8211	21116	34446	6.56	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8211	21116	34447	6.56	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8212	21117	34448	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8212	21117	34449	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8213	21118	34450	0.85	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
8213	21118	34451	0.85	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
8240	21145	34477	0.53	0.0E+00	BF590267.1	EST_HUMAN	nal22c04.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3263214 3' similar to contains element TAR1 repetitive element;
8254	21159	34492	1.58	0.0E+00	BE767610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
8254	21159	34493	1.58	0.0E+00	BE767610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
8287	21191	34528	0.47	0.0E+00	AI827216.1	EST_HUMAN	W09c07.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2424396 3' similar to TR:Q90808 Q90808 OLFACTORY RECEPTOR 4;
8295	21199	34535	0.63	0.0E+00	X92224.1	NT	H. sapiens germline immunoglobulin heavy chain, variable region, (6-1G1)
8298	21202	34538	0.56	0.0E+00	BE798034.1	EST_HUMAN	601305637F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640041 5'
8304	21208	34543	0.42	0.0E+00	AW402189.1	EST_HUMAN	UJHF-BKO-aat-c-07-0.U1.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054733 5'
8309	21213	34550	0.53	0.0E+00	AW955307.1	EST_HUMAN	EST368377 MAGE resequences, MAGD Homo sapiens cDNA
8317	21222		0.45	0.0E+00	BE503684.1	EST_HUMAN	7a31e04.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3220302 3' similar to gb:S67798 HYALLURONIDASE PRECURSOR (HUMAN);
8342	21247	34582	0.43	0.0E+00	Y16795.1	NT	Homo sapiens psbHba pseudogene
8350	21255	34590	0.51	0.0E+00	W52873.1	EST_HUMAN	zc90f10.1 Pancreatic islet Homo sapiens cDNA clone IMAGE:338443 5'
8351	21256	34591	0.75	0.0E+00	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (h. sapiens) (LOC83433), mRNA
8352	21257	34592	0.53	0.0E+00	AU117333.1	EST_HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001175 5'
8353	21258		0.43	0.0E+00	BE613963.1	EST_HUMAN	601504084F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905733 5'
8379	21283	34614	0.53	0.0E+00	AW668044.1	EST_HUMAN	EST360119 MAGE resequences, MAGJ Homo sapiens cDNA
8380	21284	34615	0.46	0.0E+00	AI133435.1	EST_HUMAN	HA2043 Human fetal liver cDNA library Homo sapiens cDNA
8389	21293	34625	0.46	0.0E+00	BE090733.1	EST_HUMAN	RC1-BT0721-050400-011-h05 BT0721 Homo sapiens cDNA
8403	21306	34637	0.44	0.0E+00	6965995	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8403	21306	34638	0.44	0.0E+00	6965995	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8405	21308	34840	0.51	0.0E+00	AW403220.1	EST_HUMAN	UI-HF-BK0-eay-h-04-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3055710 5'
8417	21320	34852	2.76	0.0E+00	AV707162.1	EST_HUMAN	AV707162 ADB Homo sapiens cDNA clone ADBCWED07 5'
8417	21320	34853	2.76	0.0E+00	AV707162.1	EST_HUMAN	AV707162 ADB Homo sapiens cDNA clone ADBCWED07 5'
8419	21322	34855	0.44	0.0E+00	AW403420.1	EST_HUMAN	UI-HF-BK0-abe-q-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3055068 5'
8438	21368	34709	0.67	0.0E+00	AU133187.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001807 5'
8479	21410		0.7	0.0E+00	BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
8491	21422	34761	0.76	0.0E+00	BE131013.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
8502	21433	34774	1.51	0.0E+00	AA149791.1	EST_HUMAN	z001c06.r1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:566410 5'
8515	21446	34788	0.88	0.0E+00	BF026628.1	EST_HUMAN	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
8544	21475	34817	2.47	0.0E+00	BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
8561	21492	34833	7.07	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8561	21492	34834	7.07	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8589	21620	34864	0.77	0.0E+00	AW674581.1	EST_HUMAN	bb34d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O84652
8589	21620	34865	0.77	0.0E+00	AW674581.1	EST_HUMAN	F17K2.26 PROTEIN. ;
8596	21527	34871	2.99	0.0E+00	AA397551.1	EST_HUMAN	z81804.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
8598	21529	34872	0.83	0.0E+00	AW387131.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
8600	21531		0.69	0.0E+00	AB020681.1	NT	MR0-ST0031-061099-003-at11 ST0031 Homo sapiens cDNA
8601	21532	34873	2.57	0.0E+00	AU142402.1	EST_HUMAN	Homo sapiens mRNA for KIA0884 protein, partial cds
8605	21536	34877	1	0.0E+00	BE388421.1	EST_HUMAN	AL142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
8605	21536	34878	1	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8619	21550	34891	0.53	0.0E+00	7657278	NT	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8621	21552	34893	0.9	0.0E+00	W95278.1	EST_HUMAN	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
8621	21552	34894	0.9	0.0E+00	W95278.1	EST_HUMAN	z005d01.r1 Soares fetal heart_Nb-H19W Homo sapiens cDNA clone IMAGE:358081 5'
8623	21554		6.23	0.0E+00	BF673066.1	EST_HUMAN	z005d01.r1 Soares fetal heart_Nb-H19W Homo sapiens cDNA clone IMAGE:358081 5'
8627	21558		0.53	0.0E+00	AU134114.1	EST_HUMAN	602163008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
8672	21603	34943	1.61	0.0E+00	AL120124.1	EST_HUMAN	AU134114 OVARC1 Homo sapiens cDNA clone OVARC1001296 5'
8672	21603	34944	1.61	0.0E+00	AL120124.1	EST_HUMAN	DKFZ761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8712	21643		1.18	0.0E+00	BE877693.1	EST_HUMAN	DKFZ761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8735	21665	35010	1.44	0.0E+00	AW500549.1	EST_HUMAN	601485254F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3887773 5'
							UI-HF-BNO-ak-f-01-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8743	21673	35016	13.09	0.0E+00	AW157233.1	EST_HUMAN	au03608.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
8760	21690	35033	0.83	0.0E+00	AW072395.1	EST_HUMAN	xa07d12.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2667639 3' similar to contains element OFR repetitive element;
8776	21708	35054	1.11	0.0E+00	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8781	21711	35057	0.64	0.0E+00	W01616.1	EST_HUMAN	za36d05.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:294633 5'
8782	21712	35058	1.29	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8782	21712	35059	1.29	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8785	21725	35073	1.61	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8831	21761	35107	0.56	0.0E+00	AJ367350.1	EST_HUMAN	q95c12.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN;
8843	21773	35120	2.89	0.0E+00	BE874157.1	EST_HUMAN	7d76d04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O95793 O95793 STAUFEN PROTEIN;
8845	21775	35122	1.34	0.0E+00	A188671.1	EST_HUMAN	w60b10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429276 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR;
8859	21789	35139	1.38	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8859	21789	35140	1.38	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8866	21796	35149	1.88	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8866	21796	35150	1.88	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8868	21798	35162	1.58	0.0E+00	AA403192.1	EST_HUMAN	z6602.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:766619 5' similar to TR:G1304132 G1304132 TPRD;
8868	21798	35153	1.58	0.0E+00	AA403192.1	EST_HUMAN	z6602.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:766619 5' similar to TR:G1304132 G1304132 TPRD;
8908	21836		6.06	0.0E+00	AA398511.1	EST_HUMAN	z173a08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727658 3' similar to gb:S85655 PROHIBITIN (HUMAN);
8916	21846	35201	0.85	0.0E+00	BE837593.1	EST_HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sapiens cDNA
8917	21847	35202	2.19	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8917	21847	35203	2.19	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8934	21864	35221	1.24	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8934	21864	35222	1.24	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8948	21878	35238	1.86	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8948	21878	35239	1.86	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8958	21898	35246	1.05	0.0E+00	A1884477.1	EST_HUMAN	wm33a11.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8965	21895	35252	0.83	0.0E+00	AA502284.1	EST_HUMAN	ne25d10.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1138434
8969	21899		0.72	0.0E+00	11418789	NT	G1138434 KIAA0187 PROTEIN. ;
8977	21907	35263	0.69	0.0E+00	AJ580780.1	EST_HUMAN	Homo sapiens proteodherin beta 3 (PCHB3), mRNA
8980	21910		2.13	0.0E+00	BE880797.1	EST_HUMAN	ta04f11.x1 Soares_pregnant_uterus NBHPU Homo sapiens cDNA clone IMAGE:2043117 3'
9004	21933	35288	0.65	0.0E+00	AW245765.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
9004	21933	35289	0.65	0.0E+00	AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
9005	21934	35290	2.12	0.0E+00	4768895	NT	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 6'
9005	21934	35291	2.12	0.0E+00	4759895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9008	21937	35293	0.54	0.0E+00	U88084.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9008	21937	35294	0.54	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
9073	22002	35356	0.73	0.0E+00	AJ251760.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
9077	22005	35360	1.01	0.0E+00	X98922.1	NT	Homo sapiens NESP55, GNAS1 antisense (partial) and XLalphas (partial) genes
9077	22005	35361	1.01	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
9077	22006	35362	1.01	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
9090	22019	35375	0.65	0.0E+00	U82879.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
9130	22058	35418	0.82	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9130	22058	35419	0.82	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9133	22061	35421	0.93	0.0E+00	AU131871.1	EST_HUMAN	AU131871 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
9147	22075	35437	0.62	0.0E+00	11426372	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
9150	22078		2.11	0.0E+00	AW513513.1	EST_HUMAN	xc48e01.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4
9152	22080		0.51	0.0E+00	BE783232.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
9153	22081	35439	2.82	0.0E+00	D52850.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02 5'
9182	22110	35469	4.47	0.0E+00	BE378495.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
9188	22116	35473	2.25	0.0E+00	AA410645.1	EST_HUMAN	2832e04.1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:724062 5'
9188	22117		2.14	0.0E+00	BF313946.1	EST_HUMAN	601800571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
9196	22124	35480	0.52	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
9201	22129	35485	1.45	0.0E+00	AW139673.1	EST_HUMAN	U1-H-B11-act-e-12-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
9201	22129	35486	1.45	0.0E+00	AW139673.1	EST_HUMAN	U1-H-B11-act-e-12-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
9232	22160	35515	0.55	0.0E+00	AL193301.2	NT	Homo sapiens chromosome 21, segment HS21C101
9238	22166	35519	2.36	0.0E+00	BE260272.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'

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9243	22171	35523	2.72	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
9243	22171	35524	2.72	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
9243	22171	35525	2.72	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
9257	22185	35541	0.31	0.0E+00	AI459722.1	EST_HUMAN	ik13h11.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150948 3'
9284	22212	35570	0.81	0.0E+00	AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
9291	22219	35578	11.94	0.0E+00	AA892527.1	EST_HUMAN	cr80g02.s1 NCJ_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S
9297	22225	35584	0.53	0.0E+00	10947037	NT	RIBOSOMAL PROTEIN L7A (HUMAN);
9297	22225	35585	0.53	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
9321	22249	35613	1.51	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
9323	22251	35615	1.64	0.0E+00	BE278917.1	EST_HUMAN	601156330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
9338	22261		2.66	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAAF11 5'
9339	22267	35630	1.86	0.0E+00	AW337277.1	EST_HUMAN	xy73e07.x1 NCJ_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587
9344	22272	35634	1.67	0.0E+00	AU124051.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
9421	22349	35714	0.85	0.0E+00	AU140704.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
9430	22358	35721	0.53	0.0E+00	AB007923.1	NT	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5'
9438	22366	35726	6.3	0.0E+00	AW592233.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
9438	22366	35727	6.3	0.0E+00	AW592233.1	EST_HUMAN	Hf48e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
9484	22412	35773	1.84	0.0E+00	AV714764.1	EST_HUMAN	Hf48e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
9499	22427	35788	3.12	0.0E+00	AL040428.1	EST_HUMAN	AV714764 DOB Homo sapiens cDNA clone DOBAUA06 5'
9499	22427	35789	3.12	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9505	22432	35795	1.43	0.0E+00	AF133901.1	NT	DKFZp434C1814.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9507	22434	35798	2.04	0.0E+00	AB040945.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
9514	22441		0.88	0.0E+00	BF088289.1	EST_HUMAN	Homo sapiens mRNA for KIAA1512 protein, partial cds
9542	22469	35828	4.05	0.0E+00	11422857	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9552	22479	35838	1.35	0.0E+00	K01241.1	NT	7k2b003.x1 NCJ_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476692 3' similar to TR:O36448 O36448
9559	22483	35840	7.51	0.0E+00	AB020630.1	NT	S GAG. ;
9559	22486	35847	7.51	0.0E+00	AB020630.1	NT	Homo sapiens tumor protein p73 (TP73), mRNA
9564	22491	35853	1.48	0.0E+00	AV660739.1	EST_HUMAN	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
9569	22496	35859	4.11	0.0E+00	7706638	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9574	22501	35864	0.55	0.0E+00	BE793326.1	EST_HUMAN	Homo sapiens mRNA for KIAA0823 protein, partial cds
							Homo sapiens mRNA for KIAA0823 protein, partial cds
							AV660739 GLC Homo sapiens cDNA clone GLCGKG12 3'
							Homo sapiens polycystin-L (PKDL), mRNA
							601588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9588	22514		0.74	0.0E+00	H73637.1	EST_HUMAN	y03h08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:232767 5'
9599	22525	35889	4.06	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9599	22525	35890	4.06	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9608	22534	36004	0.71	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858100 5'
9608	22534	35905	0.71	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858100 5'
9611	22537		0.59	0.0E+00	M89886.1	NT	Human polymorphic loci in Xq28
9613	22539	35909	1.86	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9628	22554	35924	2.36	0.0E+00	A061386.1	EST_HUMAN	an29e04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700084 3'
9632	22558	35927	2.3	0.0E+00	A1954607.1	EST_HUMAN	wq34a12.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MG83_HUMAN
9637	22563	35933	5.32	0.0E+00	9258595	NT	OT5480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
9647	22573	35944	1.62	0.0E+00	AW958311.1	EST_HUMAN	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
9657	22583	35954	3.01	0.0E+00	9635487	NT	EST370381 IMAGE resequences, IMAGE Homo sapiens cDNA
9673	22598	35972	1.26	0.0E+00	AU142662.1	EST_HUMAN	Human endogenous retrovirus, complete genome
9686	22612	35986	1.31	0.0E+00	11438995	NT	AU142662 Y79AA1 Homo sapiens cDNA clone Y79AA1000678 5'
9687	22613		0.94	0.0E+00	BE410768.1	EST_HUMAN	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
9701	22628	36005	1.57	0.0E+00	BF002024.1	EST_HUMAN	601301676F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9714	22639	36019	1.46	0.0E+00	AB011150.1	NT	7q97h12.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q8UH62
9715	22640	36020	4.58	0.0E+00	BE794823.1	EST_HUMAN	Q8UH62 HYPOTHETICAL 42.5 KD PROTEIN ;
9719	22644	36025	0.58	0.0E+00	BE810292.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9719	22644	36026	0.58	0.0E+00	BE810292.1	EST_HUMAN	601589294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943483 5'
9722	22647	36029	0.71	0.0E+00	AU136228.1	EST_HUMAN	RC3-PT0161-230600-011-c05 PTO161 Homo sapiens cDNA
9726	22651	36033	1.23	0.0E+00	BE883843.1	EST_HUMAN	RC3-PT0161-230600-011-c05 PTO161 Homo sapiens cDNA
9726	22651	36034	1.23	0.0E+00	BE883843.1	EST_HUMAN	AU136229 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
9744	22658	36050	0.75	0.0E+00	AB011168.1	NT	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9747	22671	36054	1.85	0.0E+00	AA344801.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9747	22671	36055	1.85	0.0E+00	AA344801.1	EST_HUMAN	Homo sapiens mRNA for KIAA0594 protein, partial cds
9805	22711	36093	0.89	0.0E+00	AW673469.1	EST_HUMAN	EST50505 Gall bladder 1 Homo sapiens cDNA 5' end
9805	22711	36094	0.89	0.0E+00	AW673469.1	EST_HUMAN	EST50505 Gall bladder 1 Homo sapiens cDNA 5' end
9838	22743	36124	1.88	0.0E+00	BE207063.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800387 5' similar to TR:O60275 O60275
							KIAA0522 PROTEIN ;
							ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800387 5' similar to TR:O60275 O60275
							KIAA0522 PROTEIN ;
							ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus
							Bcl-xL mRNA, complete cds (MOUSE);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9838	22743	36125	1.68	0.0E+00	BE207063.1	EST_HUMAN	ba0605.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus
9849	22957	36346	1.93	0.0E+00	BF348013.1	EST_HUMAN	Bel-xL mRNA, complete cds (MOUSE);
9883	22708	36184	3.23	0.0E+00	BE712515.1	EST_HUMAN	602023150F1 NCI CGAP_Br67 Homo sapiens cDNA clone IMAGE:4158300 5'
9916	22904	36291	0.72	0.0E+00	BF034377.1	EST_HUMAN	QV2-HT0696-250700-282-508 HT0696 Homo sapiens cDNA
9916	22904	36292	0.72	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9923	22911	36299	0.79	0.0E+00	5803069	NT	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9923	22911	36300	0.78	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9932	22837	36226	1.29	0.0E+00	AL042278.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9965	22870	36259	1.88	0.0E+00	AI088043.1	EST_HUMAN	DKFZP434L0120.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434L0120 5'
9972	21330	34682	0.57	0.0E+00	BF303962.1	EST_HUMAN	ow60H01.x1 Soares_NSF_P8_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to
9973	21331	34663	4.02	0.0E+00	11550151	NT	TR-Q14677 Q14677 KIAA0171 PROTEIN.;
9973	21331	34664	4.02	0.0E+00	11550151	NT	601892245F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138066 5'
9975	21333	34687	8.83	0.0E+00	AI290809.1	EST_HUMAN	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9975	21333	34668	8.83	0.0E+00	AI290809.1	EST_HUMAN	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9976	21334	34669	1.41	0.0E+00	AIW953836.1	EST_HUMAN	qim09a06.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN
10003	22820	36207	4.26	0.0E+00	AF163463.1	NT	P28316 60S RIBOSOMAL PROTEIN L23A.;
10006	22823	36211	0.73	0.0E+00	BE885128.1	EST_HUMAN	qim09a06.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL2B_HUMAN
10006	22823	36212	0.73	0.0E+00	BE885128.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A.;
10015	22915	36307	9.31	0.0E+00	BE255829.1	EST_HUMAN	EST36026 MAGC resequences; MAGC Homo sapiens cDNA
10018	22918	36307	1.72	0.0E+00	BE781382.1	EST_HUMAN	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
10018	22918	36308	1.72	0.0E+00	BE781382.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
10020	22920	36309	15.09	0.0E+00	AW163779.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
10040	22940	36329	3.44	0.0E+00	BE263191.1	EST_HUMAN	601108942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:39560722 5'
10057	22973	36363	5.14	0.0E+00	C06158.1	EST_HUMAN	60146828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
10057	22973	36364	5.14	0.0E+00	C06158.1	EST_HUMAN	60146828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
10059	22975	36367	2.77	0.0E+00	BE748215.1	EST_HUMAN	60146828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
10068	22984	36375	2.2	0.0E+00	11437282	NT	601576683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927648 5'
							Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10068	22984	36376	2.2	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10068	22984	36377	2.2	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10088	22881	36287	1.92	0.0E+00	BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
10105	22996	36391	1.14	0.0E+00	AV701829.1	EST_HUMAN	AV701829 ADB Homo sapiens cDNA clone ADBBYH01 5'
10117	23008	36403	2.68	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
10117	23008	36404	2.68	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
10148	23039	36438	1.16	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA
10167	23058	36458	2.11	0.0E+00	AW500293.1	EST_HUMAN	U1HF-BND-akg-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
10167	23058	36459	2.11	0.0E+00	AW500293.1	EST_HUMAN	U1HF-BND-akg-b-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
10176	23087	36465	1.5	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10176	23037	36468	1.5	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10178	23069	36467	0.68	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3874037 5'
10178	23069	36468	0.68	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3874037 5'
10185	23076	36477	0.82	0.0E+00	W56829.1	EST_HUMAN	zdf16e11.r1 Soares fetal heart NbrH19W Homo sapiens cDNA clone IMAGE:340844 5'
10185	23076	36478	0.82	0.0E+00	W56829.1	EST_HUMAN	zdf16e11.r1 Soares fetal heart NbrH19W Homo sapiens cDNA clone IMAGE:340844 5'
10198	23089	36490	1.09	0.0E+00	AB035356.1	NT	Homo sapiens mRNA for neurexin I-alpha protein, complete cds
10202	23093		0.64	0.0E+00	AU124780.1	EST_HUMAN	am58a11.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639548 3'
10204	23095	36495	2.27	0.0E+00	AW500526.1	EST_HUMAN	U1HF-BND-akg-c-07-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
10245	23136	36541	2.24	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
10272	23162	36572	2.9	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
10272	23162	36573	2.9	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
10275	23165	36578	3.07	0.0E+00	BE563320.1	EST_HUMAN	601334803F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688680 5'
10293	23183	36594	1.9	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Homo sapiens cDNA
10319	23208	36619	0.99	0.0E+00	BE206710.1	EST_HUMAN	bb26c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2664000 3'
10334	23223	36637	2.47	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10334	23223	36638	2.47	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10343	23232	36650	0.84	0.0E+00	AW500838.1	EST_HUMAN	U1HF-BPOp-af-f-05-0-U1.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
10348	23238	36656	19.64	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948383 5'
10349	23238	36657	19.64	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948383 5'
10361	23250	36670	1.96	0.0E+00	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10378	23267	36889	1.53	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
10392	23281	36701	3.06	0.0E+00	AU192349.1	EST_HUMAN	AU192349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10393	23282	36702	2.33	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
10419	23308	36728	2.26	0.0E+00	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
10419	23308	36729	2.26	0.0E+00	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
10435	23324	36742	1.13	0.0E+00	BF082868.1	EST_HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
10461	23349	36766	2.86	0.0E+00	BE280793.1	EST_HUMAN	601159227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
10470	23358	36772	3.26	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
10470	23358	36773	3.26	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
10479	23367	36779	2.47	0.0E+00	AW236269.1	EST_HUMAN	x172b01.x1 NOL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gbX02152_cds1 L-
10480	23368	36780	0.75	0.0E+00	AA341305.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10509	23396	36808	1.13	0.0E+00	AW1984113.1	EST_HUMAN	EST46740 Fetal kidney II Homo sapiens cDNA 5' end
10519	23406	36817	6.12	0.0E+00	AU143673.1	EST_HUMAN	EST376166 MAGC resequences, MAGH Homo sapiens cDNA
10519	23406	36818	6.12	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10522	23409	36821	4.18	0.0E+00	AF072408.1	NT	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10525	23411	36823	2.44	0.0E+00	11421001	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10558	23441	36824	2.44	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10558	23444	36866	3.24	0.0E+00	AU136637.1	EST_HUMAN	Homo sapiens HEF like Protein (HEFL), mRNA
10558	23444	36867	3.24	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10574	23460	36881	2.02	0.0E+00	AJ295844.1	NT	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10574	23460	36882	2.02	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7/importin7 and partial ZNF143 gene
10579	23465	36889	0.99	0.0E+00	AV695712.1	EST_HUMAN	Homo sapiens partial RANBP7 gene for RANBP7/importin7 and partial ZNF143 gene
10579	23465	36890	0.99	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKX Homo sapiens cDNA clone GKDXA07 5'
10585	23471	36897	0.72	0.0E+00	AF072408.1	NT	AV695712 GKX Homo sapiens cDNA clone GKDXA07 5'
10587	23473	36900	2.46	0.0E+00	AA196387.1	EST_HUMAN	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10612	23498	36929	0.99	0.0E+00	AA131248.1	EST_HUMAN	zp97h11.1 Streptococcus muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
10612	23498	36930	0.99	0.0E+00	AA131248.1	EST_HUMAN	zp97h11.1 Streptococcus muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
10653	23539	36973	1.91	0.0E+00	AF178308.1	NT	z31f01.1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:503945 5'
10657	23563	37013	0.9	0.0E+00	BE880958.1	EST_HUMAN	z31f01.1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:503945 5'
10708	23594	37021	5.26	0.0E+00	BE730772.1	EST_HUMAN	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10708	23594	37022	5.26	0.0E+00	BE730772.1	EST_HUMAN	601491569F1 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:3893657 5'
10713	23599	37028	0.96	0.0E+00	BE127403.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10722	23608	37037	1.14	0.0E+00	BE988611.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10722	23608	37038	1.14	0.0E+00	BE988511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10738	23624	37058	0.98	0.0E+00	BE987487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10747	23633	37065	0.84	0.0E+00	AA311824.1	EST_HUMAN	EST182363 Jurkat T-cells Vi Homo sapiens cDNA 5' end
10748	23634	37067	0.6	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
10769	23645	37078	0.72	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10762	23648	37081	0.9	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10772	23658	37087	0.84	0.0E+00	AB029280.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds
10779	23665	37092	4.32	0.0E+00	AB006560.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10779	23665	37093	4.32	0.0E+00	AB006560.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10784	23670	37099	1.4	0.0E+00	AA704457.1	EST_HUMAN	Z19b06.s1 Soares, fetal liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gbM14123.cd1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10786	23672	37100	0.86	0.0E+00	M22921.1	NT	Human beta 1,4-galactosyl-transferase mRNA, complete cds
10788	23674	37103	4.73	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184939 5'
10788	23674	37104	4.73	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184939 5'
10813	23689	37126	0.9	0.0E+00	BE897148.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10813	23689	37127	0.9	0.0E+00	BE897148.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10872	23758	37183	0.73	0.0E+00	A1631818.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10872	23758	37184	0.73	0.0E+00	A1631818.1	EST_HUMAN	Q61204 NOTCH2-LIKE ;
10884	23769	37194	1.3	0.0E+00	T03078.1	EST_HUMAN	wa36e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10905	23791	37220	0.82	0.0E+00	AU122429	EST_HUMAN	FB23A4 Fetal brain, Stratagene Homo sapiens cDNA clone FB23A4 3' end
10931	23819	37245	2.41	0.0E+00	BF436218.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002388 5'
10932	23817		1.75	0.0E+00	AV654765.1	EST_HUMAN	na645612.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10950	23834	37281	3.78	0.0E+00	AW517980.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLCDZC07 3'
10954	23838	37285	5.05	0.0E+00	BE549213.1	EST_HUMAN	xu174601.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gbM69066 MOESIN (HUMAN);
10970	23854	37281	0.7	0.0E+00	X69693.1	NT	(HUMAN);
10997	23881	37311	0.61	0.0E+00	X69693.1	NT	601078784F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10997	23881	37312	2.07	0.0E+00	BE781742.1	EST_HUMAN	Homo sapiens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
11016	23900	37337	2.27	0.0E+00	BE082720.1	EST_HUMAN	H. sapiens mRNA for NK receptor (183 Act)
11016	23900	37338	2.27	0.0E+00	BE082720.1	EST_HUMAN	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
11021	23905	37344	0.84	0.0E+00	Y08032.1	NT	RC2-BT0642-150200-012-003 BT0642 Homo sapiens cDNA
11027	23911	37353	0.76	0.0E+00	A1656890.1	EST_HUMAN	RC2-BT0642-150200-012-003 BT0642 Homo sapiens cDNA
							Human endogenous retrovirus-K, LTR U5 and gag gene
							i154e07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2244612 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11033	23917	37359	3.04	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
11033	23917	37360	3.04	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
11038	23920	37361	0.88	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
11038	23920	37362	0.88	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
11054	23938	37376	0.54	0.0E+00	H39805.1	EST_HUMAN	yp01a10.t1 Scores breast 3NdbHst Homo sapiens cDNA clone IMAGE:186138 5'
11072	23956	37392	2.22	0.0E+00	D87675.1	NT	Homo sapiens DNA for amygd precursor protein, complete cds
11075	23959	37394	0.58	0.0E+00	BE172254.1	EST_HUMAN	MRO-HT0559-270300-006-e12 HT0559 Homo sapiens cDNA
11075	23959	37395	0.58	0.0E+00	BE172254.1	EST_HUMAN	MRO-HT0559-270300-006-e12 HT0559 Homo sapiens cDNA
11081	24013	37454	3.41	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAG005 6'
11081	24013	37455	3.41	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAG005 6'
11083	24015		2.06	0.0E+00	AW813783.1	EST_HUMAN	EST3755368 IMAGE resequences, MAGH Homo sapiens cDNA
11090	24021	37463	6.48	0.0E+00	AW863563.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11102	24033	37477	2.25	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11102	24033	37478	2.25	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11104	24035	37480	1.94	0.0E+00	AW057621.1	EST_HUMAN	wy61609.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2563065 3' similar to TR:Q60566 Q60566 VDX:
11113	24043	37488	1.83	0.0E+00	BE243270.1	EST_HUMAN	TCAAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) BAYOR-HQSC project=TCAA Homo sapiens cDNA clone TCAAAP0917
11114	24044	37489	3.23	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
11114	24044	37490	3.23	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
11124	24054	37500	4.29	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
11124	24054	37501	4.29	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
11140	24069	37515	1.98	0.0E+00	AW404795.1	EST_HUMAN	UI-HF-BLO-ecm-d-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 6'
11144	24073	37520	3.87	0.0E+00	11424828	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
11145	24074	37521	8.6	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
11145	24074	37522	8.6	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
11146	24075	37523	3.45	0.0E+00	AI991827.1	EST_HUMAN	wu32805.x1 Scores Dielgraeve_colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
11149	24078	37527	2.03	0.0E+00	BE582109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
11153	24082	37529	7.78	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'
11155	24084	37530	2.4	0.0E+00	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11155	24084	37531	2.4	0.0E+00	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11161	24089	37536	1.74	0.0E+00	AB014608.1	NT	Homo sapiens mRNA for KIAA0708 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11161	24039	37537	1.74	0.0E+00	AB014608.1	NT	Homo sapiens mRNA for KIAA0708 protein, partial cds
11169	24097	37544	3.32	0.0E+00	BE903304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
11172	10052	32177	1.88	0.0E+00	AA195905.1	EST_HUMAN	z95b11.1 Stragelene muscle 897209 Homo sapiens cDNA clone IMAGE:627633 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
11192	24118	37565	3.77	0.0E+00	AA809090.1	EST_HUMAN	hw17c08.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1240718 3' similar to gb:X57609 IG
11193	24119	37566	5.68	0.0E+00	BE793498.1	EST_HUMAN	LAMBDA CHAIN C REGIONS (HUMAN);
11200	24126	37572	18.68	0.0E+00	AV727362.1	EST_HUMAN	601588828F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
11200	24126	37573	18.68	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
11214	24140	37592	23.51	0.0E+00	AW516055.1	EST_HUMAN	xy04g10.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S
11220	24146	37597	1.6	0.0E+00	AU136741.1	EST_HUMAN	RIBOSOMAL PROTEIN S16 (HUMAN);
11225	24151	37600	3.11	0.0E+00	AW593333.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'
11225	24151	37601	3.11	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11225	24151	37602	3.11	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11228	24154	37604	1.86	0.0E+00	Z34897.1	NT	H. sapiens mRNA for H1 histamine receptor
11229	24155	37605	3.08	0.0E+00	F13069.1	EST_HUMAN	HSC31C031 normalized infant brain cDNA Homo sapiens cDNA clone c-3ic03
11255	24179	37628	3.12	0.0E+00	AW338094.1	EST_HUMAN	hw66t01.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2892985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);
11259	24180	37629	4.38	0.0E+00	AW451230.1	EST_HUMAN	UJH-B13-ali-a-01-Q-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11256	24180	37630	4.38	0.0E+00	AW451230.1	EST_HUMAN	UJH-B13-ali-a-01-Q-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11258	13328		4.43	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
11260	24183	37632	1.73	0.0E+00	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
11274	24196	37649	1.7	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
11285	24205	37656	1.86	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
11302	24221	37670	1.58	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'
11303	24222		73.49	0.0E+00	BF694061.1	EST_HUMAN	602141406F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'
11305	24224	37672	3.86	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
11308	24225		1.7	0.0E+00	AW239269.1	EST_HUMAN	xy72b01.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152 cds1 L- LACTATE DEHYDROGENASE M CHAIN (HUMAN);
11311	24230	37676	5.79	0.0E+00	AU149809.1	EST_HUMAN	qf43c03.x1 Scores_NHT Homo sapiens cDNA clone IMAGE:1762772 3'

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11311	24230	37677	5.79	0.0E+00	AI149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1762772 3'
11312	24231	37678	2.28	0.0E+00	AW391637.1	EST_HUMAN	QV4-ST0234-121199-032-b06 ST0234 Homo sapiens cDNA
11326	24244		2.16	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
11329	24248	37686	9.87	0.0E+00	11424728	NT	Homo sapiens insulin receptor (INSR), mRNA
11336	24255	37683	3.74	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-d06 UM0093 Homo sapiens cDNA
11336	24255	37694	3.74	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-d06 UM0093 Homo sapiens cDNA
11337	24258	37685	1.77	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184979 5'
11339	24258	37687	28.65	0.0E+00	BE281209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
11343	24262	37702	1.82	0.0E+00	AB028040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
11348	24266	37707	4.38	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
11375	24291	37735	65.99	0.0E+00	AA740782.1	EST_HUMAN	0532e07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element
11382	24298	37744	3.06	0.0E+00	AF252303.1	NT	MSR1 repetitive element
11396	24312	37758	5.59	0.0E+00	C05089.1	EST_HUMAN	Homo sapiens signalling lymphocytic activation molecule (SLAM) gene, exon 2
11403	24319	37766	2.44	0.0E+00	AA746375.1	EST_HUMAN	C05089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NH04817
11403	24319	37767	2.44	0.0E+00	AA746375.1	EST_HUMAN	0a56h01.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11411	24327		1.98	0.0E+00	BE392589.1	EST_HUMAN	0a56h01.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11414	24330	37778	1.57	0.0E+00	BF353625.1	EST_HUMAN	601307409F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625560 5'
11415	24331	37779	5.98	0.0E+00	AL157603.1	EST_HUMAN	QV2-HT0698-020800-285-407 HT0698 Homo sapiens cDNA
11427	24343	37788	7.08	0.0E+00	AU116988.1	EST_HUMAN	DKFZp761J2116_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
11440	24356	37804	1.98	0.0E+00	AV693656.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
11448	24364	37813	1.4	0.0E+00	BF368563.1	EST_HUMAN	AV693656 GKC Homo sapiens cDNA clone GKCCNC03 5'
11474	24387	37837	2.7	0.0E+00	BE182360.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
11474	24387	37838	2.7	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
11484	24397	37847	1.72	0.0E+00	AW408390.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
11488	24400	37850	3.66	0.0E+00	BE896423.1	EST_HUMAN	UIHF-BL0-acc-c-09-0-J1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060089 5'
11496	24407	37860	1.63	0.0E+00	AW500307.1	EST_HUMAN	60143092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
11496	24407	37861	1.63	0.0E+00	AW500307.1	EST_HUMAN	UIHF-BNO-akg-d-02-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							UIHF-BNO-akg-d-02-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							bb78c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb:Y00345_cds1
							POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:XB5553 M.musculus mRNA for poly(A) binding protein (MOUSE);
11499	24410	37864	1.71	0.0E+00	BE018293.1	EST_HUMAN	AU121677 MAMMA1 Homo sapiens cDNA clone MAMMA1000731 5'
11524	24434	37892	1.52	0.0E+00	AU121677.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
11538	24446	37907	3.94	0.0E+00	BE897953.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
11538	24448	37910	1.68	0.0E+00	AI459545.1	EST_HUMAN	ea86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'

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Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11538	24448	37911	1.68	0.0E+00	AI45945.1	EST_HUMAN	ac98g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11578	24487	37958	3.1	0.0E+00	4759827	NT	Homo sapiens neuraxn III (NRXN3) mRNA
11578	24488	37957	3.31	0.0E+00	BF206561.1	EST_HUMAN	601870902F1 NIH_MGC_1p Homo sapiens cDNA clone IMAGE:4101433 5'
11585	24494	37963	13.79	0.0E+00	AW207734.1	EST_HUMAN	UIH-B12-age-b-01-0-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11588	24497	37964	3.18	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11588	24497	37965	3.18	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11690	24499	37967	4.97	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-
11690	24499	37968	4.97	0.0E+00	BE206846.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN ;
11613	24521	37989	2.4	0.0E+00	11024711	NT	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-
11617	20818	34124	1.92	0.0E+00	L32832.1	NT	55KDA-ASSOCIATED PROTEIN ;
11621	24528	37996	2.44	0.0E+00	BE148076.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11621	24528	37997	2.44	0.0E+00	BE148076.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11643	24549	38020	1.56	0.0E+00	AW673469.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11643	24549	38021	1.56	0.0E+00	AW673469.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11663	24569	38044	5.1	0.0E+00	BF507876.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275
11663	24569	38045	5.1	0.0E+00	BF507876.1	EST_HUMAN	KIAA0522 PROTEIN ;
11671	24675	38051	1.68	0.0E+00	AU135170.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275
11675	24579	38055	1.63	0.0E+00	BF576138.1	EST_HUMAN	KIAA0522 PROTEIN ;
11675	24579	38056	1.63	0.0E+00	BF576138.1	EST_HUMAN	KIAA0522 PROTEIN ;
11676	24580	38057	7.13	0.0E+00	BE876401.1	EST_HUMAN	UIH-B14-ekb-b-10-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11676	24580	38058	7.13	0.0E+00	BE876401.1	EST_HUMAN	UIH-B14-ekb-b-10-0-U1.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11686	24589	38077	3.79	0.0E+00	BF240536.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001981 5'
11700	24602	38078	2.21	0.0E+00	AB037737.1	NT	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11704	24606	38081	3.42	0.0E+00	11430868	NT	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11704	24606	38082	3.42	0.0E+00	11430868	NT	601488828F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3889207 5'
11721	24623	38103	9.05	0.0E+00	4503544	NT	601488828F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3889207 5'
11730	24632	38113	3.17	0.0E+00	AW328173.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
11733	24635		25.52	0.0E+00	M55083.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
							Homo sapiens mRNA for KIAA1316 protein, partial cds
							Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
							Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
							Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
							ar04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2947177 5'
							Human gamma actin-like pseudogene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11737	24639	38119	2.9	0.0E+00	A1600988.1	EST_HUMAN	w20e11.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
11740	24642	38121	2.51	0.0E+00	BF306986.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11740	24642	38122	2.51	0.0E+00	BF306986.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11747	24648	38129	42.39	0.0E+00	BF362462.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
11768	24659		2.58	0.0E+00	BE997051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11769	24670		1.93	0.0E+00	4503786	NT	Homo sapiens fyn-related kinase (FRK) mRNA
11780	24679	38168	1.79	0.0E+00	8923698	NT	Homo sapiens golgin-like protein (GLP) mRNA
11782	24681		1.82	0.0E+00	BF207662.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11793	24715	38206	4.01	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN.;
11793	24715	38207	4.01	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN.;
11795	24717	38208	1.82	0.0E+00	AW763028.1	EST_HUMAN	QV0-CT0226-101299-071-f06 CT0226 Homo sapiens cDNA
11800	24722		2.1	0.0E+00	AA558707.1	EST_HUMAN	m42c08.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11801	18537	31379	4.92	0.0E+00	A1934954.1	EST_HUMAN	wp06g08.x1 NCL_CGAP_K12 Homo sapiens cDNA clone IMAGE:2464084 3'
11802	24723	38215	11.66	0.0E+00	AW327896.1	EST_HUMAN	dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11821	25699	38233	1.73	0.0E+00	AW282776.1	EST_HUMAN	UI-H-BW0-ajl-d-07-0-U1.e1 NCL_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2728509 3'
11826	23961	37397	1.54	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
11834	24695	38174	4.25	0.0E+00	BE185656.1	EST_HUMAN	IL5-HT0731-020500-077-f05 HT0731 Homo sapiens cDNA
11846	24696	38186	5.71	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G178 5'
11846	24696	38187	5.71	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G178 5'
11853	24703	38194	7.61	0.0E+00	A1923116.1	EST_HUMAN	w183g03.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11856	24746	38237	5.43	0.0E+00	AA760913.1	EST_HUMAN	n211c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13688
11856	24746	38238	5.43	0.0E+00	AA760913.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN.;
11861	24751	38244	1.71	0.0E+00	BE910546.1	EST_HUMAN	n211c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13688
11871	23971	37408	4.99	0.0E+00	BE676347.1	EST_HUMAN	601501030F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902928 5'
11873	23973	37410	1.5	0.0E+00	A1893358.1	EST_HUMAN	712712.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3285919 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1.;
							665b09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2274521 3' similar to gb:M55542 INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (HUMAN);

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11875	23975	37412	1.93	0.0E+00	BE615693.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11875	23975	37413	1.93	0.0E+00	BE615693.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11882	23982	37420	1.97	0.0E+00	AV757420.1	EST_HUMAN	AV757420 BM Homo sapiens cDNA clone BMFAGH03 5'
11911	24758	38263	1.76	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11911	24758	38254	1.76	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11925	24770	38267	3.99	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
11944	24788	38284	29.97	0.0E+00	A1207425.1	EST_HUMAN	HA2767 Human fetal liver cDNA library Homo sapiens cDNA
11944	24788	38285	29.97	0.0E+00	A1207425.1	EST_HUMAN	HA2767 Human fetal liver cDNA library Homo sapiens cDNA
11972	24815	38308	7.56	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3839012 3'
11972	24815	38310	7.56	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3839012 3'
11983	24828	38322	2.01	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11983	24828	38323	2.01	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11986	24829	38326	9	0.0E+00	AW006022.1	EST_HUMAN	wz91h01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2 CE11040 ZINC FINGER, C2H2 TYPE ;
11990	25700	38330	2.7	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO ;
12010	24852	38352	2.96	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
12010	24852	38353	2.96	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
12031	24873	38377	4.58	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
12031	24873	38378	4.58	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
12036	24878	38384	6.4	0.0E+00	U36263.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
12039	24881	38386	5.52	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
12039	24881	38387	5.52	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
12046	24887	38392	9.95	0.0E+00	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
12051	24892	38395	1.61	0.0E+00	AA488894.1	EST_HUMAN	aa55g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824900 3' similar to gb:M37766 B- LYMPHOCYTE ACTIVATION MARKER BLAST-1 PRECURSOR (HUMAN);
12058	24899	38404	2.49	0.0E+00	BE794758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
12062	24903	38406	38.48	0.0E+00	BE879693.1	EST_HUMAN	601491621F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
12067	24908	38410	2.31	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
12067	24908	38411	2.31	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
12071	24912	38415	1.75	0.0E+00	AF053643.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7 za34c02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294494 5' similar to SW:NABA_RAT P26435 SODIUM/BILE ACID COTRANSPORTER ;
12078	24919	38419	2.18	0.0E+00	W01479.1	EST_HUMAN	

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12078	24919	38420	2.18	0.0E+00	W01479.1	EST_HUMAN	zab4c02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294434 5' similar to
12080	24921	38423	2.68	0.0E+00	BE409893.1	EST_HUMAN	SW:NABA_RAT P28435 SODIUMBILE ACID COTRANSPORTER ;
12081	24922	38424	1.48	0.0E+00	BE148650.1	EST_HUMAN	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3625644 5'
12082	24923	38425	1.52	0.0E+00	11427345	NT	MFO-HTD241-150300-011-402 HTD241 Homo sapiens cDNA
12082	24923	38426	1.52	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
12082	24923	38427	1.52	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
12083	24924	38428	2.76	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12083	24924	38429	2.76	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12092	24933	38440	2	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000929 5'
12095	24938	38442	2.75	0.0E+00	BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
12111	24952	38455	5.84	0.0E+00	X51755.1	NT	Human lambdaIda-immunoglobulin constant region complex (germline)
12111	24952	38458	5.84	0.0E+00	X51755.1	NT	Human lambdaIda-immunoglobulin constant region complex (germline)
12118	24959		1.47	0.0E+00	W88984.1	EST_HUMAN	zh73d05.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:417705 3'
12149	25701		13.89	0.0E+00	BF309120.1	EST_HUMAN	601880534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
12155	24994	38493	31.03	0.0E+00	BE297176.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632988 5'
12164	25000	38501	5.75	0.0E+00	AL040793.1	EST_HUMAN	DKFZp434D0415_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0416 6'
12240	25954	31368	5.31	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3603020 5'
12249	25908		2.36	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12251	25916		7.98	0.0E+00	AI180993.1	EST_HUMAN	ge17b12.x1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
12259	25078		4.27	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12279	25083		5.73	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12287	25089		4.11	0.0E+00	11417862	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
12304	25112		6.72	0.0E+00	5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
12347	25789		4.25	0.0E+00	AL041931.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5'
12369	25919		2.12	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
12378	25158		5.28	0.0E+00	AL048544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5'
12389	26619		1.45	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
12423	25940		2.21	0.0E+00	N54484.1	EST_HUMAN	y440e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to
12437	25195		3.31	0.0E+00	AF106656.1	NT	SW:POL_BAEVM P10272 POL POLYPROTEIN ;
12440	13921	26867	7.53	0.0E+00	4507500	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
							Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA

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12440	13921	26868	7.53	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12449	25822		2.17	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
12474	13638		3.25	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12503	25613	31736	2.44	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12562	25784	31575	2.62	0.0E+00	AW550082.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
12586	25738		1.51	0.0E+00	L20493.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
12613	25817		3.04	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12650	25325		4.02	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12685	25912		1.57	0.0E+00	A1204914.1	EST_HUMAN	an05h04.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12719	25397		2.09	0.0E+00	A1904546.1	EST_HUMAN	QV-BT065-020396-103 BT065 Homo sapiens cDNA
12727	25809		1.6	0.0E+00	BE439792.1	EST_HUMAN	HTM1-854F HTM1 Homo sapiens cDNA
12766	14738	27706	4.46	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbhBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
12768	14738	27707	4.46	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN);
12777	25405		16.85	0.0E+00	D50659.1	NT	GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN);
12781	25410	31783	4.86	0.0E+00	11418189	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
12781	25410	31784	4.86	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12784	25413		1.57	0.0E+00	AB026898.1	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12827	25445		2.96	0.0E+00	AW684999.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12871	25473		1.74	0.0E+00	11528291	NT	h86a08.x1 Soares NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2979154 3'
12897	16403	28304	2.66	0.0E+00	4886312	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12905	18430	31353	1.96	0.0E+00	6806918	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12908	25492	31773	2.45	0.0E+00	AB028900.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12945	25511		1.95	0.0E+00	9558724	NT	Homo sapiens GST gene for cerebrosis sulfotransferase, exon 1, 2, 3, 4, 5
12969	25584		3.31	0.0E+00	AL163246.2	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF-1), mRNA
12976	13711	26618	1.58	0.0E+00	6806918	NT	Homo sapiens chromosome 21 segment HS21C046
13044	25579		3.08	0.0E+00	7657020	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13060	25586		2.03	0.0E+00	AB026898.1	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

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Table 4

Single Exon Probes Expressed in Adult Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13087	25606		1.58	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV8)

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human adult liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,109 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,110 - 25,995.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in, any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.
11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.
13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human adult liver comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,109 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human adult liver.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,110 - 25,995 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human adult liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
10 of SEQ ID NOs.: 25,996 - 38,578, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human adult liver.

15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human adult liver, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human adult liver; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the adult liver of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

- 5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 25,995 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,995.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,996 - 38,578.

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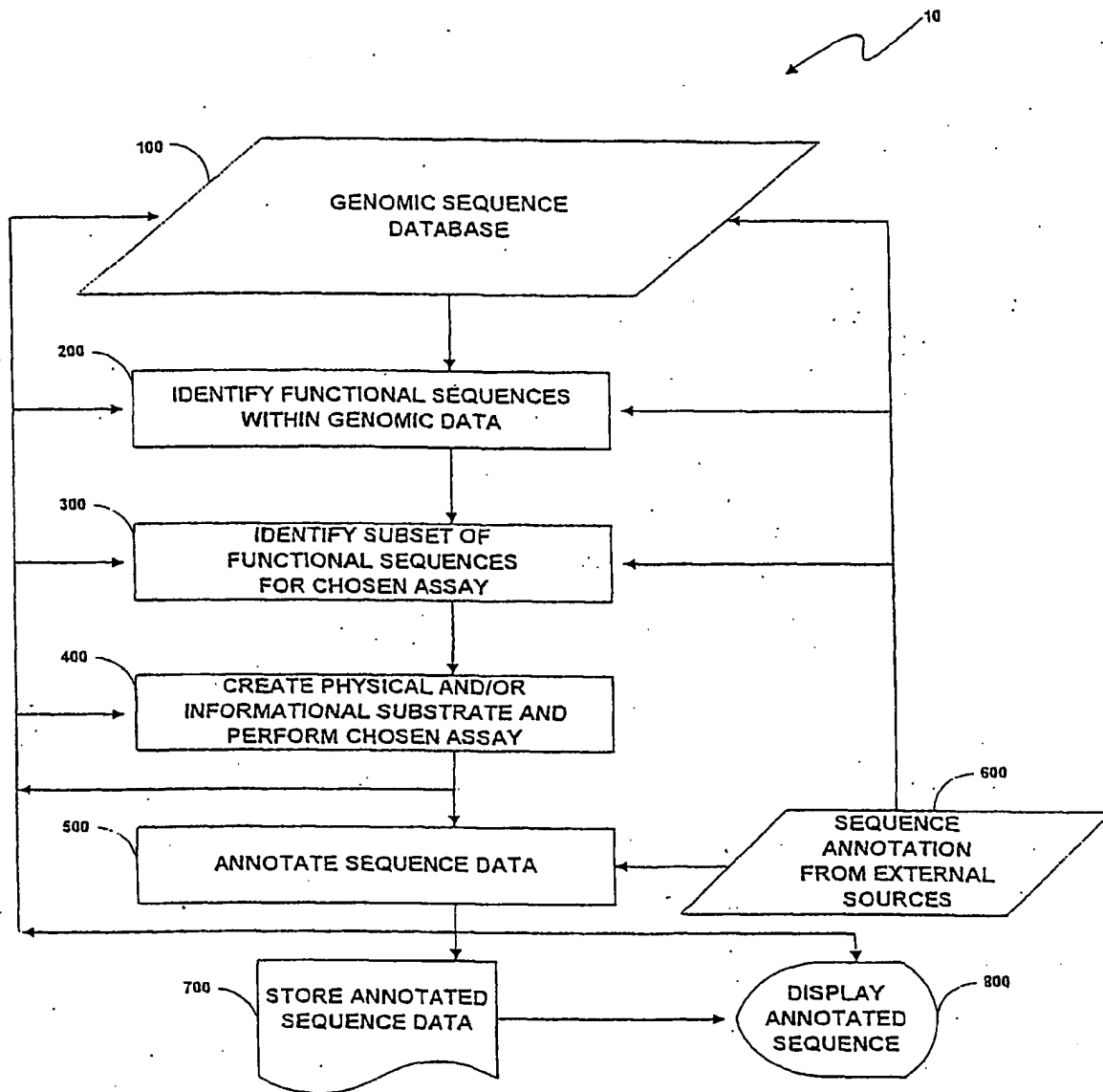


Fig. 1

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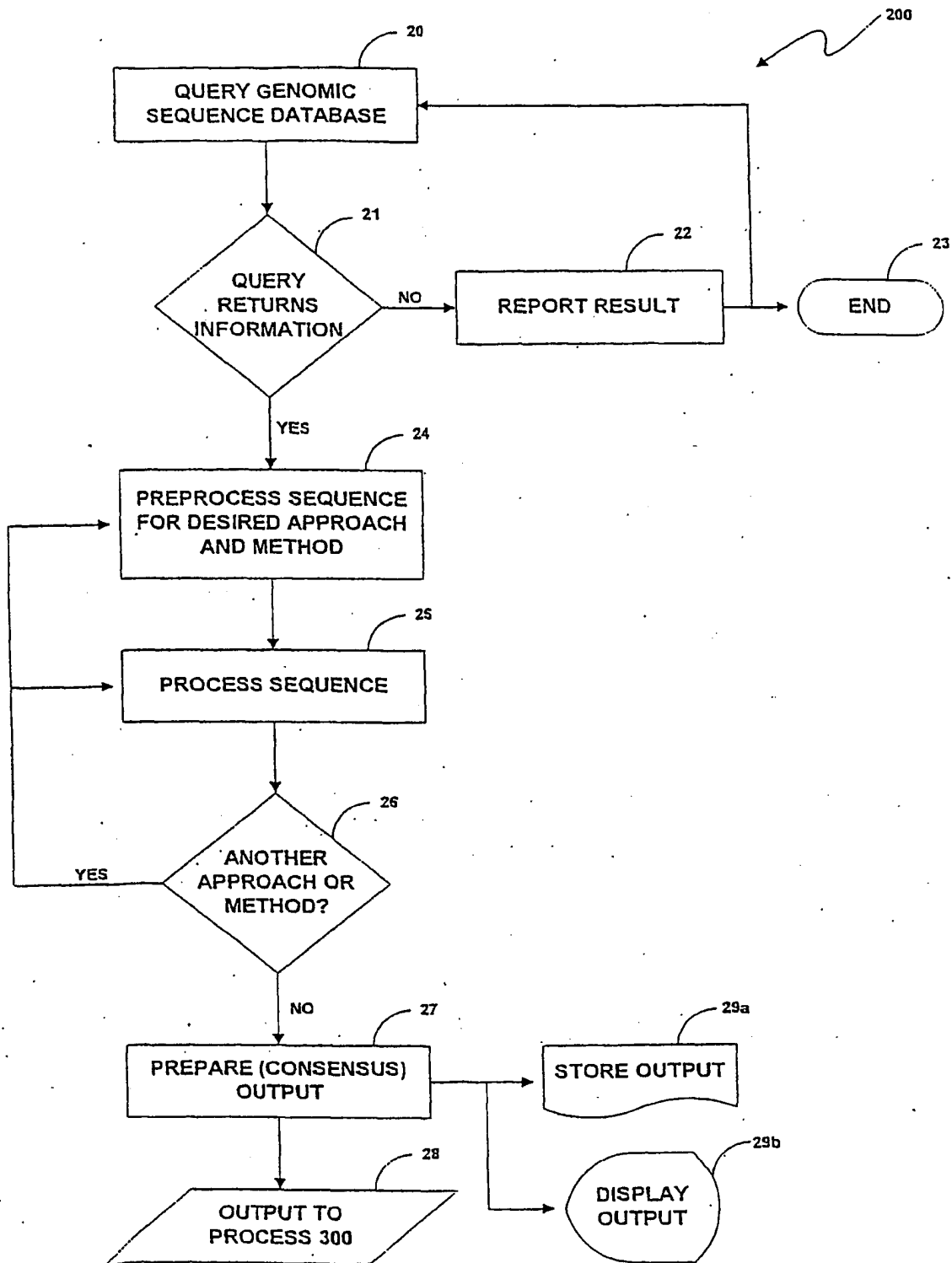


Fig. 2

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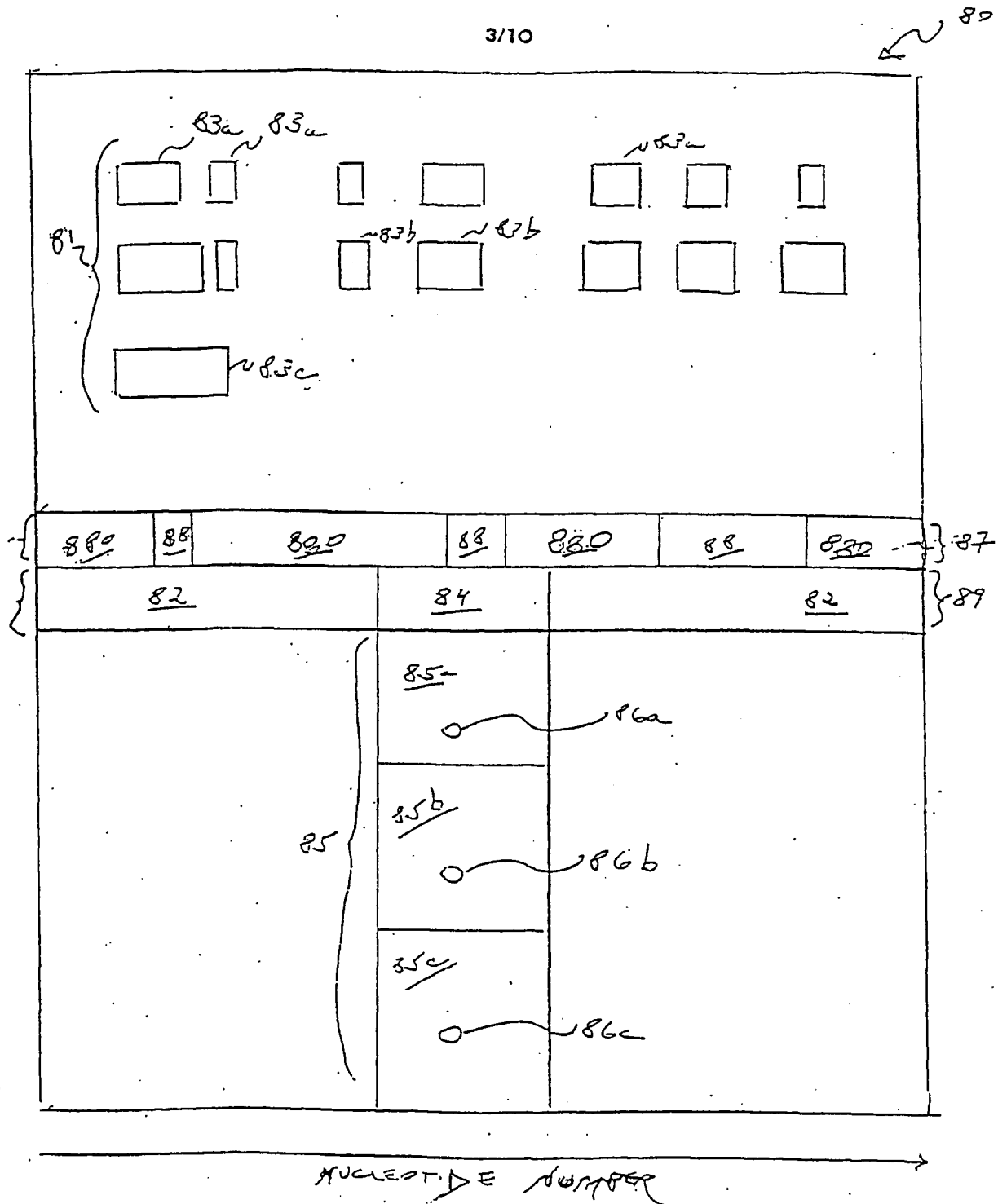


Fig. 3

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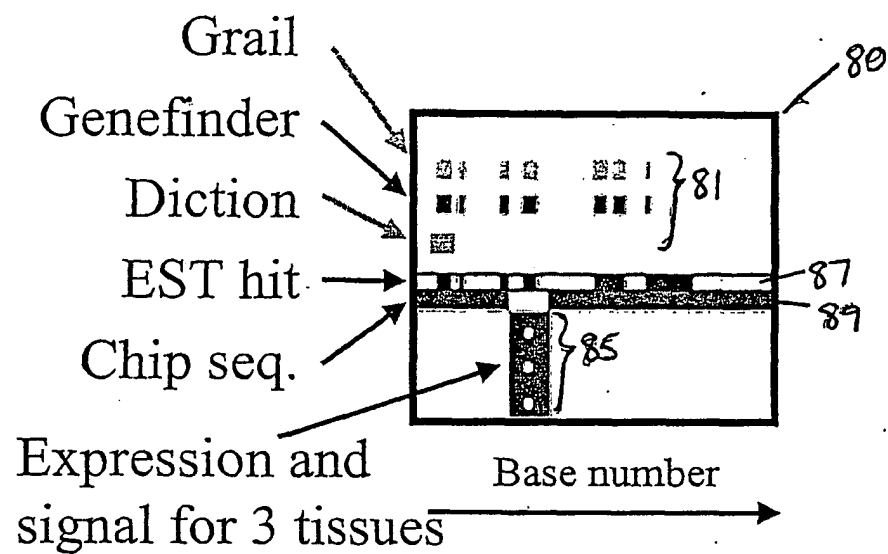


Fig. 4

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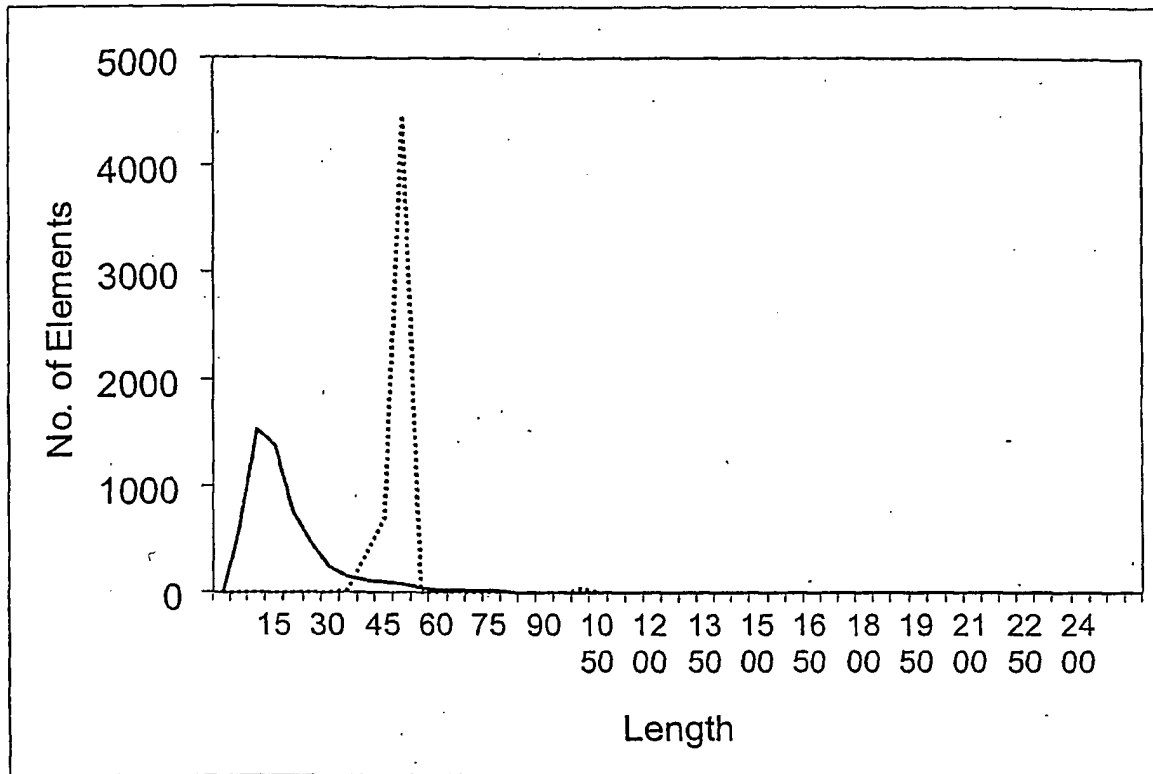


Fig. 5

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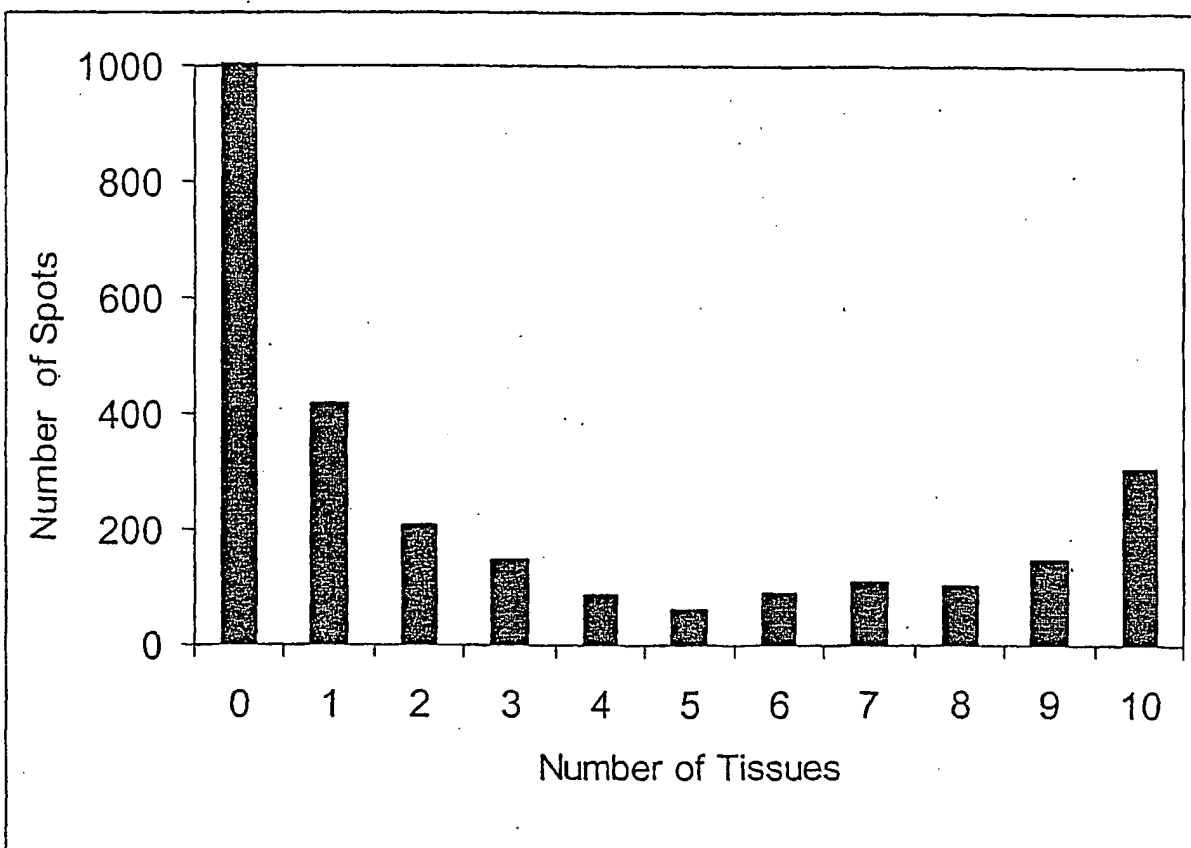


Fig. 6

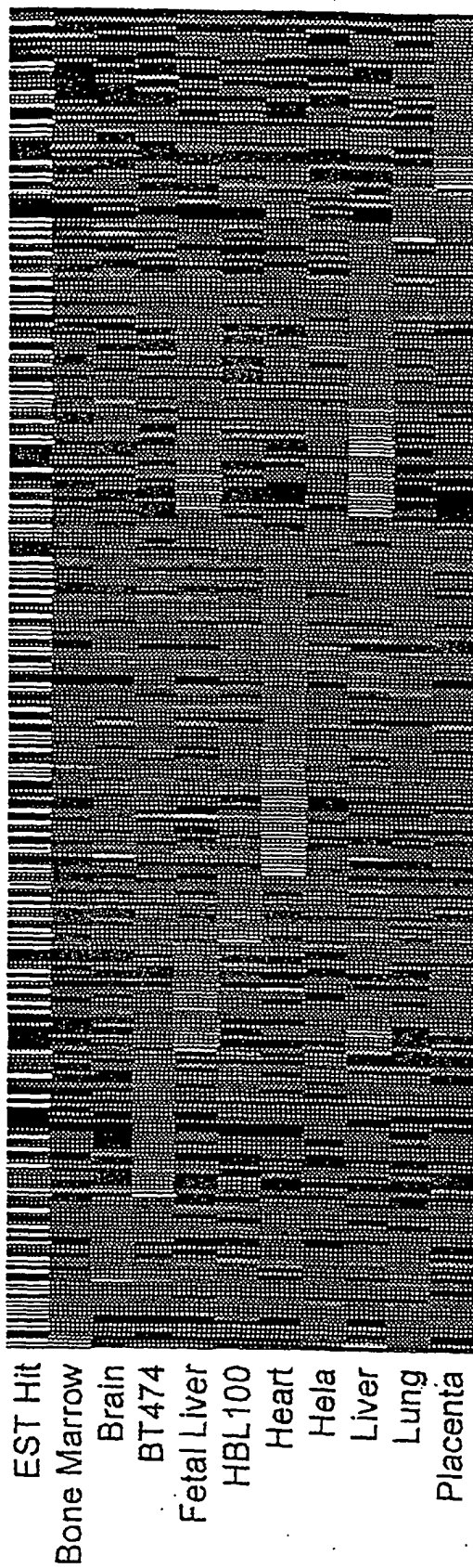


Fig. 7a

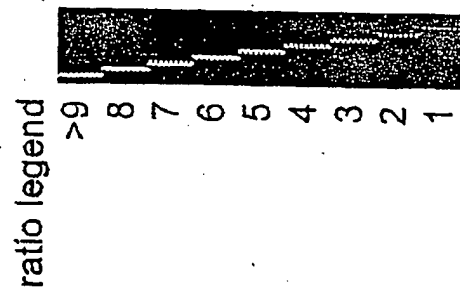


Fig. 7b

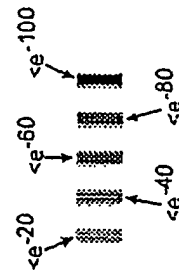


Fig. 7c

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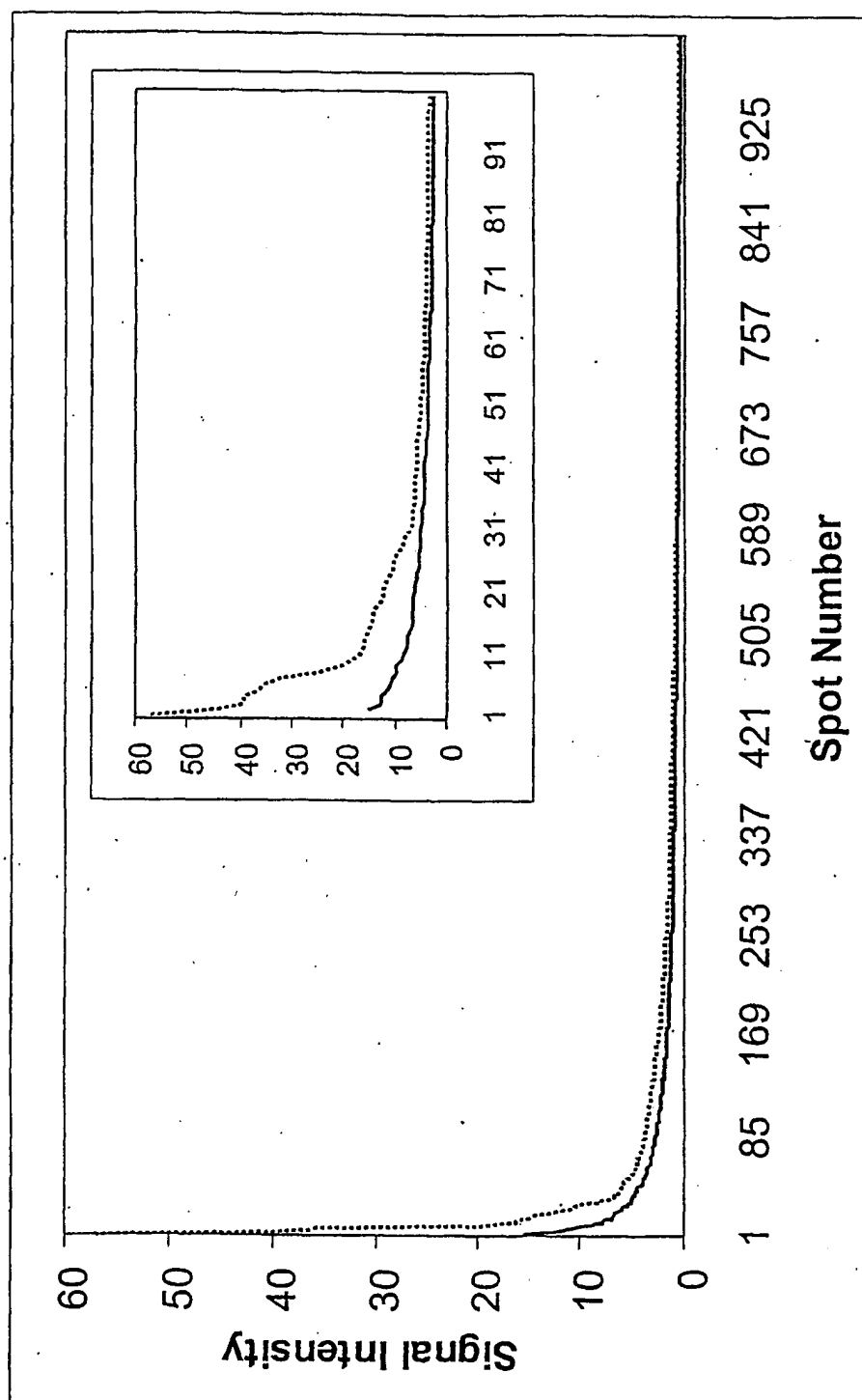


Fig. 8

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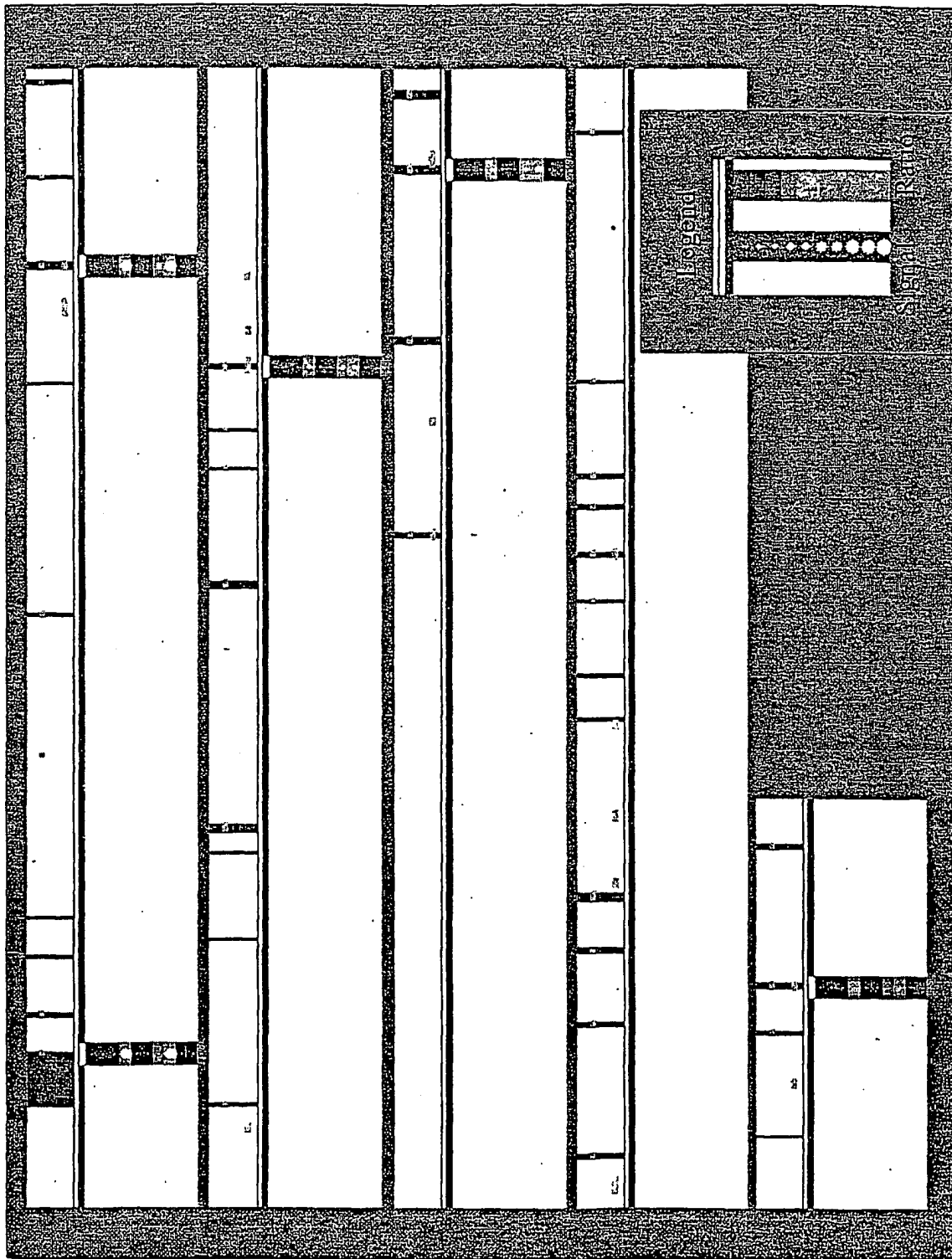
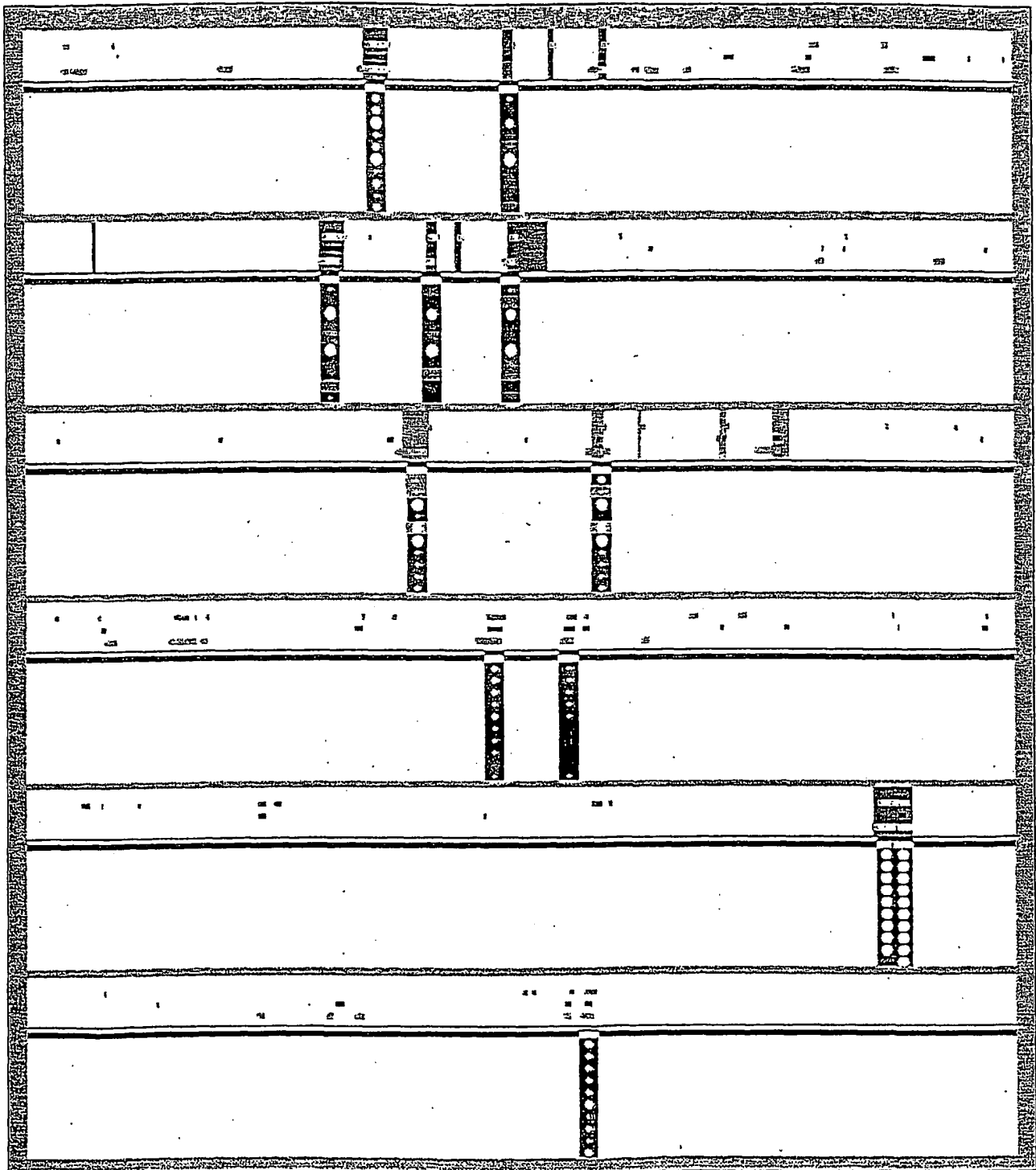


Fig. 9

10/10

Fig. 10



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9 August 2001 (09.08.2001)

PCT

(10) International Publication Number
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| 60/236,359 | 27 September 2000 (27.09.2000) | US |
| 0024263.6 | 4 October 2000 (04.10.2000) | GB |
- (71) Applicant (for all designated States except US): **AEOM-ICA, INC.** [US/US]; 928 East Arques Avenue, Sunnyvale, CA 94085 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **PENN, Sharron, G.** [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). **HANZEL, David, K.** [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). **CHEN, Wen-sheng** [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). **RANK, David, R.** [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).
- (74) Agent: **RONNING, Royal, N., Jr.**; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:
- with international search report
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see PCT Gazette No. 09/2002 of 28 February 2002, Section II
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human adult liver is described. Also described are single exon nucleic acid probes expressed in the adult liver and their use in methods for detecting gene expression.

WO 01/057273 A3

INTERNATIONAL SEARCH REPORT

National Application No
PCT/US 01/00664

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, EPO-Internal, SEQUENCE SEARCH, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 23254 A (AFFYMETRIX INC ;NAIR ARCHANA (US); LOCKHART DAVID J (US); WARRINGT) 14 May 1999 (1999-05-14) the whole document	1-27
X	EP 0 321 362 A (PASTEUR INSTITUT) 21 June 1989 (1989-06-21) the whole document specially page 11, paragraph 1	1-27
X	PATENT ABSTRACTS OF JAPAN vol. 015, no. 373 (C-0869), 19 September 1991 (1991-09-19) & JP 03 147799 A (HOECHST JAPAN LTD), 24 June 1991 (1991-06-24) abstract	1-27
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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

11 July 2002

Date of mailing of the international search report

07. 08. 2002

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Molina Galan, E

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00664

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	STEENBERGH P H ET AL: "COMPLETE NUCLEOTIDE SEQUENCE OF THE HIGH MOLECULAR WEIGHT HUMAN IGF-I MESSENGER RNA" BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 175, no. 2, 1991, pages 507-514, XP002185752 ISSN: 0006-291X the whole document	1-27
X	DATABASE EBI 'Online! EMBL; Accession Number AC007372, 27 April 1999 (1999-04-27) DICKHOFF ET AL: "Sequencing of human chromosome 14q31 region" XP002182131 sequence	13
X	DATABASE EBI 'Online! EMBL; ADAMS ET AL.: "Use of random BAC end sequence database for sequence ready map building" Database accession no. B57793 XP002185753 Sequence	13
X	DATABASE SWISSPROT 'Online! EMBL; AN: 002711, 1 July 1997 (1997-07-01) BENIT ET AL.: "Cloning of a new murine endogenous retrovirus" XP002037954 the whole document	13
X	DATABASE EBI 'Online! embl; AN: AA414703, 9 May 1997 (1997-05-09) MARRA ET AL.: "The WashU-HHMI Mouse EST Project" XP002205620 the whole document	13
A	US 5 618 671 A (LINDSTROEM PER) 8 April 1997 (1997-04-08) column 1, line 60 -column 2, line 19 column 4, line 36 -column 5, line 29; claims	1-27

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00664

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EISEN M B ET AL: "Cluster analysis and display of genome-wide expression patterns" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 95, December 1998 (1998-12), pages 14863-14868, XP002140966 ISSN: 0027-8424 the whole document ----	1,12
P,X	PENN S G ET AL: "Mining the human genome using microarrays of open reading frames." NATURE GENETICS, (2000 NOV) 26 (3) 315-8., XP002183793 the whole document -----	1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/00664**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 1-12, 15-21 (partially)
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27 (partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-12, 15-21 (partially)

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first and second inventions in form 206 PCT.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq. Id. 1 or 2 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising Seq. Id. 1 or 2 has been limited to the Seq. Id. as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 26004. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 13118).

Likewise, claim 26, which refers to peptides encoded by Seq. Id. 1 or 2 and 13118, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide disclosed, identified by Seq. Id. 26004.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

Invention 1

A nucleic acid probe comprising SEQ ID 1, complementary sequences or fragments thereof (in particular comprising Seq. Id. 13110). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. 1 (in particular the one defined by Seq. Id. 25996).

2. Claims: 1-27 (partially)

Invention 2

A nucleic acid probe comprising SEQ ID 2, complementary sequences or fragments thereof (in particular comprising Seq. Id. 13118). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. 2 (in particular the one defined by Seq. Id. 26004).

3. Claims: 1-27 (partly)

Inventions 3-13109

A nucleic acid probe comprising SEQ ID n (where n ranges from 3-13109 according to the invention number above), complementary sequences or fragments thereof, in particular comprising the SEQ ID no. which is listed in the column "Exon Seq. Id. no." in the same row that contains Seq. Id. n in table 4. Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. n, in particular the one defined by the Seq. Id. no. in the column "ORF Seq. Id. no." of the same row where Seq. Id. n is listed.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/00664

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
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			EP 1027456 A1	16-08-2000
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			JP 7508407 T	21-09-1995
			WO 9400597 A1	06-01-1994

CORRECTED VERSION

(19) World Intellectual Property Organization
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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human adult liver is described. Also described are single exon nucleic acid probes expressed in the adult liver and their use in methods for detecting gene expression.

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